

STIC-Biotech/ChemLib

109561

From: Chan, Christina
Sent: Wednesday, December 03, 2003 8:48 AM
To: Swope, Sheridan; STIC-Biotech/ChemLib
Subject: RE: 09830144

Please rush this one. Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Swope, Sheridan
Sent: Tuesday, December 02, 2003 8:12 PM
To: Chan, Christina
Subject: FW: 09830144

I made a mistake on the search request.

-----Original Message-----

From: Swope, Sheridan
Sent: Tuesday, December 02, 2003 8:08 PM
To: Chan, Christina
Subject: 09830144

Chris, May I have this rushed?--overdue amdt.

For 09/830,144, pls search and interference search:

SID 1, nt 408-1091 against the NT and AA data bases.

SID 2, aa76-303 against the NT and AA data bases.

SID 3, nt1338-1541 against the NT and AA data bases.

SID 4, aa437-504 against the NT and AA data bases.

Thanks!

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
sheridan.swope@uspto.gov
703-305-1696 (voice)
703-308-3014 (FAX)
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Office: CM1 Rm12D12

Point of Contact
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 11:40:09 ; Search time 137.149 Seconds
(without alignments)
1647.882 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPULTLQSTWHTQSSSSS.....AEFYRLWSVDHGEQSVVTP 68

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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- 12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
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- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	359	100.0	1560	12	US-10-384-743-1 DR Sequence 1, Appli

2	359	100.0	1560	13	US-10-123-427-1	Sequence 1, Appli
3	359	100.0	1560	13	US-10-123-427-5	Sequence 5, Appli
4	359	100.0	1560	13	US-10-158-895-1	Sequence 1, Appli
5	359	100.0	1560	12	US-10-384-743-42	Sequence 42, Appli
6	359	100.0	1560	13	US-10-158-895-42	Sequence 42, Appli
7	359	100.0	1560	12	US-10-384-743-10	Sequence 10, Appli
8	359	100.0	1560	13	US-10-158-895-10	Sequence 10, Appli
9	359	100.0	16877	10	US-09-764-877-3349	Sequence 3349, Ap
10	352	98.1	696	10	US-09-925-300-330	Sequence 330, App
11	346	96.4	409	11	US-09-918-995-32946	Sequence 32946, A
12	75.5	21.0	672	12	US-09-928-267-16	Sequence 16, Appli
13	75.5	21.0	833	12	US-09-928-267-8	Sequence 8, Appli
14	75	20.9	1610	12	US-09-971-392-119	Sequence 119, App
15	71	19.8	996	10	US-09-974-300-6219	Sequence 6219, Ap
16	69.5	19.4	1492	10	US-09-941-831-7	Sequence 7, Appli
17	69.5	19.4	9507	11	US-09-764-891-9785	Sequence 9785, Ap
18	69	19.2	12409	11	US-09-989-442-156	Sequence 156, App
19	68.5	19.1	3068	14	US-10-259-453-1	Sequence 1, Appli
20	68.5	19.1	3082	14	US-10-259-453-2	Sequence 2, Appli
21	68.5	19.1	32767	12	US-10-004-113-4	Sequence 4, Appli
22	68	18.9	273	9	US-09-864-761-22569	Sequence 22569, A
23	68	18.9	8918	10	US-09-764-864-1682	Sequence 1682, Ap
24	68	18.9	8919	10	US-09-764-864-1683	Sequence 1683, Ap
25	67.5	18.8	2377	12	US-10-374-979-65	Sequence 65, Appli
26	67.5	18.8	2377	14	US-10-037-534-2	Sequence 2, Appli
27	67.5	18.8	2678	11	US-09-919-039-234	Sequence 234, App
28	66.5	18.5	743	12	US-10-027-632-147810	Sequence 147810,
29	66.5	18.5	743	12	US-10-027-632-147811	Sequence 147811,
30	66.5	18.5	743	13	US-10-027-632-147810	Sequence 147810,
31	66.5	18.5	743	13	US-10-027-632-147811	Sequence 147811,
32	66	18.4	684	12	US-10-029-386-24794	Sequence 24794, A
33	66	18.4	728	12	US-10-029-386-24125	Sequence 24125, A
34	66	18.4	902	12	US-10-027-632-31743	Sequence 31743, A
35	66	18.4	902	12	US-10-027-632-31744	Sequence 31744, A
36	66	18.4	902	13	US-10-027-632-31743	Sequence 31743, A
37	66	18.4	902	13	US-10-027-632-31744	Sequence 31744, A
38	66	18.4	1173	14	US-10-156-761-1415	Sequence 1415, Ap
39	66	18.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
40	65.5	18.2	499	11	US-09-918-995-20193	Sequence 20193, A
41	65.5	18.2	4753	13	US-10-098-841-18	Sequence 18, Appli
42	65	18.1	895	10	US-09-764-891-5489	Sequence 5489, Ap
43	64.5	18.0	966	10	US-09-938-842A-2555	Sequence 2555, Ap
44	64.5	18.0	1409	14	US-10-012-542-82	Sequence 82, Appli
45	64.5	18.0	42432	12	US-10-029-120-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-384-743-1
; Sequence 1, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JF98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (30)..(1541)
US-10-384-743-1

Alignment Scores:
Pred. No.: 1.16e-41 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-384-743-1 (1-1560)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1338 CAAAGCCGACCTTAACCTTGAGTCCACCAACGACGACGAGCAGCAGCTCCAGC 1397
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGGAGCGCTCTTCCGCTCCGCGCCGCCACCTCGCTCCGCGCTGGCGAGGACGGT 1457
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGAGCTTTGCTGAGTTTACCGCTCTGGACGCTGGACCATGGC 1517
Qy 61 GluGlnSerValThrAlaPro 68
Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 2
US-10-123-427-1
; Sequence 1, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/123,427
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1541
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 30..1541
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-123-427-1

Alignment Scores:
Pred. No.: 1.16e-41 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-123-427-1 (1-1560)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1338 CAAAGCCGACCTTAACCTTGAGTCCACCAACGACGACGAGCAGCAGCTCCAGC 1397
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGGAGCGCTCTTCCGCTCCGCGCCGCCACCTCGCTCCGCGCTGGCGAGGACGGT 1457
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGAGCTTTGCTGAGTTTACCGCTCTGGACGCTGGACCATGGC 1517
Qy 61 GluGlnSerValThrAlaPro 68
Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 3
US-10-123-427-5
; Sequence 5, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/123,427
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 24-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 17981/111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1560 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 30..1541
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 30..1541
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-123-427-5

Alignment Scores:
 Pred. No.: 1,16e-41 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-123-427-5 (1-1560)

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 Db 1338 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397
 Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1398 TCTGACGAGGCGCTTCTCCGCTCCGCGCCGCCACTCGCTCCGCGCTGCGAGGACGGT 1457
 Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
 Db 1458 CGTGTGAGCCCTAATGAGCTTTGCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1517
 Qy 61 GluGlnSerValValThrAlaPro 68
 Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 4
 US-10-158-895-1
 ; Sequence 1, Application US/10158895
 ; Publication No. US20020155624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/158,895
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1560
 ; TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (30) .. (1541)
 US-10-158-895-1
 Alignment Scores:
 Pred. No.: 1,16e-41 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-158-895-1 (1-1560)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 1338 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397
 Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1398 TCTGACGAGGCGCTTCTCCGCTCCGCGCCGCCACTCGCTCCGCGCTGCGAGGACGGT 1457
 Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
 Db 1458 CGTGTGAGCCCTAATGAGCTTTGCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1517
 Qy 61 GluGlnSerValValThrAlaPro 68
 Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 5
 US-10-384-743-42

US-10-384-743-42
 ; Sequence 42, Application US/10384743
 ; Publication No. US20030162228A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/384,743
 ; CURRENT FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 1568
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11) .. (1549)
 US-10-384-743-42

Alignment Scores:
 Pred. No.: 1,17e-41 Length: 1568
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-384-743-42 (1-1568)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20

Db 1346 CAAAGCCGACCTTAACCTCGAGTCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 1405
QY 21 SerAspGlyClyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1406 TCTGACGGAGGCTCTTCGCTCCGCGCCGACCTCGCTCCGCTGGCGAGGACGGT 1465
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1466 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1525
QY 61 GluGlnSerValValThrAlaPro 68
Db 1526 GAGCAGAGCGTGTGACAGCAGCG 1549

RESULT 6

US-10-158-895-42
; Sequence 42, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 42
; LENGTH: 1568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(1549)
US-10-158-895-42

Alignment Scores:
Pred. No.: 1,17e-41 Length: 1568
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-158-895-42 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1346 CAAAGCCGACCTTAACCTCGAGTCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 1405
QY 21 SerAspGlyClyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1406 TCTGACGGAGGCTCTTCGCTCCGCGCCGACCTCGCTCCGCTGGCGAGGACGGT 1465
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1466 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1525
QY 61 GluGlnSerValValThrAlaPro 68
Db 1526 GAGCAGAGCGTGTGACAGCAGCG 1549

RESULT 7

US-10-384-743-10
; Sequence 10, Application US/10384743
; Publication No. US2003016228A1

; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-10-384-743-10

Alignment Scores:
Pred. No.: 1,17e-41 Length: 1569
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-384-743-10 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1315 CAAAGCCGACCTTAACCTCGAGTCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 1374
QY 21 SerAspGlyClyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1375 TCTGACGGAGGCTCTTCGCTCCGCGCCGACCTCGCTCCGCTGGCGAGGACGGT 1434
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1435 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1494
QY 61 GluGlnSerValValThrAlaPro 68
Db 1495 GAGCAGAGCGTGTGACAGCAGCG 1518

RESULT 8

US-10-158-895-10
; Sequence 10, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-10-158-895-10

Alignment Scores:

Pred. No.: 1,17e-41 Length: 1569
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps:

US-09-830-144-4_COPY_437_504 (1-68) x US-10-158-895-10 (1-1569)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1315 CAAAGCCCGACCTTAACCTCGAGTCGAGTCACCAACAGCGACGAGCAGCAGCTCCAGC 1374
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1375 TCTGAGGAGGCGCTCTTCGCGTCCCGCGCCGCCCACTCGCTCCCGCTGCGGAGACGGT 1434
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1435 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTTACCGCCTCTGGAGCGTGGACCATGGC 1494
Qy 61 GluGlnSerValThrAlaPro 68
Db 1495 GAGCAGAGCGTGGTACGACCG 1518

RESULT 9

US-09-764-877-3349
; Sequence 3349, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3349

Alignment Scores:
Pred. No.: 2,17e-40 Length: 16877
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps:

US-09-830-144-4_COPY_437_504 (1-68) x US-09-764-877-3349 (1-16877)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 15011 CAAAGCCCGACCTTAACCTCGAGTCGAGTCACCAACAGCGACGAGCAGCAGCTCCAGC 15070
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 15071 TCTGAGGAGGCGCTCTTCGCGTCCCGCGCCGCCCACTCGCTCCCGCTGCGGAGACGGT 15130
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 15131 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTTACCGCCTCTGGAGCGTGGACCATGGC 15190

Qy 61 GluGlnSerValThrAlaPro 68
Db 15191 GAGCAGAGCGTGGTACGACCG 15214

RESULT 10

US-09-925-300-330
; Sequence 330, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (657)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (685)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-330

Alignment Scores:
Pred. No.: 4,38e-41 Length: 696
Score: 352.00 Matches: 67
Percent Similarity: 98.53% Conservative: 0
Best Local Similarity: 98.53% Mismatches: 1
Query Match: 98.05% Indels: 0
DB: 10 Gaps:

US-09-830-144-4_COPY_437_504 (1-68) x US-09-925-300-330 (1-696)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 49 CAAAGCCCGACCTTAACCTCGAGTCGAGTCACCAACAGCGACGAGCAGCAGCTCCAGC 108
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 109 TCTACGAGGAGCGCTCTTCGCGTCCCGCGCCGCCCACTCGCTCCCGCTGCGGAGACGGT 168
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 169 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTTACCGCCTCTGGAGCGTGGACCATGGC 228

Qy 61 GluGlnSerValThrAlaPro 68
Db 229 GAGCAGAGCGTGGTACGACCG 252

RESULT 11

US-09-918-995-32946
; Sequence 32946, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 204111-756

;
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32946
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-32946

Alignment Scores:
Pred. No.: 1,66e-40 Length: 409
Score: 346.00 Matches: 65
Percent Similarity: 97.06% Conservative: 1
Best Local Similarity: 95.59% Mismatches: 2
Query Match: 96.38% Indels: 0
DB: 11 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-918-995-32946 (1-409)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 48 CAAAGCCGACCTTAACCTCGAGGCGCACCAACACGACGACGAGCAGCTCCAGC 107
QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
DB 108 TCTGACGAGGCGCTCTTCGCTCCCGCGCGCCGCTCCGCTCCGCGGAGGAGCGT 167
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
DB 168 CGTGTGACCCCTAAGTGACCTTGTGAGCTTACCGCTCTGGAGCGTGGACCAATGC 227
QY 61 GluGlnSerValValThrAlaPro 68
DB 228 GAGCAGGCGCGGTGACAGCAGC 251

RESULT 12

US-09-928-267-16
; Sequence 16, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Fodor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; TYPE: DNA
; ORGANISM: porcine
US-09-928-267-16

Alignment Scores:
Pred. No.: 0.233 Length: 672
Score: 75.50 Matches: 21
Percent Similarity: 51.92% Conservative: 6
Best Local Similarity: 40.38% Mismatches: 14
Query Match: 21.03% Indels: 11
DB: 12 Gaps: 2

US-09-830-144-4_COPY_437_504 (1-68) x US-09-928-267-16 (1-672)

QY 6 ThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerSer 25
DB 156 ACAACGGTGAACACACACTATACCCAGAGCTCGTTTCGACGGCTCCAGGCCCACTG 215
QY 26 PheArgSerArgProAlaHisSerLeu-----Pro 35

DB 216 TCACGACGCGCGCGCGCGTGGTCTACTGACTTCAGACACGCGCGTGTATATGACACCT 275
QY 36 ProGlyGlu---AspGlyArgValGluProTyrVal 46
DB 276 CCTACTCAACTGAGAGGAACACTACTGAGATGTACGTG 311

RESULT 13

US-09-928-267-8
; Sequence 8, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Fodor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 833
; TYPE: DNA
; ORGANISM: pig and human
US-09-928-267-8

Alignment Scores:
Pred. No.: 0.303 Length: 833
Score: 75.50 Matches: 21
Percent Similarity: 51.92% Conservative: 6
Best Local Similarity: 40.38% Mismatches: 14
Query Match: 21.03% Indels: 11
DB: 12 Gaps: 2

US-09-830-144-4_COPY_437_504 (1-68) x US-09-928-267-8 (1-833)

QY 6 ThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerSer 25
DB 163 ACAACGGTGAACACACACTATACCCAGAGCTCGTTTCGACGGCTCCAGGCCCACTG 222
QY 26 PheArgSerArgProAlaHisSerLeu-----Pro 35
DB 223 TCACGACGCGCGCGCGCGTGGTCTACTGACTTCAGACACGCGCGTGTATATGACACCT 282
QY 36 ProGlyGlu---AspGlyArgValGluProTyrVal 46
DB 283 CCTACTCAACTGAGAGGAACACTACTGAGATGTACGTG 318

RESULT 14

US-09-971-392-119
; Sequence 119, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 119
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 215481.15
US-09-971-392-119

Alignment Scores:

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GenCore version 5.1.6
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(without alignments)
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Perfect score: 359
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	359	100.0	1560	2	US-08-752-891-5
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4	359	100.0	1560	2	US-09-144-178-5
5	359	100.0	1560	3	US-09-406-854-1
6	359	100.0	1560	3	US-09-406-854-5
7	359	100.0	1560	4	US-09-529-279-1
8	359	100.0	1560	4	US-10-158-895-1
9	359	100.0	1568	4	US-09-529-279-42
10	359	100.0	1568	4	US-10-158-895-42
11	359	100.0	1569	4	US-09-529-279-10
12	359	100.0	1569	4	US-10-158-895-10

c 13	71.5	19.9	1108	5	PCT-US93-03035-1	Sequence 1, Appli
14	67.5	18.8	2559	2	US-09-070-060-2	Sequence 2, Appli
15	67.5	18.8	2559	3	US-09-357-746-2	Sequence 2, Appli
16	67.5	18.8	5359	2	US-09-070-060-1	Sequence 1, Appli
17	67.5	18.8	5372	3	US-09-357-746-1	Sequence 1, Appli
c 18	65	18.1	951	4	US-09-252-991A-7708	Sequence 7708, Ap
19	65	18.1	1008	4	US-09-252-991A-7923	Sequence 7923, Ap
20	65	18.1	1227	4	US-09-252-991A-7853	Sequence 7853, Ap
c 21	64.5	18.0	1409	4	US-09-461-325-82	Sequence 82, Appl
22	64.5	18.0	2259	4	US-09-252-991A-6446	Sequence 6446, Ap
c 23	64	17.8	564	4	US-09-252-991A-15454	Sequence 15454, A
24	64	17.8	2319	4	US-09-252-991A-15284	Sequence 15284, A
c 25	64	17.8	2427	4	US-09-252-991A-15396	Sequence 15396, A
26	63.5	17.7	1101	4	US-09-152-060-23	Sequence 23, Appl
27	63.5	17.7	1173	3	US-08-706-216-5	Sequence 5, Appli
28	63.5	17.7	1473	4	US-09-152-060-43	Sequence 43, Appl
c 29	63.5	17.7	2784	3	US-08-857-076-39	Sequence 39, Appl
c 30	63.5	17.7	3017	3	US-08-857-076-52	Sequence 52, Appl
c 31	63.5	17.7	3119	3	US-08-857-076-53	Sequence 53, Appl
32	62	17.3	336	4	US-09-252-991A-1069	Sequence 1069, Ap
c 33	62	17.3	1395	2	US-08-553-367A-1	Sequence 1, Appli
c 34	62	17.3	1395	3	US-09-295-306-1	Sequence 1, Appli
c 35	62	17.3	1395	4	US-09-734-719-1	Sequence 1, Appli
c 36	62	17.3	1575	4	US-09-252-991A-1139	Sequence 1, Appli
c 37	62	17.3	2859	4	US-09-252-991A-944	Sequence 944, App
38	62	17.3	5977	3	US-09-024-020B-1	Sequence 1, Appli
39	62	17.3	5977	4	US-09-425-043-1	Sequence 1, Appli
40	62	17.3	6007	3	US-09-024-020B-2	Sequence 2, Appli
41	62	17.3	6007	4	US-09-425-043-2	Sequence 2, Appli
42	62	17.3	6556	3	US-09-024-020B-7	Sequence 7, Appli
43	62	17.3	6556	4	US-09-425-043-7	Sequence 7, Appli
44	62	17.3	6586	3	US-09-024-020B-43	Sequence 43, Appl
45	62	17.3	6586	4	US-09-425-043-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-752-891-1
; Sequence 1, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; .TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1541
; NAME/KEY: mat_peptide
; LOCATION: 30..1541
; US-08-752-891-1
;
; Alignment Scores:
; Pred. No.: 9.72e-37 Length: 1560
; Score: 359.00 Matches: 68
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 2 Gaps: 0
;
; US-09-830-144-4_COPY_437_504 (1-68) x US-08-752-891-1 (1-1560)
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; Db 1338 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCTCCAGC 1397
;
; QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
; Db 1398 TCTGACGAGCGCTTTCGCTCCGCGCCGCCACCTCGCTCCGCGGAGGACGGT 1457
;
; QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
; Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGACGCTGGACCAATGCC 1517
;
; QY 61 GluGlnSerValValThralaPro 68
; Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541
;
; RESULT 2
; US-08-752-891-5
; Sequence 5, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
;
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; .TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1541
; NAME/KEY: mat_peptide
; LOCATION: 30..1541
; US-08-752-891-5
;
; Alignment Scores:
; Pred. No.: 9.72e-37 Length: 1560
; Score: 359.00 Matches: 68
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 2 Gaps: 0
;
; US-09-830-144-4_COPY_437_504 (1-68) x US-08-752-891-5 (1-1560)
;
; QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
; Db 1338 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCTCCAGC 1397
;
; QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
; Db 1398 TCTGACGAGCGCTTTCGCTCCGCGCCGCCACCTCGCTCCGCGGAGGACGGT 1457
;
; QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
; Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGACGCTGGACCAATGCC 1517
;
; QY 61 GluGlnSerValValThralaPro 68
; Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541
;
; RESULT 3
; US-09-144-178-1
; Sequence 1, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
;
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; .TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1541
; NAME/KEY: mat_peptide
; LOCATION: 30..1541
; US-08-752-891-5
;
; Alignment Scores:
; Pred. No.: 9.72e-37 Length: 1560
; Score: 359.00 Matches: 68
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 2 Gaps: 0
;
; US-09-830-144-4_COPY_437_504 (1-68) x US-08-752-891-5 (1-1560)
;
; QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
; Db 1338 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCTCCAGC 1397
;
; QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
; Db 1398 TCTGACGAGCGCTTTCGCTCCGCGCCGCCACCTCGCTCCGCGGAGGACGGT 1457
;
; QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
; Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGACGCTGGACCAATGCC 1517
;
; QY 61 GluGlnSerValValThralaPro 68
; Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541
;
; RESULT 3
; US-09-144-178-1
; Sequence 1, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-144-178-1

Alignment Scores:
Pred. No.: 9.72e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-1 (1-1560)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1338 CAAAGCCGACCTTAACCTTCAGTCCACACGACGACGACGACGACGACGACGACG 1397
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGACCTTCTCCGCTCCCGCCGCCCACTCGCTCCCGCTGGGAGGACGGT 1457
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGACCATGGC 1517
Qy 61 GluGlnSerValValThrAlaPro 68
Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 4
US-09-144-178-5
Sequence 5, Application US/09144178
Patent No. 5989862
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-144-178-5

Alignment Scores:
Pred. No.: 9.72e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-5 (1-1560)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1338 CAAAGCCGACCTTAACCTTCAGTCCACACGACGACGACGACGACGACGACGACG 1397
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGACCTTCTCCGCTCCCGCCGCCCACTCGCTCCCGCTGGGAGGACGGT 1457
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGACCATGGC 1517
Qy 61 GluGlnSerValValThrAlaPro 68
Db 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 5
US-09-406-854-1
Sequence 1, Application US/09406854
Patent No. 6140042
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-406-854-1

Alignment Scores:
Pred. No.: 9.72e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-406-854-1 (1-1560)

Qy	1	GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer	20
Db	1338	CAAAAGCCGACCTTAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCAGCTCCAGC	1397
Qy	21	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	40
Db	1398	TCTGACGAGGCGCTTTCCTCCGCGCCGCCACCTCGCTCCCGCTGGGAGGACGGT	1457
Qy	41	ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly	60
Db	1458	CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGGAGGCTGACCATGGC	1517
Qy	61	GluGlnSerValThrAlaPro	68
Db	1518	GAGCAGACGCTGGTGACAGCACCG	1541

RESULT 6
US-09-406-854-5
Sequence 5, Application US/09406854
Patent No. 6140042
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-406-854-5

Alignment Scores:
Pred. No.: 9.72e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-406-854-5 (1-1560)

Qy	1	GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer	20
Db	1338	CAAAAGCCGACCTTAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCAGCTCCAGC	1397
Qy	21	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	40
Db	1398	TCTGACGAGGCGCTTTCCTCCGCGCCGCCACCTCGCTCCCGCTGGGAGGACGGT	1457

Alignment Scores:	9.79e-37	Length:	1568
Pred. No.:	359.00	Matches:	68
Score:			

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-529-279-42 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 1346 CAAAGCCGACCTTAACCTGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1405
 QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1406 TCTGACGAGGCGCTTCCGCTCCCGCCGCCACTCGCTCCCGCTGCGAGGACGGT 1465
 QY 41 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1466 CGTGTGAGCCCTATGTGACTTGTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 1526 GAGCAGAGCGTGTGACAGCAGCG 1549

RESULT 10

US-10-158-895-42
 ; Sequence 42, Application US/10158895
 ; Patent No. 6551840
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/158,895
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 1568
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11)..(1549)
 US-10-158-895-42

Alignment Scores:
 Pred. No.: 9,796-37 Length: 1568
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-158-895-42 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 1346 CAAAGCCGACCTTAACCTGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1405
 QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1406 TCTGACGAGGCGCTTCCGCTCCCGCCGCCACTCGCTCCCGCTGCGAGGACGGT 1465
 QY 41 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1466 CGTGTGAGCCCTATGTGACTTGTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525

QY 61 GluGlnSerValValThrAlaPro 68
 Db 1526 GAGCAGAGCGTGTGACAGCAGCG 1549

RESULT 11

US-09-529-279-10
 ; Sequence 10, Application US/09529279
 ; Patent No. 6451617
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/09/529,279
 ; CURRENT FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 1569
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(1557)
 US-09-529-279-10

Alignment Scores:
 Pred. No.: 9,8e-37 Length: 1569
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-529-279-10 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 1315 CAAAGCCGACCTTAACCTGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1374
 QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1375 TCTGACGAGGCGCTTCCGCTCCCGCCGCCACTCGCTCCCGCTGCGAGGACGGT 1434
 QY 41 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1435 CGTGTGAGCCCTATGTGAGTCTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1494
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 1495 GAGCAGAGCGTGTGACAGCAGCG 1518

RESULT 12

US-10-158-895-10
 ; Sequence 10, Application US/10158895
 ; Patent No. 6551840
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/158,895
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796

;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: JP 9/290188
;; PRIOR FILING DATE: 1997-10-22
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 10
;; LENGTH: 1569
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (7)..(1557)
US-10-158-895-10

Alignment Scores:
Pred. No.: 9, 8e-37 Length: 1569
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-10-158-895-10 (1-1569)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1315 CAAAGCCGAGCTTAACCTGCAGTCCACCAACACGACACGACGAGCAGCTCCAGC 1374
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1375 TCTGACGAGGAGCCTCTCCGCTCCGCGCCGCGCCACTCCGCTCCGCGAGGACGGT 1434
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 1435 CGTGTGAGCCCTATGTGAGATTCTGAGTTTTACCGCCCTCTGGAGCGTGACCATGGC 1494
Qy 61 GlnGlnSerValValThrAlaPro 68
Db 1495 GAGCAGAGCGTGGTGACAGCACCG 1518

RESULT 13
PCT-US93-03035-1/c
; Sequence 1, Application PC/TUS9303035
; GENERAL INFORMATION:
; APPLICANT: ABBOTT LABORATORIES
; TITLE OF INVENTION: PURIFIED THERMOSTABLE ENDONUCLEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: D-377 AP6D, ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03035
; FILING DATE: 19930330
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,306
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/860,702
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAINARD, THOMAS D
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5145.PC.01

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 708-937-4884
;; TELEFAX: 708-937-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1108 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 114..926
PCT-US93-03035-1

Alignment Scores:
Pred. No.: 4, 82 Length: 1108
Score: 71.50 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 7
Query Match: 19.92% Indels: 1
DB: 5 Gaps: 1

US-09-830-144-4_COPY_437_504 (1-68) x PCT-US93-03035-1 (1-1108)

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Db 203 AGCGGTGAGCGCGAGCGGCGGTCTCTCCACGCCGCCGCCGCTTTTCCCGC 144
Qy 38 GluAspGlyArgValGluPro 44
Db 143 ---GATGAAAGGTGGAACCC 126

RESULT 14
US-09-070-060-2
; Sequence 2, Application US/09070060
; Patent No. 5976849
; GENERAL INFORMATION:
; APPLICANT: Hustad, Carolyn M.
; TITLE OF INVENTION: Human E3 Ubiquitin Protein
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Pharmaceuticals, Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850-5437
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,060
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/073,839
; FILING DATE: 05-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Higgins, Patrick H
; REGISTRATION NUMBER: 39,709
; REFERENCE/DOCKET NUMBER: PHM.70312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302.886.4889
; TELEFAX: 302.886.8221
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 09:07:25 ; Search time 121.703 Seconds
(without alignments)
2090.550 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 1252

Sequence: 1 gtatagcttgcgcagttatc.....cattacagatccttgcag 684

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 1368560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCUI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09830144 @CGN_1_78 @runat_03122003_122347_21456
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

1	1252	100.0	518	15	US-10-283-023-2
2	1252	100.0	579	12	US-10-384-743-4
3	1252	100.0	579	14	US-10-158-895-4
4	1252	100.0	590	12	US-10-384-743-15
5	1252	100.0	590	14	US-10-158-895-15
6	371	29.6	349	15	US-10-106-698-6345
7	371	29.6	455	9	US-09-757-982-5
8	371	29.6	455	12	US-10-094-749-2477
9	363.5	29.0	394	10	US-09-862-027-19
10	355	28.4	1036	12	US-10-354-358-24
11	355	28.4	1036	14	US-10-014-882-2
12	353.5	28.2	746	15	US-10-153-668-436
13	353.5	28.2	859	15	US-10-153-668-324
14	353.5	28.2	892	15	US-10-153-668-438
15	349.5	27.9	1097	12	US-10-288-798-12
16	346	27.6	328	10	US-09-862-027-18
17	345.5	27.6	847	14	US-10-143-133-2
18	341	27.2	252	12	US-09-976-782-41
19	341	27.2	254	12	US-09-976-782-30
20	341	27.2	256	12	US-09-863-776-41
21	338.5	27.0	835	10	US-09-947-199-2
22	335.5	26.8	835	10	US-09-947-199-8
23	331.5	26.5	966	10	US-09-771-161A-197
24	326.5	26.1	256	12	US-09-976-782-40
25	326.5	26.1	257	12	US-09-976-782-29
26	323	25.8	257	11	US-09-823-187-46
27	323	25.8	257	12	US-09-863-776-42
28	323	25.8	821	12	US-10-171-404A-48
29	320	25.6	263	10	US-09-840-704-5
30	313.5	25.0	850	10	US-09-904-389-2
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33	312	24.9	277	9	US-09-815-915-13
34	312	24.9	277	10	US-09-882-166-4
35	312	24.9	277	12	US-10-393-316-13
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38	312	24.9	278	9	US-09-797-039-13
39	312	24.9	278	9	US-09-922-138-18
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44	312	24.9	278	10	US-09-934-406-4
45	312	24.9	278	12	US-10-170-789-13

ALIGNMENTS

RESULT 1
US-10-283-023-2
; Sequence 2, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; diagnosis and treatment of hematological disorders using
; FILE REFERENCE: NPI01-239PIRM
; TITLE OF INVENTION: 16319
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-283-023-2

Alignment Scores: 4.12e-125 Length: 518
Pred. No.: 518

Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-283-023-2 (1-518)

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QY 61 TCGTTGAATCCAGTGTCTTGTGATGCAATATGCTGAAGGGGCTTTATATATG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
QY 121 CTGTCATGGTCTGAACCATTCATATCTGCTGCTGCCACCAATGAGTTCGTGTTA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTTCACAGAGTGTCTTATCTTCACAGCATGCAACCAAGCGCTTAATTCACAGG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTGAGGGGGACAGTCTTAAATTTGTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAGGGGAGTGTCTTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGCGACCTCAAGTTTGAAGTAGTAATTAACAGTGAAGAAATGTGAGCTTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 215
QY 421 GGTATTATCTTTGGGAAGTGAACCGCTGCGGAAACCTTGTGATGAGATTGGTGCCCA 480
Db GlyIleLeuLeuTyrGluValIleThrArgLysProPheAspGluIleGlyPro 235
QY 481 GCTTTCGGAATCATGTGGGCTGTCTCAATATGCTGACCATGATAAAAAATTTA 540
Db AlaPheArgIleMetTyrPalaValHisAsnGlyThrArgProProLeuLysAsnLeu 255
QY 541 CCTAAGCCCATGAGAGCTGTGATCGCTGTGTGGTCTTAAGATCCTTCCAGCGCCT 600
Db ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGGAATTTGTGAATAATCACTCACTTGTATGCGGTACTTCCAGGAGCAGAT 660
Db SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCATTACAGTATCTTGTTCAG 684
Db GluProLeuGlnTyrProCysGln 303
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RESULT 2

US-10-384-743-4
; Sequence 4, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, TOSHIIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-4

Alignment Scores:
Pred. No.: 4,23e-125 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-384-743-4 (1-579)

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QY 61 TCGTTGAATCCAGTGTCTTGTGATGCAATATGCTGAAGGGGCTTTATATATG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
QY 121 CTGTCATGGTCTGAACCATTCATATCTGCTGCTGCCACCAATGAGTTCGTGTTA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
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Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGCGACCTCAAGTTTGAAGTAGTAATTAACAGTGAAGAAATGTGAGCTTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 215
QY 421 GGTATTATCTTTGGGAAGTGAACCGCTGCGGAAACCTTGTGATGAGATTGGTGCCCA 480
Db GlyIleLeuLeuTyrGluValIleThrArgLysProPheAspGluIleGlyPro 235
QY 481 GCTTTCGGAATCATGTGGGCTGTCTCAATATGCTGACCATGATAAAAAATTTA 540
Db AlaPheArgIleMetTyrPalaValHisAsnGlyThrArgProProLeuLysAsnLeu 255
QY 541 CCTAAGCCCATGAGAGCTGTGATCGCTGTGTGGTCTTAAGATCCTTCCAGCGCCT 600
Db ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGGAATTTGTGAATAATCACTCACTTGTATGCGGTACTTCCAGGAGCAGAT 660
Db SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCATTACAGTATCTTGTTCAG 684
Db GluProLeuGlnTyrProCysGln 303
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RESULT 3

US-10-158-895-4
; Sequence 4, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO

```
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

Alignment Scores:
Pred. No.: 4,23e-125 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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QY 121 CTGATGCTGTGAACCATCTCCCATATTATATCTGCCACGCAATGAGTGTGTTA 180
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QY 421 GGTATTATCTTTGGGAGTGAACCGTCGGAACCCCTTTGATGAGATTGFGGCCCA 480
Db 216 GlyIleLeuLeuTrpGluValIleThrArgLysProPheAspGluIleGlyPro 235
QY 481 GCTTTCCGAATCATGTGGGTGTTTCAATAGTGTACTGACACACATGACCACTGATAAATAATTA 540
Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CTTAAGCCCATTCAGAGCTTGATCTGTTGTGTGTTAAGATCTCTCCAGCGCCCT 600
Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
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QY 661 GAGCCATTACAGTATCCTTGTCTCAG 684
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RESULT 4

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US-10-384-743-15
; Sequence 15, Application US/10384743
; Publication NO. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-15

Alignment Scores:
Pred. No.: 4,25e-125 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-384-743-15 (1-590)
QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTCTAATATTGTAAGCTTTATGGAGCC 60
Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAla 95
QY 61 TGGTTGAATCCAGTCTGCTTGTGATGGAATATCTGAAGGGGCTCTTTATATAATGTG 120
Db 96 CysLeuAsnProValCysLeuValMetGluTyAlaGluGlyGlySerLeuTyAsnVal 115
QY 121 CTGATGCTGTGAACCATCTCCCATATTATATCTGCCACGCAATGAGTGTGTTA 180
Db 116 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCCTCCAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAGG 240
Db 136 GlnCysSerGlnGlyValAlaTyLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCAACCACTTACTCTGCTGAGTGAAGTAAATGACGCTTCAGCTGG 300
Db 156 AsnLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGACATTCACACATGACCAATAACAGGGGAGTGTCTGTGG 360
Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCACCTCAAGTCTTTTGAAGTAGTAAATGACGTGAATAAATGTCAGCTGG 420
Db 196 MetAlaProGluValPheGluGlySerAsnTySerGlnLysCysAspValPheSerTrp 215
QY 421 GGTATTATCTTTGGGAGTGAACCGTCGGAACCCCTTTGATGAGATTGFGGCCCA 480
Db 216 GlyIleLeuLeuTrpGluValIleThrArgLysProPheAspGluIleGlyPro 235
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QY 481 GCTTTCGGAATCATGTGGCTCTTCATATAGTGTACTCGACCCACTGATATAAAATTTA 540
Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CTAAGCCCATTCAGAGCCTGATGACTCGTGTGTGTCTAAAGATCCTTCCAGGCGCCT 600
Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGGAGAAATGTGAAATAATGACTCACTTCATCGGCTGCTTCCAGGAGCAGAT 660
Db 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
Db 296 GluProLeuGlnTyrProCysGln 303
RESULT 5
US-10-158-895-15
; Sequence 15, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: CHOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/00/26524
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15
Alignment Scores:
Pred. No.: 4,25e-125 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-15 (1-590)
QY 1 GTAGAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60
Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
QY 61 TGCTTGAATCCAGTGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTATATAAGTG 120
Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGCTGTGAACCATTCGCATATATATCTGCTGCCACGCAATGAGTTGGTTTA 180
Db 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerIleProCysLeu 135
QY 181 CAGTGTTCACCAAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTTAATTCACAGG 240
Db 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTCAGGGGGGACAGTCTTAAAAATTGTGAT 300
Db 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTGTGTACAGCCTGTGACATTTCAGACACACATGACCAATAACAAGGGGAGTGCTGTGG 360

Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGACCTGAAGTGTTCAGAGCTAGTAATTAACAGTGAATAATGACGCTTTCAGCTGG 420
Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 215
QY 421 GGTATATATCTTTCGGAAGTGAACGCTCGGAAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 216 GlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
QY 481 GCTTTCGGAATCATGTGGCTCTTCATATAGTGTACTCGACCCACTGATATAAAATTTA 540
Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CTAAGCCCATTCAGAGCCTGATGACTCGTGTGTGTCTAAAGATCCTTCCAGGCGCCT 600
Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGGAGAAATGTGAAATAATGACTCACTTCATCGGCTGCTTCCAGGAGCAGAT 660
Db 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
Db 296 GluProLeuGlnTyrProCysGln 303
RESULT 6
US-10-106-698-6345
; Sequence 6345, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6345
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (340)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6345
Alignment Scores:
Pred. No.: 8,23e-31 Length: 349
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 15 Gaps: 8
US-09-830-144-1_COPY_408_1091 (1-684) x US-10-106-698-6345 (1-349)
QY 4 GAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCTGC 63
Db 109 GluAlaGluIleLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 128
QY 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGGCTCTTATATAAT 117
Db 129 LeuGluProProAsnTyrGlyIleValThrGluIleAlaSerLeuGlySerLeuTyrAsp 148

[illegible]

```

RESULT 8
US-10-094-749-2477
; Sequence 2477, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, KYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094, 749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 455
; TYPE: PRT

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ORGANISM: Homo sapiens
US-10-094-749-2477

Alignment Scores:
Pred. No.: 8, 78e-31 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 12 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-094-749-2477 (1-455)

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QY 4 GAGCTTCGGCAGTTATCCGCTGTAACCATCTATATTTGTAAGCTTTATGAGCGCTGC 63
Db 53 GluAlaGluLeuSerValLeuSerHisArgAsnIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGGT-----GCTGAACCATTTGCCATATTAATCTGCTGCCCGCCAGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
QY 172 TGGTGTTCAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCCAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCAGGAGCCTGAAACCCAACTTACTGCTGTTGCGAGGGGAGCAGTTCTAAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTTGTGATTTTGGTACAGCCTGTGACATTCAGACACACATCAACCAATCAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGAGTGTCTGCTGGATGGACCTGAAGTTTTCAGAGTAGTAATACATGGAATAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GAGCTCTTCAGCTGGGTATTTCTTTGGGAAGTGAACCGCTCGAAACCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValLeuTrpGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTCGTGGCCAGCTTTCCGAATCATCTGG---GCTCTTCATAATGCTACGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
QY 523 CCACTGATAAAATTTACCTAAGCCCATTCAGAGCCTGATGACTGCTGTTGCTCTAAA 582
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuHisGlnCysTrpGluAla 245
QY 583 GATCCTTCCAGCGCCCTTCAATCGAGGAATTCGAAATAATG 627
Db 246 AspAlaLysArgProSerPheLysGlnIleSerIleLeu 260

```

RESULT 9

US-09-862-027-19
Sequence 19, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. US20020142428A1 Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 394

TYPE: PRT
ORGANISM: Homo sapiens
US-09-862-027-19

Alignment Scores:
Pred. No.: 5, 39e-30 Length: 394
Score: 363.50 Matches: 83
Percent Similarity: 54.09% Conservative: 36
Best Local Similarity: 37.73% Mismatches: 84
Query Match: 29.03% Indels: 17
DB: 10 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-862-027-19 (1-394)

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QY 4 GAGCTTCGGCAGTTATCCGCTGTAACCATCTATATTTGTAAGCTTTATGAGCGCTGC 63
Db 50 GluAlaLysLeuPheAlaMetLeuLysHisProAsnIleIleAlaLeuArgGlyValCys 69
QY 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAAT 117
Db 70 LeuLysGluProAsnLeuCysLeuValMetGluPheAlaArgGlyGlyProLeuAsnArg 89
QY 118 GTGCTGCATGGTGAACCATTTGCCATATTAATCTGCTGCCCGCCAGCAATGAGTGGTGT 177
Db 90 ValLeuSerGlyLysArgIleProAspIle-----LeuValAsnTrpAla 105
QY 178 TTACAGTGTTCCTCAAGAGTGGCTTATCTTCACAGCATGCAACCCAGCGCTAATTCAC 237
Db 106 ValGlnIleAlaArgGlyMetAsnTyrLeuHisAspGluAlaIleValProIleIleHis 125
QY 238 AGGAGCCTGAAACCCAACTTACTGCTGTT-----GCAGGG 276
Db 126 ArgAspLeuLysSerSerAsnIleLeuIleLeuGlnLysValGluAsnGlyAspLeuSer 145
QY 277 GGGACAGTCTTAAATTTGTGATTTGTACAGCCTGTGAC---ATTACAGACACACATG 333
Db 146 AsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTrpHisArgThrLys 165
QY 334 ACCAATAACAAGGGAGTGTCTGCTGGATGGCACCTGAAAGTTTGAAGTAGTAATTCAC 393
Db 166 MetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIleArgAlaSerMetPhe 185
QY 394 AGTGAATAATGTCAGCTTTCAGCTGGGTATTTATTTCTTGGGAAGTGAACCGCTCGG 453
Db 186 SerLysGlySerAspValTrpSerTyrGlyValLeuLeuTrpGluLeuLeuThrGlyGlu 205
QY 454 AAACCCCTTCATGAGTGTGGTGGCCAGCTTCCGAATCATCTGGGCTGT---CATAAAT 510
Db 206 ValProPheArgGlyIleAspGly-----LeuArgValAlaTyrGlyValAlaMetAsn 223
QY 511 GGTACTCGACCCACCATCTGATAAAAAATTTACCTAAGCCCATTCAGACCTGATGACTCGT 570
Db 224 LysLeuAlaLeuProIleProSerThrCysProGluProPheAlaLysLeuMetGluAsp 243
QY 571 TGTGTTCTAAAGATCCTTCCCGCGCCCTTCAATGAGGAATTTGAAATAATGACT 630
Db 244 CysTrpAsnProAspProHisSerArgProSerPheThrAsnIleLeuAspGlnLeuThr 263

```

RESULT 10

US-10-354-358-24
Sequence 24, Application US/10354358
Publication No. US20030157082A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
HUNTER, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Lescon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,

; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
 ; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
 ; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
 ; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
 ; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
 ; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 56428 MOLECULES
 ; FILE REFERENCE: MP102-020PIRNONIM
 ; CURRENT APPLICATION NUMBER: US/10/354,358
 ; CURRENT FILING DATE: 2003-01-30
 ; PRIOR APPLICATION NUMBER: US 60/353,600
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/364,517
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/371,075
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: US 60/371,507
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: US 60/372,984
 ; PRIOR FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: US 60/374,194
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/382,995
 ; PRIOR FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: US 60/385,023
 ; PRIOR FILING DATE: 2002-05-31
 ; PRIOR APPLICATION NUMBER: US 60/388,853
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: US 60/389,395
 ; PRIOR FILING DATE: 2002-06-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 1036
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-354-358-24

Alignment Scores:
 Pred. No.: 5,55e-29 Length: 1036
 Score: 355.00 Matches: 83
 Percent Similarity: 53.48% Conservative: 40
 Best Local Similarity: 36.09% Mismatches: 85
 Query Match: 28.35% Indels: 22
 DB: 12 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-354-358-24 (1-1036)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGGAGCCTGC 63
 Db 171 GluAlaArgLeuPheAlaMetLeuArgHisProAsnIleIleGluLeuArgGlyValCys 190
 QY 64 TTGAATCCA-----GTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
 Db 191 LeuGlnGlnProHisLeuCysLeuValLeuPheAlaArgGlyGlyAlaLeuAsnArg 210
 QY 118 GTGCTGATGCTGCTGAACCATTCGCTATATTACTGCT----- 156
 Db 211 AlaLeuAlaAlaAlaAlaProAspProArgAlaProGlyProArgAlaArg 230
 QY 157 -----GCCACGCAATG---AGTTGGTGTGTATACAGTGTCCCAAGGAGTGGCTTAT 204
 Db 231 ArgileProProHisValLeuValAsnTrpAlaValGlnIleAlaArgGlyMetLeuTrp 250
 QY 205 CTTACAGCATCAACCCAAAGCGTAATTCACAGGAGCTGAACCAACCAACTTACTG 264
 Db 251 LeuHisGlnGluAlaPheValProIleLeuHisArgAspLeuLysSerSerAsnIleLeu 270
 QY 265 CTGCTGTCAGGG-----GGCAGAGTCTTAAATTTGTGATTTT 303
 Db 271 LeuLeuGlnLysIleGluHisAspAspIleCysAsnLysThrLeuLysIleThrAspPhe 290
 QY 304 GGTACAGCTGTGAC---ATTCAGACACATGACCAATAACAAGGGAGTGTCTTGG 360

Db 291 GlyLeuAlaArgGluTrpHisArgThrThrLysMetSerThrAlaGlyThrTyAlaTrp 310
 QY 361 ATGGCACCTGAAGTTTTTGAAGGTAGTAATATACAGTGAATAATGTGACGCTCTTACGCTGG 420
 Db 311 MetAlaProGluValIleLysSerSerLeuPheSerLysGlySerAspIleTrpSerTrp 330
 QY 421 GGTATTATCTTTGGGAAGTGAATACCGGTGGAAACCCCTTTGATGAGATTGGTGGCCCA 480
 Db 331 GlyValLeuLeuTrpGluLeuThrGlyGluValProTyrArgGlyIleAspGlyLeu 350
 QY 481 GCTTTCGGAATCATGTGGCTGTTCAATAATGGTACTGCACCACTCATGATAAAAAATTAA 540
 Db 351 AlaValAlaTyrGlyValAlaValAsnLysLeuThrLeu---ProIleProSerThrCys 369
 QY 541 CCTAAGCCCATTTGAGAGCTGATGCTGTTGGTCTAAAGATCCCTCCAGCGCCCT 600
 Db 370 ProGluProPheAlaLysLeuMetLysGluCysTrpGlnGlnAspProHisIleArgPro 389
 QY 601 TCAATGGAGGAATTTGAAATAATGACT 630
 Db 390 SerPheAlaLeuIleLeuGluGlnLeuThr 399

RESULT 11

US-10-014-882-2

; Sequence 2, Application US/10014882

; Publication No. US20020107384A1

; GENERAL INFORMATION:

; APPLICANT: Kieke, James

; APPLICANT: Donoho, Gregory

; TITLE OF INVENTION: No. US20020107384A1 Human Kinase and Polynucleotides Encoding ti

; FILE REFERENCE: LEX-0279-USA

; CURRENT APPLICATION NUMBER: US/10/014,882

; CURRENT FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: US 60/254,744

; PRIOR FILING DATE: 2000-12-11

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1036

; TYPE: PRT

; ORGANISM: homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(1036)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-014-882-2

Alignment Scores:
 Pred. No.: 5,55e-29 Length: 1036
 Score: 355.00 Matches: 83
 Percent Similarity: 53.48% Conservative: 40
 Best Local Similarity: 36.09% Mismatches: 85
 Query Match: 28.35% Indels: 22
 DB: 14 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-014-882-2 (1-1036)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGGAGCCTGC 63
 Db 171 GluAlaArgLeuPheAlaMetLeuArgHisProAsnIleIleGluLeuArgGlyValCys 190
 QY 64 TTGAATCCA-----GTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
 Db 191 LeuGlnGlnProHisLeuCysLeuValLeuPheAlaArgGlyGlyAlaLeuAsnArg 210
 QY 118 GTGCTGATGCTGCTGAACCATTCGCTATATTACTGCT----- 156
 Db 211 AlaLeuAlaAlaAlaAlaProAspProArgAlaProGlyProArgAlaArg 230
 QY 157 -----GCCACGCAATG---AGTTGGTGTGTATACAGTGTCCCAAGGAGTGGCTTAT 204

Db 231 ArgilleProProHisValLeuValAsnTrpAlaValGlnIleAlaAargGlyMetLeuTyr 250
QY 205 CTTACAGCATGCAACCCAAACGCGTAATTCACAGGACCTGAAACACCAACTTACTG 264
Db 251 LeuHisGluGluAlaPheValProIleLeuHisAargAspLeuLysSerSerAsnIleLeu 270
QY 265 CTGGTTGCAGGG-----GGACAGTTCTCTAAATAATTGTCATTTT 303
Db 271 LeuLeuGluLysIleGluHisAspAspIleCysAsnLysThrLeuLysIleThrAspPhe 290
QY 304 GGTACAGCCTGTGAC---ATTACAGACACACATGACCAATAACAAAGGGAGTCTGCTGG 360
Db 291 GlyLeuAlaAargGluTrpHisargThrThrLysMetSerThrAlaGlyThrTrpAlaTrp 310
QY 361 ATGGCAGCCTGAAGTTTGAAGTAGTAATTCAGTGAATAATGTCAGCTCTTCAGCTGG 420
Db 311 MetAlaProGluValIleLysSerSerLeuPheSerLysGlySerAspIleTrpSerTyr 330
QY 421 GGTATTATCTTTGGGAAGTGATAACGCTCGGAACCCCTTTGATGAGATTGTTGGCCCA 480
Db 331 GlyValLeuLeuTrpGluLeuLeuThrGlyGluValProTyrArgGlyIleAspGlyLeu 350
QY 481 GCTTTCCGAATCATGTGGCTGTTTCATAATGTGTACTCGACCACTGATAAAAAATTTA 540
Db 351 AlaValAlaTyrGlyValAlaValAsnLysLeuThrLeu---ProIleProSerThrCys 369
QY 541 CCTAACCCCATTTGAGAGCCTGATGACTCGTGTGTGTCTTAAGACTCTTCCACAGCCCT 600
Db 370 ProGluProPheAlaLysLeuMetLysGluCysTrpGlnGlnAspProHisIleArgPro 389
QY 601 TCATGGAGGAATTTGTGAATAATGACT 630
Db 390 SerPheAlaLeuIleLeuGluGlnLeuThr 399

RESULT 12

US-10-153-668-436
; Sequence 436, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 436
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-436
Alignment Scores:
Pred. No.: 7,41e-29 Length: 746
Score: 353.50 Matches: 75
Percent Similarity: 54.63% Conservative: 43
Best Local Similarity: 34.72% Mismatches: 81
Query Match: 28.23% Indels: 17

DB: 15 Gaps: 8
US-09-830-144-1_COPY_408_1091 (1-684) x US-10-153-668-436 (1-746)
QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTATATATTGTAAGCTTTATGGAGCTGC 63
Db 194 AspIleLysHisLeuAargLysLeuLysHisProAsnIleIleThrPheLysGlyValCys 213
QY 64 TTGAATCCA-----GTGTGCTTCTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 214 ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlyGlnLeuTyrGlu 233
QY 118 GTGTGTCATGTGCTGAACCATTCATATATATATCTGCTGCCACCAATGATGTGGTCT 177
Db 234 ValLeuAargAlaGlyArgProVal-----ThrProSerLeuLeuValAspTrpSer 250
QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCAACGCGTAAATTCAC 237
Db 251 MetGlyIleAlaGlyGlyMetAsnTyrLeuHisLeuHisLys-----IleIleHis 267
QY 238 AGGGACCTGAAACCAACCACTTACTGCTGTGTCAGGGGGGACAGTCTTAAATAATTTGT 297
Db 268 ArgAspLeuLysSerProAsn---MetLeuIleThrTyrAspValValLysIleSer 286
QY 298 GATTTTGTACAGCCTGTGACATTCAGACACATGACCAATACAAAG-----GGAGT 351
Db 287 AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr 306
QY 352 GCTGCTGTGATGCGCCTGAACTTTTGAAGTAGTAATTCACAGTGAATAATGTGACGTC 411
Db 307 ValAlaTrpMetAlaProGluValIleAargAsnGluProValSerGluLysValAspIle 326
QY 412 TTCAGCTGGGTATTATCTTTGGGAAGTGATAACCGCTCGGAACCCCTTTGATGAGATT 471
Db 327 TrpSerPheGlyValValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspVal 346
QY 472 GTGGCCCGAGCTTCCGAATCATGTGGCTGT---CATATATGCTACTCGACCCACTG 528
Db 347 AspSerSerAla-----IleIleTrpGlyValGlySerAsnSerLeuHisLeuProVal 364
QY 529 ATAAAAATTTACCTAAGCCCATTTGAGAGCTCATGACTCGTTGTTGGTCTAAAGATCCT 588
Db 365 ProSerSerCysProAspGlyPheLysIleLeuLeuAargLncysTrpAsnSerLysPro 384
QY 589 TCCACGCGCCTTCAATGGAGGAAATTTGAAATAATATGACTCACTG 636
Db 385 ArgAsnArgProSerPheArgGln-----IleLeuLeuHisLeu 397
RESULT 13
US-10-153-668-324
; Sequence 324, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10


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; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 324
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153668-324

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Alignment Scores:

Pred. No.:	7.67e-29	Length:	859
Score:	353.50	Matches:	75
Percent Similarity:	54.63%	Conservative:	43
Best Local Similarity:	34.72%	Mismatches:	81
Query Match:	28.23%	Indels:	17
DB:	15	Gaps:	8

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QY	64	TTGAATCA	-----GTGTCCTCTGTGATGAATATCTGAAGGGGCTCTTTATATAAT	117
Db	181	ThrGlnAlaProCysTyrCysIleLeuMetGluPheCys	AlaGlnGlyGlnLeuTyrGlu	200
QY	118	GTGCTGCATGGTGTGCTGAAACCATTC	ATATATATCTCTCCGCCACCAATGAGTTCGTGT	177
Db	201	ValLeuArgAlaGlyArgProVal	-----ThrProSerLeuLeuValAspTrpSer	217
QY	178	TTACAGTGTTCCTCCAGGAGTGGCTTATCT	TCACAGCATGCAACCCAAAGCGCTAATTCAC	237
Db	218	MetGlyIleAlaGlyGlyMetAsnTyrLeuHis	HisLys-----IleIleHis	234
QY	238	AGGACCTGAAACACCACCAACTTACTCTGCT	GTGTGTGCAGGGGGGACAGTCTTAAAAAATTCGT	297
Db	235	ArgAspLeuLysSerProAsn	--MetLeuIleThrTyrAspAspValValLysIleSer	253
QY	298	GATTTTGTGTACAGCTGTGCATTCACACACAT	CACCATTAACAG-----GGAGAT	351
Db	254	AspPheGlyThrSerLysGluLeuSerAspLysSer	ThrLysMetSerPheAlaGlyThr	273
QY	352	GCTGCTTGGATGGACCTGAAGTTTTTGAAGGTAGT	AAATTTACAGTCAAAATCTGACGTC	411
Db	274	ValAlaTrpMetAlaProGluValIleArgAsnGlu	ProValSerGlnLysValAspIle	293
QY	412	TTCACTGGGTATATTCCTTTGGGAAGTGATAC	CGCTGGAAACCTTTTGATGAGATT	471
Db	294	TrpSerPheGlyValValLeuTrpGluLeuLeuThr	GlyGluIleProTyrLysAspVal	313
QY	472	GGTGGCCAGCTTCCGAATCATGTGGCTGTT	---CATAAATGGTACTCGACCAACCACTG	528
Db	314	AspSerSerAla	-----IleIleTrpGlyValGlySerAsnSerLeuHisLeuProVal	331
QY	529	ATAAAAAATTTACCTAAAGCCCATGAGAGCGCT	GATGACTGTTGTGGTCTTAAGATCTCT	588
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QY	589	TCCAGCGCCCTTCATGGAGGAATTTGTAATAAT	AATGACTCACTG	636
Db	352	ArgAsnArgProSerPheArgGln	-----IleLeuLeuHisLeu	364

RESULT 14

US-10-153-668-438
 ; Sequence 438, Application US/10153668
 ; Publication No. US20030092616A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HONDA, Goichi
 ; APPLICANT: MATSUDA, Akio
 ; APPLICANT: MURAWATSU, Shuji
 ; APPLICANT: ISHIZAWA, Kenya
 ; TITLE OF INVENTION: STAT6 Activating
 ; FILE REFERENCE: 1254-0207P

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; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260691
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 892
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-153-668-438

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Alignment Scores:

Pred. No.:	7.74e-29	Length:	892
Score:	353.50	Matches:	75
Percent Similarity:	54.63%	Conservative:	43
Best Local Similarity:	34.7%	Mismatches:	81
Query Match:	28.23%	Indels:	17
DB:	15	Gaps:	8

US-09-830-144-1 COPY 408 1091 (1-684) x US-10-153-668-438 (1-892)

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	QY	64	TGTAATCCA-----GTGTGTCCTGCATGCAATATGCTGAAGGGGGCTCTTTATAAAT
	Db	214	ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlyGlnLeuTyrGlu
	QY	118	GTGTGCATGGTGTGAACCATGCCATATTATCTGCTGCTCCACCACAATGACTTGGTGT
	Db	234	VallLeuArgAlaGlyArgProVal-----ThrProSerLeuLeuValAspTrpSer
	QY	178	TTACAGTGTCCCAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATCAC
	Db	251	MetGlyIleAlaGlyGlyMetAsnTyrLeuHisLeuHisLys-----IleIleHis
	QY	238	AGGACCTGAAACACCAAACCTACTGCTGGTTCAGGGGGGACAGTCTCTAAAAATTTCT
	Db	268	ArgAspLeuLysSerProAsn--MetLeuIleThrTyrAspAspValValLysIleSer
	QY	298	CATTTTGGTAGCGCTGTGACATTCACACACACATGACCAATAACAAAG-----GGGAGT
	Db	287	AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr
	QY	352	GCTGCTTGGATGGACCTGAAGTTTTTGAAGGTAGTAGTAATTCACAGTGAAAATGTGACGTC
	Db	307	ValAlaTrpMetAlaProGluValIleArgAsnGluProValSerGluLysValAspIle
	QY	412	TTACAGCTGGGGTATTATCTTTGGGAAGTGATAACGGTCGGAAACCCCTTCATGAGATT
	Ddb	327	TrpSerPheGlyValValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysaspVal
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238 AGGGACCTGAAACACCACCAACTTACTGCTGTT-----GCAGGG 276
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277 GGCACAGTCTTAAAAATTTGCAITTTGGTACAGCTGTGAC---ATTGACACACACATG 333
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287 AsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTrpHisArgThrTrpLys 306
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334 ACCAATAACACAGGGAGTCTGCTGGATGGACCTGAAGTTTTCGAAGGTAGTAATTAC 393
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394 AGTGAATAATGTGACGCTCTTCAGCTGGGGTATTATTCTTTGGGAAGTGATAAGCGTCGG 453
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RESULT 15
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; Sequence 12, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Damiel B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURUPAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dying Alina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 1097
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 55052990CD1
US-10-288-798-12

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Score: 349.50 Matches: 82
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Query Match: 27.92% Indels: 15
DB: Gaps: 5

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|||||
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118 GTGCTGTCATGCTGTGTAACCATTCGCATATTATATCTGCTGCCACGCAATGAGTTGGTGT 177
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1252	100.0	579	4	US-10-158-895-4
3	1252	100.0	590	4	US-09-529-279-15
4	1252	100.0	590	4	US-10-158-895-15
5	371	29.6	455	3	US-09-221-235-5
6	371	29.6	455	3	US-09-221-928-5
7	371	29.6	455	3	US-09-221-928-5
8	371	29.6	455	3	US-09-221-236-5
9	371	29.6	455	3	US-09-221-416-5
10	371	29.6	455	3	US-09-221-245-5
11	371	29.6	455	3	US-09-163-115-5
12	371	29.6	455	3	US-09-221-528-5

13	371	29.6	455	3	US-09-593-553-5	Sequence 5, Appli
14	371	29.6	455	3	US-09-221-237-5	Sequence 5, Appli
15	371	29.6	455	3	US-09-399-588-2	Sequence 2, Appli
16	363.5	29.0	394	4	US-09-345-473E-19	Sequence 19, Appli
17	353.5	28.2	668	1	US-08-205-018-2	Sequence 2, Appli
18	353.5	28.2	859	1	US-08-395-580-2	Sequence 2, Appli
19	353.5	28.2	859	5	PCT-US95-02792-2	Sequence 2, Appli
20	346	27.6	328	4	US-09-345-473E-18	Sequence 18, Appli
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25	323	25.8	821	1	US-08-003-311B-2	Sequence 2, Appli
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28	320	25.6	263	3	US-09-035-706-5	Sequence 5, Appli
29	320	25.6	263	3	US-08-955-841-5	Sequence 5, Appli
30	320	25.6	263	4	US-09-390-425-5	Sequence 5, Appli
31	320	25.6	263	4	US-09-566-906-5	Sequence 5, Appli
32	309.5	24.7	269	2	US-07-857-224B-79	Sequence 79, Appli
33	307.5	24.6	276	2	US-07-857-224B-72	Sequence 72, Appli
34	306	24.4	275	2	US-07-857-224B-71	Sequence 71, Appli
35	305.5	24.4	590	4	US-09-312-283C-409	Sequence 409, App
36	305.5	24.4	786	4	US-09-509-802-2	Sequence 2, Appli
37	305.5	24.4	787	3	US-09-188-930-334	Sequence 334, App
38	305.5	24.4	787	4	US-09-312-283C-334	Sequence 334, App
39	304.5	24.3	304	2	US-08-701-191A-27	Sequence 27, Appli
40	302.5	24.2	316	1	US-08-278-089A-16	Sequence 16, Appli
41	302.5	24.2	316	2	US-08-838-957A-15	Sequence 15, Appli
42	299.5	23.9	527	4	US-08-426-509A-10	Sequence 10, Appli
43	299.5	23.9	527	4	US-08-232-545-10	Sequence 10, Appli
44	299.5	23.9	527	5	PCT-US95-05008-10	Sequence 10, Appli
45	299.5	23.9	625	1	US-08-391-615-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-529-279-4
; Sequence 4, Application US/09529279

; Patent No. 6451617

; GENERAL INFORMATION:

; APPLICANT: ONO, KOICHIRO

; APPLICANT: OHTOMO, TOSHIHIKO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/09/529,279

; CURRENT FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-529-279-4

Alignment Scores: 4.53e-145 Length: 579
Pred. No.: 1252.00 Matches: 228
Score: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-529-279-4 (1-579)

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 QY 121 CTGCATGGTCTGAACCATTCATATATCTGCTGCCACCGCAATGATGGTGTGTTA 180
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 Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 195
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 Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTrp 215
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 Db 256 ProIysProIleGluSerLeuMetThrArgCysTrpSerIysAspProSerGlnArgPro 275
 QY 601 TCAATGAGGAATGTGAAATAATGACTCATCTGTGATGGGTACTTCCAGAGCGAGAT 660
 Db 276 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
 Db 296 GluProLeuGlnTyrProCysGln 303

RESULT 2

US-10-158-895-4
 ; Sequence 4, Application US/10158895
 ; Patent No. 6551840
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/158,895
 ; PRIOR FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 579
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-158-895-4
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-4 (1-579)
 QY 1 GTAGACCTCGGAGTATCCCGTGTGAACCATCTTAATATCTTAAGCTTTATGAGCC 60
 Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
 QY 61 TGGTGAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
 Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
 QY 121 CTGCATGGTCTGAACCATTCATATATCTGCTGCCACCGCAATGATGGTGTGTTA 180
 Db 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
 QY 181 CAGTGTTCACAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAAATTCACAGG 240
 Db 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
 QY 241 GACCTGAACCAACCACTTACTGCTGGTGGAGGGGAGCAGTCTTAAATAATTTGTAT 300
 Db 156 AspLeuIysProAsnLeuLeuValAlaGlyThrValLeuIysIleCysAsp 175
 QY 301 TTTGGTACAGCTGTGACATTCACACACATGACCAATAACAGGGGAGTGGCTTGG 360
 Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 195
 QY 361 ATGGCCACTGAAGTTTTGAAGGTAGTAATTACAGTGAATAAATGTCAGCTCTTCAGCTGG 420
 Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTrp 215
 QY 421 GGTATTATCTTTGGGAAGTGATAACCGCTGCGAAACCTTTGATGAGATGGTGGCCCA 480
 Db 216 GlyIleLeuTrpGluValIleThrArgIysProPheAspGluIleGlyGlyPro 235
 QY 481 GCTTTCCGAATCATGGCTGTTTCATAATGCTACTCGACCAACACCTGATAAAAAATTTA 540
 Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleIysAsnLeu 255
 QY 541 CCTAAGCCCATTCAGACCTGATGACCTGTTGTTGTTAAAGATCTTCCACGCGCCT 600
 Db 256 ProIysProIleGluSerLeuMetThrArgCysTrpSerIysAspProSerGlnArgPro 275
 QY 601 TCAATGAGGAATGTGAAATAATGACTCATCTGTGATGGGTACTTCCAGAGCGAGAT 660
 Db 276 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
 Db 296 GluProLeuGlnTyrProCysGln 303
 RESULT 3
 US-09-529-279-15
 ; Sequence 15, Application US/09529279
 ; Patent No. 6451617
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-15

Alignment Scores:
Pred. No.: 4.57e-145 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-529-279-15 (1-590)

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Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
QY 61 TCGTTGAATCCAGTGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGCTGTGTGAACCATTCGCATATTAATCTGCTGCCAGGCATAGTGTGTTTA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACCAAACTTACTGCTGTTCAGGGGGAGTGTCTTAAAAATTTGTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAGGGAGTGTGCTTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCAGCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATGTACGCTCTTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnLysSerGlnLysCysAspValPheSerTrp 215
QY 421 GGTATTATCTTTGGGAAGTGAATAACGCGTCGGAACCCCTTTGATGAGATTGGTGCCCA 480
Db GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
QY 481 GCTTTCGAATCATGTGGCTGTTCATATGATGTAATGCTGACACACACTGATAAAAATTTA 540
Db AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CCTAAGCCCATGTGAGCGCTGATGACTCGTGTGGTCTAAAGATCCCTCCAGCGCCCT 600
Db ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGGAAATTTGAAATAATGACTCACTTGATCGGGTACTTTCCAGGAGCAGAT 660
Db SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCATTCACAGTATCTTGTGTCAG 684
Db GluProLeuGlnTyrProCysGln 303
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RESULT 4

; Sequence 15, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO

; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Alignment Scores:
Pred. No.: 4.57e-145 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-15 (1-590)

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Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
QY 61 TCGTTGAATCCAGTGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGCTGTGTGAACCATTCGCATATTAATCTGCTGCCAGGCATAGTGTGTTTA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACCAAACTTACTGCTGTTCAGGGGGAGTGTCTTAAAAATTTGTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAGGGAGTGTGCTTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCAGCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATGTACGCTCTTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnLysSerGlnLysCysAspValPheSerTrp 215
QY 421 GGTATTATCTTTGGGAAGTGAATAACGCGTCGGAACCCCTTTGATGAGATTGGTGCCCA 480
Db GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
QY 481 GCTTTCGAATCATGTGGCTGTTCATATGATGTAATGCTGACACACACTGATAAAAATTTA 540
Db AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CCTAAGCCCATGTGAGCGCTGATGACTCGTGTGGTCTAAAGATCCCTCCAGCGCCCT 600
Db ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGGAAATTTGAAATAATGACTCACTTGATCGGGTACTTTCCAGGAGCAGAT 660
Db SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
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QY 661 GAGCCATTACAGTATCCTTGTCAG 684
Db 296 GluProLeuGlnTyrProCysGln 303

RESULT 5
US-09-221-235-5
; Sequence 5, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-235-5

Alignment Scores:
Pred. No.: 9,61e-37 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-235-5 (1-455)
QY 4 GAGCTTCGGCAGTATCCCGTGTGACCATCTTAATTTGTAAGCTTTATGGAGCCTGC 63
Db 53 GluAlaGluLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTCCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAAT 117
Db 73 LeuGluProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGGT-----GCTGAACCATTCGCATATTATATCTGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
QY 172 TGGTGTTTACAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAAACCAACCAACTTACTGCTGGTTGCGAGGGGGACAGTTCTAAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTGTGATTTTGGTACAGCTGTGACATTTCAGACACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTCTCTGGATGGCAGCTGAAAGTTTTTGAAGGTAGTAGTAATTACAGTGAATAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GAGCTCTTACGTGGGGTATTATCTTTGGAGTGTATACCGGTGCGAAGCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValLeuTrpGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTGGTGGCCAGCTTTCCGAATCATGTGG---GCTGTTCAATAATGGTACTCTGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
QY 523 CCACGTATAAAATTTACCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGTCTAAA 582
Db 226 ThrIleProSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-928-5 (1-455)
QY 4 GAGCTTCGGCAGTATCCCGTGTGACCATCTTAATTTGTAAGCTTTATGGAGCCTGC 63
Db 53 GluAlaGluLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTCCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAAT 117
Db 73 LeuGluProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGGT-----GCTGAACCATTCGCATATTATATCTGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
QY 172 TGGTGTTTACAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAAACCAACCAACTTACTGCTGGTTGCGAGGGGGACAGTTCTAAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTGTGATTTTGGTACAGCTGTGACATTTCAGACACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTCTCTGGATGGCAGCTGAAAGTTTTTGAAGGTAGTAGTAATTACAGTGAATAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GAGCTCTTACGTGGGGTATTATCTTTGGAGTGTATACCGGTGCGAAGCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValLeuTrpGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTGGTGGCCAGCTTTCCGAATCATGTGG---GCTGTTCAATAATGGTACTCTGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
QY 523 CCACGTATAAAATTTACCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGTCTAAA 582
Db 226 ThrIleProSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
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Db      226 ThrileProSerSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
Qy      583 GATCCTTCCAGCGCCCTTCAATGAGGAGAAATGTGAAAAATATG 627
Db      246 AspalalysLysArgProSerPheLysGlnIleSerIleLeu 260
RESULT 7
US-09-221-527-5
; Sequence 5, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE:
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-527-5

Alignment Scores:
Pred. No.:      9.61e-37      Length:      455
Score:          371.00      Matches:      81
Percent Similarity: 56.28%      Conservative: 40
Best Local Similarity: 37.67%      Mismatches: 80
Query Match:    29.63%      Indels:      14
DB:             3          Gaps:         8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-527-5 (1-455)
Qy      4 GAGCTTCGGCAGTATCCCGTGTGAACCATCTAATATTGTAAAGCTTTATGGAGCCTGC 63
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Qy      64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAAT 117
Db      73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy      118 GTGCTGCATGCT-----GCTGAACCATTCGCATATTATATCTGCTGCCCGCAATGAGT 171
Db      93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy      172 TGGTGTGTTACAGTGTCCCAAGGAGTGGCTTATCTTACAGCATGCAACCCCAAGCGCTA 231
Db      110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy      232 ATTCACAGGGACCTGAAACCAACCAACTTACTGCTGTGTCAGGGGGGACAGTTCATAAA 291
Db      130 IleHisArgAspLeuLysSerArgAsnValValIleAlaAspGly---ValLeuLys 148
Qy      292 ATTTGTGATTTTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAG----- 345
Db      149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
Qy      346 GGGAGTGTGCTGGATGGCACCTGAAGTATTTTGAAGTAGTAATACAGTGAAAAATGT 405
Db      168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy      406 GACGCTCTTCAGTGGGGTATTATCTTTGGGAAGTGAACCGCTCGGAAACCCCTTTGAT 465
Db      188 AspThrTyrSerTyrGlyValValIleTrpGluMetLeuThrArgGluValProPheLys 207
Qy      466 GAGATTGTGTCGCCAGCTTTCCGAATCATGTGG---GCTGTTCTATAATGGTACTCGACCA 522
Db      208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
Qy      523 CCACTGATAAAAAATTTTACCTAAAGCCCATTTGAGAGCCTGATGACTCGTTGTTGTCATAA 582
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Db      226 ThrileProSerSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
Qy      583 GATCCTTCCAGCGCCCTTCAATGAGGAGAAATGTGAAAAATATG 627
Db      246 AspalalysLysArgProSerPheLysGlnIleSerIleLeu 260
RESULT 8
US-09-221-236-5
; Sequence 5, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-236-5

Alignment Scores:
Pred. No.:      9.61e-37      Length:      455
Score:          371.00      Matches:      81
Percent Similarity: 56.28%      Conservative: 40
Best Local Similarity: 37.67%      Mismatches: 80
Query Match:    29.63%      Indels:      14
DB:             3          Gaps:         8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-236-5 (1-455)
Qy      4 GAGCTTCGGCAGTATCCCGTGTGAACCATCTAATATTGTAAAGCTTTATGGAGCCTGC 63
Db      53 GlualaGluIleLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
Qy      64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAAT 117
Db      73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy      118 GTGCTGCATGCT-----GCTGAACCATTCGCATATTATATCTGCTGCCCGCAATGAGT 171
Db      93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy      172 TGGTGTGTTACAGTGTCCCAAGGAGTGGCTTATCTTACAGCATGCAACCCCAAGCGCTA 231
Db      110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy      232 ATTCACAGGGACCTGAAACCAACCAACTTACTGCTGTGTCAGGGGGGACAGTTCATAAA 291
Db      130 IleHisArgAspLeuLysSerArgAsnValValIleAlaAspGly---ValLeuLys 148
Qy      292 ATTTGTGATTTTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAG----- 345
Db      149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
Qy      346 GGGAGTGTGCTGGATGGCACCTGAAGTATTTTGAAGTAGTAATACAGTGAAAAATGT 405
Db      168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy      406 GACGCTCTTCAGTGGGGTATTATCTTTGGGAAGTGAACCGCTCGGAAACCCCTTTGAT 465
Db      188 AspThrTyrSerTyrGlyValValIleTrpGluMetLeuThrArgGluValProPheLys 207
Qy      466 GAGATTGTGTCGCCAGCTTTCCGAATCATGTGG---GCTGTTCTATAATGGTACTCGACCA 522
Db      208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
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Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
Qy 523 CCACGTGATAAAATTTACCTAACCCATTGAGAGCCTGATGACTCGTTGTTGCTCTAAA 582
Db 226 ThrileProSerSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
Qy 583 GATCCTTCCAGCGCCCTTCAATGGAGGAAATTTGAAAAATAATG 627
Db 246 AspaLalysLysArgProSerPheLysGlnIleleSerIleLeu 260

RESULT 11

US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-115-5

Alignment Scores:
Pred. No.: 9.61e-37 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-163-115-5 (1-455)

Qy 4 GAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCCTGC 63
Db 53 GluAlaGluIleLeuSerValLeuSerHisArgAsnIleleGlnPheTyrGlyValle 72
Qy 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGCTCTTTATATAAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy 118 GTGCTGCATGCT-----GCTGAACCATTTGCCATATTATATCTGCTGCCCGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy 172 TGGTGTTTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy 232 ATTCACAGGACCTGAAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAspGly---ValLeuLys 148
Qy 292 ATTTGTGATTTTGTACAGCCTGTGACATTCACAGACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrHisMetSerLeuVal 167
Qy 346 GGGAGTGTCTGGATGGACCTGAAGTTTTTGAAGTAGTAATACAGTGAAAAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy 406 GACGCTTCACGTGGGTATTATTCTTTGGAGAGTAAACGCTCGGAAACCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValLeuTrpGluMetLeuThrArgGluValProPheLys 207
Qy 466 GAGATTGTGGCCAGCTTTCCGAAATCATGTGG---GCTGTTTCATATGTTGACTCGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225

Qy 523 CCACGTGATAAAATTTACCTAACCCATTGAGAGCCTGATGACTCGTTGTTGCTCTAAA 582
Db 226 ThrileProSerSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
Qy 583 GATCCTTCCAGCGCCCTTCAATGGAGGAAATTTGAAAAATAATG 627
Db 246 AspaLalysLysArgProSerPheLysGlnIleleSerIleLeu 260

RESULT 12

US-09-221-528-5
; Sequence 5, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-528-5

Alignment Scores:
Pred. No.: 9.61e-37 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-528-5 (1-455)

Qy 4 GAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCCTGC 63
Db 53 GluAlaGluIleLeuSerValLeuSerHisArgAsnIleleGlnPheTyrGlyValle 72
Qy 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGCTCTTTATATAAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy 118 GTGCTGCATGCT-----GCTGAACCATTTGCCATATTATATCTGCTGCCCGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy 172 TGGTGTTTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy 232 ATTCACAGGACCTGAAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAspGly---ValLeuLys 148
Qy 292 ATTTGTGATTTTGTACAGCCTGTGACATTCACAGACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrHisMetSerLeuVal 167
Qy 346 GGGAGTGTCTGGATGGACCTGAAGTTTTTGAAGTAGTAATACAGTGAAAAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy 406 GACGCTTCACGTGGGTATTATTCTTTGGAGAGTAAACGCTCGGAAACCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValLeuTrpGluMetLeuThrArgGluValProPheLys 207
Qy 466 GAGATTGTGGCCAGCTTTCCGAAATCATGTGG---GCTGTTTCATATGTTGACTCGACCA 522

Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
QY 523 CCAGTATAAAATTTACCTAAGCCCATTCAGAGCGCTGATGACTCTTGTGGTCTAAA 582
Db 226 ThrileProSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
QY 583 GATCCTTCCAGGCGCCCTTCAATGAGGAAATTTGTGAAATAATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleleSerIleLeu 260

RESULT 13

US-09-593-553-5
; Sequence 5, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-553-5

Alignment Scores:
Pred. No.: 9,61e-37 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-593-553-5 (1-455)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACACCTTAATATTGTAAGCTTTTATGGAGCTGC 63
Db 53 GluAlaGluIleLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTGCTGTGATGGAATATCTGAGGGGCTCTTATATAAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGGT-----GCTGAACCAATTCGCATATTATATCTGCTGCCCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
QY 172 TGGTGTTCACAGTTCCTCCAGGAGTGCTTATCTTCACAGCATGCAACCCAAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAAACCAACCACTTACTGCTGCTGAGGGGAGCAGTCTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTGTGATTTTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTGCTTGGATGGCCCTGAGTTTTCAGAGTAGTAGTATACAGTGAATAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GACGTCTTCAGCTGGGTATTATTCTTTGGAGTGTAAACCGCTCGGAACCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValIleValThrGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTGGTGGCCCGAGCTTTCCGAATCATGTGG---GCTGTTTATAATGGTACTCGACCA 522

Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225
QY 523 CCAGTATAAAATTTACCTAAGCCCATTCAGAGCGCTGATGACTCTTGTGGTCTAAA 582
Db 226 ThrileProSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245
QY 583 GATCCTTCCAGGCGCCCTTCAATGAGGAAATTTGTGAAATAATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleleSerIleLeu 260

RESULT 14

US-09-221-237-5
; Sequence 5, Application US/09221237
; Patent No. 6214597
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,237
; CURRENT FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-237-5

Alignment Scores:
Pred. No.: 9,61e-37 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-221-237-5 (1-455)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACACCTTAATATTGTAAGCTTTTATGGAGCTGC 63
Db 53 GluAlaGluIleLeuSerValLeuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTGCTGTGATGGAATATCTGAGGGGCTCTTATATAAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGGT-----GCTGAACCAATTCGCATATTATATCTGCTGCCCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
QY 172 TGGTGTTCACAGTTCCTCCAGGAGTGCTTATCTTCACAGCATGCAACCCAAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAAACCAACCACTTACTGCTGCTGAGGGGAGCAGTCTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTGTGATTTTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAG----- 345
Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTGCTTGGATGGCCCTGAGTTTTCAGAGTAGTAGTATACAGTGAATAATGT 405
Db 168 GlyThrPheProTrpMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GACGTCTTCAGCTGGGTATTATTCTTTGGAGTGTAAACCGCTCGGAACCCCTTTGAT 465
Db 188 AspThrTyrSerTyrGlyValValIleValThrGluMetLeuThrArgGluValProPheLys 207

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OM nucleic - nucleic search, using sw model

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(without alignments)
2227.439 Million cell updates/sec

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Perfect score: 684
Sequence: 1 GTAGAGCTTCGAGTATCCGCTGTAACCATCTCTATATTTGTAAGCTTTATGAGCC 60

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues 4403344

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	1705	14	US-10-283-023-1
2	684	100.0	1705	14	US-10-283-023-3
3	684	100.0	1788	12	US-10-384-743-14
4	684	100.0	1788	13	US-10-158-895-14
5	684	100.0	2656	12	US-10-384-743-3
6	684	100.0	2656	13	US-10-158-895-3
7	65.4	9.6	1428	10	US-09-938-842A-882
8	56.6	8.3	1398	14	US-09-938-842A-633
9	54.6	8.0	1365	14	US-10-106-698-2068
10	54.6	8.0	1365	9	US-09-757-982-6
11	54.6	8.0	2120	9	US-09-757-982-4
12	54.6	8.0	2251	12	US-10-094-749-838
13	52	7.6	1737	10	US-09-862-027-13
14	52	7.6	3160	14	US-10-177-293-306
15	52	7.6	3268	11	US-09-291-417-1
16	52	7.6	3335	12	US-10-353-690-115

17	46.8	6.8	1239	10	US-09-938-842A-1190	Sequence 1190, Ap
18	46.4	6.8	1926	10	US-09-938-842A-86	Sequence 86, Appl
19	46	6.7	3538	12	US-10-288-798-36	Sequence 36, Appl
20	45.2	6.6	2466	12	US-10-171-404A-47	Sequence 47, Appl
21	45	6.6	3111	13	US-10-014-882-1	Sequence 1, Appli
22	45	6.6	3518	13	US-10-014-882-3	Sequence 3, Appli
23	45	6.6	5549	12	US-10-354-358-23	Sequence 23, Appl
24	43.8	6.4	2157	12	US-10-259-165-367	Sequence 367, Appl
25	43.8	6.4	2160	12	US-10-259-165-39	Sequence 39, Appl
26	43.6	6.4	2146	13	US-10-071-766-83	Sequence 83, Appl
27	43.6	6.4	2148	12	US-10-240-965-251	Sequence 251, App
28	43.6	6.4	2198	9	US-09-012-135A-2	Sequence 2, Appli
29	43.6	6.4	2237	12	US-10-240-965-252	Sequence 252, App
30	43.6	6.4	2283	14	US-10-198-846-10281	Sequence 10281, A
31	43.6	6.4	2284	12	US-09-814-353-21674	Sequence 21674, A
32	43.6	6.4	2342	12	US-10-292-408-27	Sequence 27, Appl
33	43.6	6.4	2347	14	US-10-209-324-1	Sequence 1, Appli
34	43.2	6.3	1887	10	US-09-938-842A-52	Sequence 52, Appl
35	43.2	6.3	2211	10	US-09-938-842A-1577	Sequence 1577, Ap
36	42.6	6.2	1857	10	US-09-764-868-220	Sequence 220, App
37	42.6	6.2	1857	11	US-09-764-891-2341	Sequence 2341, Ap
38	42.6	6.2	1857	14	US-10-205-428-202	Sequence 202, App
39	42.4	6.2	266	10	US-09-878-574-7790	Sequence 7790, Ap
40	41.8	6.1	2564	12	US-10-366-288-11	Sequence 11, Appl
41	41.4	6.1	1143	10	US-09-801-368-401	Sequence 401, App
42	40.4	5.9	2440	14	US-10-153-668-435	Sequence 435, App
43	40.4	5.9	3365	14	US-10-153-668-323	Sequence 323, App
44	40.4	5.9	3428	14	US-10-153-668-437	Sequence 437, App
45	40.4	5.9	3761	12	US-09-814-353-20138	Sequence 20138, A

ALIGNMENTS

RESULT 1

US-10-283-023-1
; Sequence 1, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
; FILE REFERENCE: MP101-239P1PM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-283-023-1

Query Match 100.0%; Score 684; DB 14; Length 1705;

Best Local Similarity 100.0%; Pred. No. 3.6e-210;

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGAGTATCCGCTGTAACCATCTCTATATTTGTAAGCTTTATGAGCC 60

Db 226 GTAGAGCTTCGAGTATCCGCTGTAACCATCTCTATATTTGTAAGCTTTATGAGCC 285

Qy 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTTTTATATAATGTG 120

Db 286 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTTTTATATAATGTG 345

Qy 121 CTGATGTGTGTAACCATCTGTCATATATATGCTGCCACGCAATGAGTGTGTTTA 180

Db 346 CTGATGTGTGTAACCATCTGTCATATATATGCTGCCACGCAATGAGTGTGTTTA 405

Qy 191 CAGTGTTCCTCCAGGAGTGGCTTAATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 240

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
Db 232 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 291
QY 61 TGCCTTGAATCCAGTGTGCTTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 292 TGCCTTGAATCCAGTGTGCTTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 351
QY 121 CTGATGCTGTGAACCATTCGCCATTAATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 180
Db 352 CTGATGCTGTGAACCATTCGCCATTAATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 411
QY 181 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
Db 412 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 471
QY 241 GACCTGAAACCCACCAACTTACTGCTGTTCAGGGGGGACAGTTCTAAAAATTGTGAT 300
Db 472 GACCTGAAACCCACCAACTTACTGCTGTTCAGGGGGGACAGTTCTAAAAATTGTGAT 531
QY 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTTGG 360
Db 532 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTTGG 591
QY 361 ATGGACCTGAAGTTTGTGAAGGTAGTAATTTACAGTGAAAAATGTGACGTCTTCAGCTGG 420
Db 592 ATGGACCTGAAGTTTGTGAAGGTAGTAATTTACAGTGAAAAATGTGACGTCTTCAGCTGG 651
QY 421 GGTATTATCTTTGGGAAGTATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 652 GGTATTATCTTTGGGAAGTATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 711
QY 481 GCTTTCCGAATCATGTGGGCTGTTTCATAATGCTACTCGACACCACTGATAAAAAATTGA 540
Db 712 GCTTTCCGAATCATGTGGGCTGTTTCATAATGCTACTCGACACCACTGATAAAAAATTGA 771
QY 541 CCTAAGCCCATTGAGAGCTGATGACTGTTGTGGTCTAAGATCCCTCCAGGCGCCT 600
Db 772 CCTAAGCCCATTGAGAGCTGATGACTGTTGTGGTCTAAGATCCCTCCAGGCGCCT 831
QY 601 TCAATGGAGGAAATGTGAAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 660
Db 832 TCAATGGAGGAAATGTGAAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 891
QY 661 GAGCCATTACAGTATCCTTTGTGAG 684
Db 892 GAGCCATTACAGTATCCTTTGTGAG 915

RESULT 4

US-10-158-895-14
; Sequence 14, Application US/10158895
; Publication No. US2002015624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Query Match 100.0%; Score 684; DB 13; Length 1788;
Best Local Similarity 100.0%; Pred. No. 3.7e-210; Indels 0; Gaps 0;
Matches 684; Conservative 0; Mismatches 0;

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
Db 232 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 291
QY 61 TGCCTTGAATCCAGTGTGCTTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 292 TGCCTTGAATCCAGTGTGCTTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 351
QY 121 CTGATGCTGTGAACCATTCGCCATTAATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 180
Db 352 CTGATGCTGTGAACCATTCGCCATTAATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 411
QY 181 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
Db 412 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 471
QY 241 GACCTGAAACCCACCAACTTACTGCTGTTCAGGGGGGACAGTTCTAAAAATTGTGAT 300
Db 472 GACCTGAAACCCACCAACTTACTGCTGTTCAGGGGGGACAGTTCTAAAAATTGTGAT 531
QY 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTTGG 360
Db 532 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTTGG 591
QY 361 ATGGACCTGAAGTTTGTGAAGGTAGTAATTTACAGTGAAAAATGTGACGTCTTCAGCTGG 420
Db 592 ATGGACCTGAAGTTTGTGAAGGTAGTAATTTACAGTGAAAAATGTGACGTCTTCAGCTGG 651
QY 421 GGTATTATCTTTGGGAAGTATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 652 GGTATTATCTTTGGGAAGTATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 711
QY 481 GCTTTCCGAATCATGTGGGCTGTTTCATAATGCTACTCGACACCACTGATAAAAAATTGA 540
Db 712 GCTTTCCGAATCATGTGGGCTGTTTCATAATGCTACTCGACACCACTGATAAAAAATTGA 771
QY 541 CCTAAGCCCATTGAGAGCTGATGACTGTTGTGGTCTAAGATCCCTCCAGGCGCCT 600
Db 772 CCTAAGCCCATTGAGAGCTGATGACTGTTGTGGTCTAAGATCCCTCCAGGCGCCT 831
QY 601 TCAATGGAGGAAATGTGAAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 660
Db 832 TCAATGGAGGAAATGTGAAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 891
QY 661 GAGCCATTACAGTATCCTTTGTGAG 684
Db 892 GAGCCATTACAGTATCCTTTGTGAG 915

RESULT 5

US-10-384-743-3
; Sequence 3, Application US/10384743
; Publication No. US2003016228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)..(1919)
US-10-384-743-3

Query Match 100.0%; Score 684; DB 12; Length 2656;
Best Local Similarity 100.0%; Pred. No. 4.6e-210;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60
Db 408 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 467
QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATCTGAAGGGGCTCTTTATATAAATGTG 120
Db 468 TGCTTGAATCCAGTGTCTTGTGATGGAATATCTGAAGGGGCTCTTTATATAAATGTG 527
QY 121 CTGCATGGTGTGAACCATCTCCCATATTAATCTGCTGCCACGCAATGAGTGTGTGTTA 180
Db 528 CTGCATGGTGTGAACCATCTCCCATATTAATCTGCTGCCACGCAATGAGTGTGTGTTA 587
QY 181 CAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
Db 588 CAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 647
QY 241 GACCTGAAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAAATAATTTGTGAT 300
Db 648 GACCTGAAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAAATAATTTGTGAT 707
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTTGG 360
Db 708 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTTGG 767
QY 361 ATGGCACTGAAGTTTTTGAAGGTAGTAATTCAGTGAATAATCTGACGCTCTTCAGCTGG 420
Db 768 ATGGCACTGAAGTTTTTGAAGGTAGTAATTCAGTGAATAATCTGACGCTCTTCAGCTGG 827
QY 421 GGTATTAATCTTTGGGAAGTGAATTAACCGTGGGAAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 828 GGTATTAATCTTTGGGAAGTGAATTAACCGTGGGAAACCCCTTTGATGAGATTGGTGGCCCA 887
QY 481 GCTTTCCGAATCATGTGGGCTGTTCAATAATGGTACTCGACCAACCATGATAAAAAATTTA 540
Db 888 GCTTTCCGAATCATGTGGGCTGTTCAATAATGGTACTCGACCAACCATGATAAAAAATTTA 947
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGGTCTAAAGATCTCTCCAGCGCCT 600
Db 948 CCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGGTCTAAAGATCTCTCCAGCGCCT 1007
QY 601 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGCGGTACTTTCCAGGAGCAGAT 660
Db 1008 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGCGGTACTTTCCAGGAGCAGAT 1067
QY 661 GAGCCATTACAGTATCCTTTGTCAG 684
Db 1068 GAGCCATTACAGTATCCTTTGTCAG 1091

RESULT 6
US-10-158-895-3
; Sequence 3, Application US/1015895
; Publication No. US20020155624A1
; GENERAL INFORMATION:

; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)..(1919)
US-10-158-895-3

Query Match 100.0%; Score 684; DB 13; Length 2656;
Best Local Similarity 100.0%; Pred. No. 4.6e-210;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60
Db 408 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 467
QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATCTGAAGGGGCTCTTTATATAAATGTG 120
Db 468 TGCTTGAATCCAGTGTCTTGTGATGGAATATCTGAAGGGGCTCTTTATATAAATGTG 527
QY 121 CTGCATGGTGTGAACCATCTCCCATATTAATCTGCTGCCACGCAATGAGTGTGTGTTA 180
Db 528 CTGCATGGTGTGAACCATCTCCCATATTAATCTGCTGCCACGCAATGAGTGTGTGTTA 587
QY 181 CAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
Db 588 CAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 647
QY 241 GACCTGAAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAAATAATTTGTGAT 300
Db 648 GACCTGAAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAAATAATTTGTGAT 707
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTTGG 360
Db 708 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTTGG 767
QY 361 ATGGCACTGAAGTTTTTGAAGGTAGTAATTCAGTGAATAATCTGACGCTCTTCAGCTGG 420
Db 768 ATGGCACTGAAGTTTTTGAAGGTAGTAATTCAGTGAATAATCTGACGCTCTTCAGCTGG 827
QY 421 GGTATTAATCTTTGGGAAGTGAATTAACCGTGGGAAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 828 GGTATTAATCTTTGGGAAGTGAATTAACCGTGGGAAACCCCTTTGATGAGATTGGTGGCCCA 887
QY 481 GCTTTCCGAATCATGTGGGCTGTTCAATAATGGTACTCGACCAACCATGATAAAAAATTTA 540
Db 888 GCTTTCCGAATCATGTGGGCTGTTCAATAATGGTACTCGACCAACCATGATAAAAAATTTA 947
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGGTCTAAAGATCTCTCCAGCGCCT 600
Db 948 CCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGGTCTAAAGATCTCTCCAGCGCCT 1007
QY 601 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGCGGTACTTTCCAGGAGCAGAT 660
Db 1008 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGCGGTACTTTCCAGGAGCAGAT 1067
QY 661 GAGCCATTACAGTATCCTTTGTCAG 684


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Db 1068 GAGCATTACAGTATCCTTGTCAG 1091
|||||
RESULT 7
US-09-938-842A-882
; Sequence 882, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-882

Query Match 9.6%; Score 65.4; DB 10; Length 1428;
Best Local Similarity 49.3%; Pred. No. 3.9e-10;
Matches 171; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 338 ATACCAAGGGAGTCTGCTTGGATGGCACCCTGAAGTCTTTTGAAGGTAGTAAATTACAGTG 397
Db 956 ATACATAGGAACTTATAGGTGGATGGCACCCTGAAGTCTTTTAAACGGATACCATGGAC 1015

QY 398 AAAAATGTGAGCTCTTCAGCTGGGGTATATATCTTTGGGAAGTGATAACGGCTCGGAAC 457
Db 1016 GGAAGTGGCATGTTTATAGTTTGGACTCTTTTATGGMAATGTAGTGGAGCACTTC 1075

QY 458 CTTTGTATGAGATTGGTGGCCAGCTTCCGNAATCATGTGGGCTGTTTATATGTCATC 517
Db 1076 CATATGAGGAGATGAATTTGCTGAACAAATTCCTACGAGTTATATACAGAAATTA 1135

QY 518 GACCACCACTGATAAAAAATTTACCTAAGCCCAATTGAGAGCCTGATGACTCGTTGTTG 577
Db 1136 GGCCAGTTATACCGACGAGTTGTCAGCGGCCATGAAGAGCTGATCGAGCATGTTGTT 1195

QY 578 CTAAGAATCTCTCCAGCGCCCTTCAATGGAGGAAATTTGGAATAATATGACTCACTTGA 637
Db 1196 CATCGAAACACAGACAGAGACCGGAATTCGGCAGATTGTCAAAGTGTGGAACATTCA 1255

QY 638 TCGGTACTTTCCAGGACAGATGAGCCATTACAGTATCCTTGTCTAG 684
Db 1256 AGAAGTCTCTAACAGCGAAGGAAAACTTAATCTTTTACCTAGCCAG 1302

RESULT 8
US-09-938-842A-633
; Sequence 633, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-633

Query Match 8.0%; Score 54.6; DB 14; Length 1063;
Best Local Similarity 48.3%; Pred. No. 1e-06;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTTGGTGTGTTTACAGTTGCCAAGAGTGGCTTATCTTCACAGCATGCA 219
Db 578 CACATTATGAGCTGGGCCCATGATGTAGCCAAAGGAATGCAATTTATCATATGAGGCT 519
QY 220 CCCAAAGCGCTAATTCACAGGAGCTGAAACACCAACTTACTGCTGTTGCGAGGGG 279
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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 633
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-633

Query Match 8.3%; Score 56.6; DB 10; Length 1398;
Best Local Similarity 52.3%; Pred. No. 2.7e-07;
Matches 150; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

QY 186 TTCCCAAGGAGTGGCTTATCTTCACAGCATCAACCCAAAGCGCTAATTCACAGGACCT 245
Db 714 TCGAATAATCGTCTCTGCGATTTCCCATCTCCATGAGAAAGGCATATGCAAGAGATCT 773

QY 246 GAAACCAACAAACTTACTGCTGGTTGAGGGGGGACAG---TTCUAAAAATTTGTGATTT 302
Db 774 GAAACCGAATAACATCTCATGATACAGATGCCACGTGATGCTAACAGATTTTGGTTT 833

QY 303 TGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTGCTTGGAT 362
Db 834 AGCAAGGAATTTGAAGAAAAACACAAGATCAAACTCCATGTGCGGAACCTACCGAGTATAT 893

QY 363 GGCACCTGAAGTTTGTGAAGTAGTAAATTACAGTGAAAAATGTGACGCTTTCAGCTGGG 422
Db 894 GGCACCTGAAGTTGTCAGGAAAGGACATGATAAGCAGCTGACTGGTGAGCGTAGG 953

QY 423 TATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGA 469
Db 954 GATTCTTCTGTATGAGATGCTCACAGGAAGCCACCGTTTCTCGGA 1000

RESULT 9
US-10-106-698-2068/c
; Sequence 2068, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2068
; LENGTH: 1063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-2068

Query Match 8.0%; Score 54.6; DB 14; Length 1063;
Best Local Similarity 48.3%; Pred. No. 1e-06;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTTGGTGTGTTTACAGTTGCCAAGAGTGGCTTATCTTCACAGCATGCA 219
Db 578 CACATTATGAGCTGGGCCCATGATGTAGCCAAAGGAATGCAATTTATCATATGAGGCT 519
QY 220 CCCAAAGCGCTAATTCACAGGAGCTGAAACACCAACTTACTGCTGTTGCGAGGGG 279
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Db 518 CCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGGTTGTTATAGCTGTGATGGA 459
Qy 280 ACAGTTCCTAAATTTGTGATTTTGGTACAGCCTGTGACATTCACACACATGACCAAT 339
Db 458 GTATTGAAGATCTGTGATCTTGGTGGCTCTCGGTTCCATACCAATACACACATGTC 399
Qy 340 AACAAAGGGAGTGTCTGTGGATGGCCACCTGAAGCTTTTGAAGTGTAGTAATTACAGTGA 399
Db 398 TTGGTTGAACCTTTCCCATGATGGCTCCAGAGTTATCCAGATCTCCCTGTGTGAGAA 339
Qy 400 AAATGTCAAGCTTTCACTGGGTTATTTCTTTGGGAAGTGAATAACGGCTCGGAACCC 459
Db 338 ACTGTGACACATATTCATGTTGGTCTCTGGGAGATGCTAAACAAGGAGGTCCCC 279
Qy 460 TTTGATGAGATTGGTG 476
Db 278 TTTAAAGGTTTGAAGG 262

RESULT 10

US-09-757-982-6
; Sequence 6, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1365)
US-09-757-982-6

Query Match 8.0%; Score 54.6; DB 9; Length 1365;
Best Local Similarity 48.3%; Pred. No. 1.2e-06;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 160 CAGCAATGAGTTGGTGTTCACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGGCCACTGTATGAGCAAGAAATGCATTTATACATATGGAGCT 375
Qy 220 CCCAAGCGCTAATTCACAGGACCTGAACCCACCAACTTACTGCTGGTTGACGGGGG 279
Db 376 CCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGGTTGTTATAGCTGTGATGGA 435
Qy 280 ACAGTTCCTAAATTTGTGATTTTGGTACAGCCTGTGACATTCACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGATTTGGTGGCTCTCGGTTCCATACCAATACACACATGTC 495
Qy 340 AACAAAGGGAGTGTCTGTGGATGGCCACCTGAAGCTTTTGAAGTGTAGTAATTACAGTGA 399
Db 496 TTGGTTGAACCTTTCCCATGATGGCTCCAGAGTTATCCAGATCTCCCTGTGTGAGAA 555
Qy 400 AAATGTCAAGCTTTCACTGGGTTATTTCTTTGGGAAGTGAATAACGGCTCGGAACCC 459
Db 556 ACTGTGACACATATTCATGTTGGTCTCTGGGAGATGCTAAACAAGGAGGTCCCC 615
Qy 460 TTTGATGAGATTGGTG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 11

US-09-757-982-4

; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(1411)
US-09-757-982-4

Query Match 8.0%; Score 54.6; DB 9; Length 2120;
Best Local Similarity 48.3%; Pred. No. 1.5e-06;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 160 CAGCAATGAGTTGGTGTTCACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAA 219
Db 362 CACATTATGACCTGGGCCACTGTATGAGCAAGAAATGCATTTATACATATGGAGCT 421
Qy 220 CCCAAGCGCTAATTCACAGGACCTGAACCCACCAACTTACTGCTGGTTGACGGGGG 279
Db 422 CCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGGTTGTTATAGCTGTGATGGA 481
Qy 280 ACAGTTCCTAAATTTGTGATTTTGGTACAGCCTGTGACATTCACACACATGACCAAT 339
Db 482 GTACTGAAGATCTGTGATTTGGTGGCTCTCGGTTCCATACCAATACACACATGTC 541
Qy 340 AACAAAGGGAGTGTCTGTGGATGGCCACCTGAAGCTTTTGAAGTGTAGTAATTACAGTGA 399
Db 542 TTGGTTGAACCTTTCCCATGATGGCTCCAGAGTTATCCAGATCTCCCTGTGTGAGAA 601
Qy 400 AAATGTGACGCTTTCACTGGGTTATTTCTTTGGGAAGTGAATAACGGCTCGGAACCC 459
Db 602 ACTGTGACACATATTCATGTTGGTCTCTGGGAGATGCTAAACAAGGAGGTCCCC 661
Qy 460 TTTGATGAGATTGGTG 476
Db 662 TTTAAAGGTTTGAAGG 678

RESULT 12

US-10-094-749-838
; Sequence 838, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 3160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-306

Query Match 7.6%; Score 52; DB 14; Length 3160;
Best Local Similarity 48.8%; Pred. No. 1.3e-05;
Matches 207; Conservative 0; Mismatches 205; Indels 12; Gaps 2;

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Qy 204 TCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGGAGCTGAAACCCAAACTTACT 263
Db 510 TCTGGACTATCTGCATTTCAGAAAAAGAAAATTCACCGAGACATAAAAGCTGCCAATGCTT 569

Qy 264 GCT-----GGTTTCAGGGGGGACAGTTCATAAAATTTTGATTTTGGTACAGCCTGTGA 317
Db 570 GCTCTCAGAACCAAGGAGATGTTAAACTTGTGATTTTGGAGTTGCTGCTCAGCTGACAGA 629

Qy 318 CATTTCAGACACACATGACCAATAACAAGGGGAGTGTCTGCTTGGATGCGACCTGAAGTTT 377
Db 630 TACACAGATTAAAGAAATACCTTTGTGGAACTCCATTTTGGATGGCTCTCTGAAGTTAT 689

Qy 378 TGAAGGTAGTAATTTACAGTGAATAATGTGACGTCTTCAGCTGGGGTATTTCTTTGGGA 437
Db 690 TCAACAGTCACTTATGACTCAAAAGAGCTGACATTTGGTTCATTTGGGAATTTACTGCTATTGA 749

Qy 438 AGTGATAACGGTTCGGAACCTTTTGATGAGATTGGTGGCCAGCTTTCGGAATCATGTG 497
Db 750 ACTAGCCAAAGGAGAGCCACTAACTCGATATGCATC-----CAATGAGAGTTCTGTT 803

Qy 498 GGCTGTTTCATAATGGTACTCGACCACTGATAAAAAATTTACCTAAGCCCATTTGAGAG 557
Db 804 TCTTATCCCAAAACAATCTCCAACTCTTGTGGAGACTTTACTAAGTCTTTTAAGGA 863

Qy 558 CCTGATGACTCGTTTGTGTTAAAGATCCCTTCCAGCGCCCTTCAATGGAGGAAATGT 617
Db 864 GTTTATTGATGCTTTCCTGGAACAAAGATCCATCATTTTCGTCTACAGCAAAAGAACTTCT 923

Qy 618 GAAA 621
Db 924 GAAA 927
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RESULT 15
US-09-291-417-1
; Sequence 1, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291.417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Mammalian (Human) STUK2
US-09-291-417-1

Query Match 7.6%; Score 52; DB 11; Length 3268;
Best Local Similarity 48.8%; Pred. No. 1.3e-05;
Matches 207; Conservative 0; Mismatches 205; Indels 12; Gaps 2;

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Qy 204 TCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGGAGCTGAAACCCAAACTTACT 263
Db 574 TCTGGACTATCTGCATTTCAGAAAAAGAAAATTCACCGAGACATAAAAGCTGCCAATGCTT 633
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Qy 264 GCT-----GGTTTCAGGGGGGACAGTTCATAAAATTTTGATTTTGGTACAGCCTGTGA 317
Db 634 GCTCTCAGAACCAAGGAGATGTTAAACTTGTGATTTTGGAGTTGCTGCTCAGCTGACAGA 693

Qy 318 CATTTCAGACACACATGACCAATAACAAGGGGAGTGTCTGCTTGGATGCGACCTGAAGTTT 377
Db 694 TACACAGATTAAAGAAATACCTTTGTGGAACTCCATTTTGGATGGCTCTCTGAAGTTAT 753

Qy 378 TGAAGGTAGTAATTTACAGTGAATAATGTGACGTCTTCAGCTGGGGTATTTCTTTGGGA 437
Db 754 TCAACAGTCACTTATGACTCAAAAGAGCTGACATTTGGTTCATTTGGGAATTTACTGCTATTGA 813

Qy 438 AGTGATAACGGTTCGGAACCTTTTGATGAGATTGGTGGCCAGCTTTCGGAATCATGTG 497
Db 814 ACTAGCCAAAGGAGAGCCACTAACTCGATATGCATC-----CAATGAGAGTTCTGTT 867

Qy 498 GGCTGTTTCATAATGGTACTCGACCACTGATATAAAAAATTTACCTAAGCCCATTTGAGAG 557
Db 868 TCTTATCCCAAAACAATCTCCAACTCTTGTGGAGACTTTACTAAGTCTTTTAAGGA 927

Qy 558 CCTGATGACTCGTTTGTGTTAAAGATCCCTTCCAGCGCCCTTCAATGGAGGAAATGT 617
Db 928 GTTTATTGATGCTTTCCTGGAACAAAGATCCATCATTTTCGTCTACAGCAAAAGAACTTCT 987

Qy 618 GAAA 621
Db 988 GAAA 991
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Job time : 1022.11 secs

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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:33:11 ; Search time 70.8649 Seconds
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598.382 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELRLSRVNHPIVYKLYGA.....MTHLMRYFPGADEPQYPCQ 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1252	100.0	518	15	US-10-283-023-2	Sequence 2, Appli
2	1252	100.0	579	12	US-10-384-743-4	Sequence 4, Appli
3	1252	100.0	579	14	US-10-158-895-4	Sequence 4, Appli
4	1252	100.0	590	12	US-10-384-743-15	Sequence 15, Appl
5	1252	100.0	590	14	US-10-158-895-15	Sequence 15, Appl
6	371	29.6	349	15	US-10-106-698-6345	Sequence 6345, Ap
7	371	29.6	455	9	US-09-757-982-5	Sequence 5, Appli
8	371	29.6	455	12	US-10-094-749-2477	Sequence 2477, Ap
9	363.5	29.0	394	10	US-09-862-027-19	Sequence 19, Appl
10	355	28.4	1036	12	US-10-354-358-24	Sequence 24, Appl
11	355	28.4	1036	14	US-10-014-882-2	Sequence 2, Appli
12	353.5	28.2	746	15	US-10-153-668-436	Sequence 436, App
13	353.5	28.2	859	15	US-10-153-668-324	Sequence 324, App
14	353.5	28.2	892	15	US-10-153-668-438	Sequence 438, App
15	349.5	27.9	1097	12	US-10-288-798-12	Sequence 12, Appl

16	346	27.6	328	10	US-09-862-027-18	Sequence 18, Appl
17	345.5	27.6	847	14	US-10-143-133-2	Sequence 2, Appli
18	341	27.2	252	12	US-09-976-782-41	Sequence 41, Appl
19	341	27.2	254	12	US-09-976-782-30	Sequence 30, Appl
20	341	27.2	256	12	US-09-863-776-41	Sequence 41, Appl
21	338.5	27.0	835	10	US-09-947-199-2	Sequence 2, Appli
22	335.5	26.8	835	10	US-09-947-199-8	Sequence 8, Appli
23	331.5	26.5	966	10	US-09-771-161A-197	Sequence 197, App
24	326.5	26.1	256	12	US-09-976-782-40	Sequence 40, Appl
25	326.5	26.1	257	12	US-09-976-782-29	Sequence 29, Appl
26	323	25.8	257	11	US-09-823-187-46	Sequence 46, Appl
27	323	25.8	257	12	US-09-863-776-42	Sequence 42, Appl
28	323	25.8	821	12	US-10-171-404A-48	Sequence 48, Appl
29	320	25.6	263	10	US-09-840-704-5	Sequence 5, Appli
30	313.5	25.0	850	10	US-09-904-389-2	Sequence 2, Appli
31	312	24.9	265	9	US-09-797-039-10	Sequence 10, Appl
32	312	24.9	265	12	US-10-170-789-10	Sequence 10, Appl
33	312	24.9	277	9	US-09-815-915-13	Sequence 13, Appl
34	312	24.9	277	10	US-09-882-166-4	Sequence 4, Appli
35	312	24.9	277	12	US-10-393-316-13	Sequence 13, Appl
36	312	24.9	277	12	US-10-170-789-17	Sequence 17, Appl
37	312	24.9	277	15	US-10-172-088-6	Sequence 6, Appli
38	312	24.9	278	9	US-09-797-039-13	Sequence 13, Appl
39	312	24.9	278	9	US-09-922-138-18	Sequence 18, Appl
40	312	24.9	278	9	US-09-922-138-27	Sequence 27, Appl
41	312	24.9	278	9	US-09-910-150-17	Sequence 17, Appl
42	312	24.9	278	9	US-09-910-150-31	Sequence 31, Appl
43	312	24.9	278	10	US-09-842-582-4	Sequence 4, Appli
44	312	24.9	278	10	US-09-934-406-4	Sequence 4, Appli
45	312	24.9	278	12	US-10-170-789-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-10-283-023-2
; Sequence 2, Application US/10283023
; PUBLICATION NO. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carrioll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
; FILE REFERENCE: MP101-239PIRM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-283-023-2

Query Match 100.0%; Score 1252; DB 15; Length 518;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VELRLSRVNHPIVYKLYGACLNIPVCLVMEYAEGLSLNVLHGAEPLPYTTAAHMSWCL	60
Db	76	VELRLSRVNHPIVYKLYGACLNIPVCLVMEYAEGLSLNVLHGAEPLPYTTAAHMSWCL	135
Qy	61	QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVLKCDGTACDIOHTMNNKGSAAW	120
Db	136	QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVLKCDGTACDIOHTMNNKGSAAW	195
Qy	121	MAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL	180
Db	196	MAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL	255

QY 181 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 228
Db 256 FKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 303

RESULT 2

US-10-384-743-4

; Sequence 4, Application US/10384743
; Publication No. US20030162228A1

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, KOICHIRO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/10/384,743

; CURRENT FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: US/09/529,279

; PRIOR FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 4

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-384-743-4

Query Match 100.0%; Score 1252; DB 12; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-112;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 60

Db 76 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 120

Db 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 195

QY 121 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180

Db 196 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 228

Db 256 FKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 303

RESULT 3

US-10-158-895-4

; Sequence 4, Application US/10158895
; Publication No. US20020155624A1

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, KOICHIRO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/10/158,895

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US/09/529,279

; PRIOR FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 4

; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

Query Match 100.0%; Score 1252; DB 14; Length 579;

Best Local Similarity 100.0%; Pred. No. 1.1e-112;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 60

Db 76 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 120

Db 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 195

QY 121 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180

Db 196 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 228

Db 256 FKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 303

RESULT 4

US-10-384-743-15

; Sequence 15, Application US/10384743
; Publication No. US20030162228A1

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, KOICHIRO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/10/384,743

; CURRENT FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: US/09/529,279

; PRIOR FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 15

; LENGTH: 590

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-384-743-15

Query Match

Best Local Similarity

Matches 228; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 60

Db 76 VELRQLSRVNHNPNIKLYGACLNPNVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 120

Db 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQTHTMNNKGSAAW 195

QY 121 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180

Db 196 MAPEVFEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 228

Db 256 FKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFFGADPELOYPCQ 303

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RESULT 5
US-10-158-895-15
; Sequence 15, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Query Match      100.0%; Score 1252; DB 14; Length 590;
Best Local Similarity 100.0%; Pred. No. 1.1e-112;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRLSRVNHPIVVKLYGACLNPPVCLVMEYAEAGSLYNNVLHGAEPLPYTTAAHAMSWCL 60
DB 76 VELRLSRVNHPIVVKLYGACLNPPVCLVMEYAEAGSLYNNVLHGAEPLPYTTAAHAMSWCL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKSAAW 195
QY 121 MAPEVFEGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFEGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 KPPIESLMTRCWSKDPSPORPSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 228
DB 256 KPPIESLMTRCWSKDPSPORPSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 303

RESULT 6
US-10-106-698-6345
; Sequence 6345, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6345
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (340)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-10-106-698-6345

Query Match      29.6%; Score 371; DB 15; Length 349;
Best Local Similarity 37.7%; Pred. No. 1e-27;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRQLSRVNHPIVVKLYGACLNPPVCLVMEYAEAGSLYNNVLHGAEPLPYTTAAHAMSW 57
DB 109 EABLISVLSHRNIIQFYGVILEPPNYGIVTEVASIGSLYDYNRSRSEM---DMDHMT 165
QY 58 WCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
DB 166 WATDVAKGMHYLHMEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 223
QY 116 GSAAMAPVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMW-AVHNGTRP 174
DB 224 GTFPWMAPEVIQSLPVSCTCDTYSYGVVLWEMLTREVFPKGLEG--LQVAVLWVEKNERL 281
QY 175 PLIKNLKPPIESLMTRCWSKDPSPORPSMEEIVKIM 209
DB 282 TIPSSCPRSPAEHLHQWEADAKKRPSPKQIISIL 316

RESULT 7
US-09-757-982-5
; Sequence 5, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-982-5

Query Match      29.6%; Score 371; DB 9; Length 455;
Best Local Similarity 37.7%; Pred. No. 1.4e-27;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRQLSRVNHPIVVKLYGACLNPPVCLVMEYAEAGSLYNNVLHGAEPLPYTTAAHAMSW 57
DB 53 EABLISVLSHRNIIQFYGVILEPPNYGIVTEVASIGSLYDYNRSRSEM---DMDHMT 109
QY 58 WCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
DB 110 WATDVAKGMHYLHMEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
QY 116 GSAAMAPVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMW-AVHNGTRP 174
DB 168 GTFPWMAPEVIQSLPVSCTCDTYSYGVVLWEMLTREVFPKGLEG--LQVAVLWVEKNERL 225
QY 175 PLIKNLKPPIESLMTRCWSKDPSPORPSMEEIVKIM 209
DB 226 TIPSSCPRSPAEHLHQWEADAKKRPSPKQIISIL 260

RESULT 8
US-10-094-749-2477
; Sequence 2477, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
```

APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAWAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAGHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/09/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2477
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2477

Query Match 29.6%; Score 371; DB 12; Length 455;
Best Local Similarity 37.7%; Pred. No. 1.4e-27;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;
Qy 2 ELRQLSRVNHPIVVKLYGACINP--VCLVMEYABGSSLYNVHLHG--AEPLPYTAAHAMS 57
Db 53 EAEILSVLSHRNLIQFVGVILEPPNYGIVTEYASLSGLDYDINSRSEEM--DMDHMT 109
Qy 58 WLCQSGVAYLHSMQPKALIHRLDKPNNLLVAGGVVVKICDPTGACDQTHMNNK-- 115
Db 110 WATDVAKGMHYLHMEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy 116 GSAAWMAPEVFGSNYSKCDVFSWGLILWEVITRRKPEDEIGGPAFRIMV-AVHNGTRP 174
Db 168 GTFPWWMAPEVLIQSPVSETCDTYSYGVVLWEMLTREVFPFKGLEG--LQVAMLVVEKNRL 225
Qy 175 PLIKNLKPIESLMTRCWSKDPSPQSPSMEETVKIM 209
Db 226 TIPSSCPSPFAELLHQWEADAKKRPSPFKQIISIL 260

RESULT 9
US-09-862-027-19
Sequence 19, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
US-09-862-027-19

Query Match 29.0%; Score 363.5; DB 10; Length 394;
Best Local Similarity 37.7%; Pred. No. 6.5e-27;

Matches 83; Conservative 36; Mismatches 84; Indels 17; Gaps 6;
Qy 2 ELRQLSRVNHPIVVKLYGACINP--VCLVMEYABGSSLYNVHLHGAEPLPYTAAHAMS 59
Db 50 EAKLFAMLKHPNIIALRGVCLKEPNLCLVMEFARGGPNRVLSGRIPPD--LVNWA 105
Qy 60 LQCSQGVAYLHSMQPKALIHRLDKPNNLLV-----AGTVLKIODEGTACD-IQTHM 111
Db 106 VQIARGMNYLHDEAIVPIIHRDLKSSNIILOKVENGDLNSKILKITDFGLARBWHRTK 165
Qy 112 TNKGSAAWMAPEVFGSNYSKCDVFSWGLILWEVITRRKPEDEIGGPAFRIMVAV-HN 170
Db 166 MSAAGTYANWMAPEVIRASMEKSGSDVWSYGVLLWELLTGEVFPFGIDG--LRVAYGVAMN 223
Qy 171 GTRPPLIKNLKPIESLMTRCWSKDPSPQSPSMEETVKIM 210
Db 224 KLALPIPTCTPEPEFAKLMECDWNPDPHSPFSFTNILDQLT 263

RESULT 10

US-10-354-358-24
Sequence 24, Application US/10354358
Publication No. US20030157082A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Hunter, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REFERENCE: MP102-020PIRNONMIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 1036
TYPE: PRT
ORGANISM: Homo sapiens
US-10-354-358-24

Query Match 28.4%; Score 355; DB 12; Length 1036;


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; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-324

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QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTGVLKICDFGTACDIQTHMTNKK--GS 117
Db 218 MGIAGGMNLYLHLK---IIHRDLKSPN-MLITYDDVVVKISDFGTSKELSDKSTKWSFAGT 273
QY 118 AAWMAPEVFGSNYSEKCDVFSWGIILWEVITRKKPDEIGGPAFRIMWAV--HNGTRPPL 176
Db 274 VAWMAPEVIRNEPVSEKVDIWSFGVLWELLTGIPYKVDSSA--IILHL 364
QY 177 IKNLKPKIESLMTRCWSKDPSPRSMEEIVKIMTHL 212
Db 332 PSSCPDGFKILLRQCNWSKPRNRPFRQ---IILHL 364

RESULT 14
US-10-153-668-438
; Sequence 438, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STATs Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-438

Query Match      28.2%; Score 353.5; DB 15; Length 892;
Best Local Similarity 34.7%; Pred. No. 1.6e-25;
Matches 75; Conservative 43; Mismatches 81; Indels 17; Gaps 8;

QY 2 ELRLSRVNHNPNIKLYGACLNIP--VCLWMEYABGGSLYNVLHGAELPYYTAHAHMSWC 59
Db 194 DIKHLRLKHPNIITFGVCTQAPCYCILMEFCAGQQLYEVLRAGRPV---TPSLLYDWS 250
QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTGVLKICDFGTACDIQTHMTNKK--GS 117
Db 251 MGIAGGMNLYLHLK---IIHRDLKSPN-MLITYDDVVVKISDFGTSKELSDKSTKWSFAGT 306
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QY 118 AAWMAPEVFGSNYSEKCDVFSWGIILWEVITRKKPDEIGGPAFRIMWAV--HNGTRPPL 176
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QY 177 IKNLKPKIESLMTRCWSKDPSPRSMEEIVKIMTHL 212
Db 365 PSSCPDGFKILLRQCNWSKPRNRPFRQ---IILHL 397

RESULT 15
US-10-288-798-12
; Sequence 12, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B.;
; APPLICANT: WALIA, Narinder K.; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameeta R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Valda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 1097
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 55052990CD1
US-10-288-798-12

Query Match      27.9%; Score 349.5; DB 12; Length 1097;
Best Local Similarity 37.4%; Pred. No. 5e-25;
Matches 82; Conservative 35; Mismatches 87; Indels 15; Gaps 5;

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Db 191 EAKLFAMLKHPNIITALRGVCLKEPNLCVMEFARGGPNLRLSGKRIPDDI---LVNWA 246
QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLV-----AGTVLKI CDFGTACD-IOTHM 111
Db 247 VQIARGMNYLLDEAIVPIIHRDLKSNLILQKVENGDLSNLIKILITDFGLAREWHRTTK 306
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:28:31 ; Search time 29.2703 Seconds
(without alignments)
329.579 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELQLSRVNHNPVLYGALG.....MTHLMRYFPGADEPLQYPCQ 228

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1252	100.0	579	4	US-10-158-895-4
3	1252	100.0	590	4	US-09-529-279-15
4	1252	100.0	590	4	US-10-158-895-15
5	371	29.6	455	3	US-09-221-233-5
6	371	29.6	455	3	US-09-221-928-5
7	371	29.6	455	3	US-09-221-527-5
8	371	29.6	455	3	US-09-221-236-5
9	371	29.6	455	3	US-09-221-416-5
10	371	29.6	455	3	US-09-221-245-5
11	371	29.6	455	3	US-09-163-115-5
12	371	29.6	455	3	US-09-221-528-5
13	371	29.6	455	3	US-09-593-553-5
14	371	29.6	455	3	US-09-221-237-5
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17	353.5	28.2	668	1	US-08-205-018-2
18	353.5	28.2	859	1	US-08-395-580-2
19	353.5	28.2	859	5	PCT-US95-02792-2
20	346	27.6	328	4	US-09-345-473E-18
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22	338.5	27.0	835	4	US-09-458-457-2
23	335.5	26.8	835	4	US-09-458-457-8
24	323	25.8	821	1	US-07-928-464-2
25	323	25.8	821	1	US-08-003-311B-2
26	323	25.8	821	1	US-08-261-432-2
27	323	25.8	821	5	PCT-US93-07347-2

28	320	25.6	263	3	US-09-035-706-5	Sequence 5, Appli
29	320	25.6	263	3	US-08-955-841-5	Sequence 5, Appli
30	320	25.6	263	4	US-09-390-425-5	Sequence 5, Appli
31	320	25.6	263	4	US-09-566-906-5	Sequence 5, Appli
32	309.5	24.7	269	2	US-07-857-224B-79	Sequence 79, Appl
33	307.5	24.6	276	2	US-07-857-224B-72	Sequence 72, Appl
34	306	24.4	275	2	US-07-857-224B-71	Sequence 71, Appl
35	305.5	24.4	590	4	US-09-312-283C-409	Sequence 409, App
36	305.5	24.4	786	4	US-09-503-802-2	Sequence 2, Appli
37	305.5	24.4	787	3	US-09-188-930-334	Sequence 334, App
38	305.5	24.4	787	4	US-09-312-283C-334	Sequence 334, App
39	304.5	24.3	304	2	US-08-701-191A-27	Sequence 27, Appl
40	302.5	24.2	316	1	US-08-278-089A-16	Sequence 16, Appl
41	302.5	24.2	316	2	US-08-838-957A-15	Sequence 15, Appl
42	299.5	23.9	527	4	US-08-428-509A-10	Sequence 10, Appl
43	299.5	23.9	527	4	US-08-232-545-10	Sequence 10, Appl
44	299.5	23.9	527	5	PCT-US95-05008-10	Sequence 10, Appl
45	299.5	23.9	625	1	US-08-391-615-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-529-279-4
; Sequence 4, Application US/09529279

; Patent No. 6451617

; GENERAL INFORMATION:

; APPLICANT: ONO, KOICHIRO

; APPLICANT: OHTOMO, TOSHIHIKO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/09/529, 279

; CURRENT FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-529-279-4

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Best Local Similarity 100.0%; Pred. No. 4e-133;

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DB 76 VELQLSRVNHNPVLYGACINPVCLVMEYAEAGSLYNVLHGABPLPYTTAAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALTHRDLPENLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120

DB 136 QCSQGVAYLHSMQPKALTHRDLPENLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 195

QY 121 MAPEVFGSNVSEKCDVFSWGIILWEVITRRKPFDEIGGPAPRIMWAVHNGTRPPLKNL 180

DB 196 MAPEVFGSNVSEKCDVFSWGIILWEVITRRKPFDEIGGPAPRIMWAVHNGTRPPLKNL 255

QY 181 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFPGADEPLQYPCQ 228

DB 256 PKPIESLMTRCWSKDPQSRPSMEEIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 2

US-10-158-895-4

; Sequence 4, Application US/10158895

; Patent No. 6551840

; GENERAL INFORMATION:

; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

Query Match 100.0%; Score 1252; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 4e-133;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTNNKGSAAW 195
Qy 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 180
Db 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 255
Qy 181 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 228
Db 256 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 303

RESULT 3
US-09-529-279-15
; Sequence 15, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-15

Query Match 100.0%; Score 1252; DB 4; Length 590;
Best Local Similarity 100.0%; Pred. No. 4.1e-133;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTNNKGSAAW 120
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Db 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 255
Qy 181 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 228
Db 256 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 303

RESULT 4

US-10-158-895-15
; Sequence 15, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Query Match 100.0%; Score 1252; DB 4; Length 590;
Best Local Similarity 100.0%; Pred. No. 4.1e-133;
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Qy 1 VELQLSRVNHNPVTKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPPLPYTAAHANGWCL 60
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Qy 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTNNKGSAAW 120
Db 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTNNKGSAAW 195
Qy 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 180
Db 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 255
Qy 181 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 228
Db 256 PKPIESLMTRCWSKDPQRSMEIEIVKIMTHLMRYFFGADEPLOYPCQ 303

RESULT 5

US-09-221-235-5
; Sequence 5, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: WNI-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:


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QY 175 PLIKNLKPYESLMTRCWSKDPSPORPSMEEIVKIM 209
Db 226 TIPSSCRPSFAELLHQWEADAKKRPSPFKQIISIL 260

RESULT 9
US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5

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Best Local Similarity 37.7%; Pred. No. 1.7e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

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QY 175 PLIKNLKPYESLMTRCWSKDPSPORPSMEEIVKIM 209
Db 226 TIPSSCRPSFAELLHQWEADAKKRPSPFKQIISIL 260

RESULT 10
US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-245-5

Query Match 29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 1.7e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

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US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-115-5

Query Match 29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 1.7e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRQLSRVNHNPVIVKLYGACINP--VCLVMEYAEAGGSLYVNLHG--AEPLPYTAAHAMS 57
Db 53 EAEILSVLSHRNIIQFYGVILEPNNYIGVTEYASLSGLYDINSNRSEEM---DMDHMT 109
QY 58 WCLQCSOGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNK-- 115
Db 110 WATDVAKGMHYLHWEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRPHNHTTHMSLV 167
QY 116 GSAAWMAPEVFEKGSNYSEKCDVFSWGLLMEVITRRKPFDEIGGPAFRIMW-AVHNGTRP 174
Db 168 GTFPMAPEVIQSLPVSETCDTYSYGVVLMELTREVFPFKGLEG--LQVAWLVVVEKNERL 225
QY 175 PLIKNLKPYESLMTRCWSKDPSPORPSMEEIVKIM 209
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RESULT 12
US-09-221-528-5
; Sequence 5, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-528-5
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QY 58 WCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDGTACDIQTHMTNKK-- 115
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QY 116 GSAAMMAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMW-AVHNGTRP 174
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; Sequence 5, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-553-5

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Best Local Similarity 37.7%; Pred. No. 1.7e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

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US-09-221-237-5
; Sequence 5, Application US/09221237
; Patent No. 6214597
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,237
; CURRENT FILING DATE: 1998-12-28
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; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
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; ORGANISM: Homo sapiens
US-09-221-237-5

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US-09-399-588-2
; Sequence 2, Application US/09399588
; Patent No. 6511825
; GENERAL INFORMATION:
; APPLICANT: Ruggieri, Rosamaria
; APPLICANT: Callow, Marinella
; APPLICANT: Diaz, Paul W.
; TITLE OF INVENTION: No. 6511825el Cell Signaling Polypeptides and Nucleic Acids
; FILE REFERENCE: 1044-US
; CURRENT APPLICATION NUMBER: US/09/399,588
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: 60/104,088
; EARLIER FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Human J42
US-09-399-588-2

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Best Local Similarity 37.7%; Pred. No. 1.7e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

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us-09-830-144-2 copy_76_303.ra1

Page 6

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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 4403344

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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3	1252	100.0	1788	12 US-10-384-743-14	Sequence 14, Appli
4	1252	100.0	1788	13 US-10-158-895-14	Sequence 14, Appli
5	1252	100.0	2656	12 US-10-384-743-3	Sequence 3, Appli
6	1252	100.0	2656	13 US-10-158-895-3	Sequence 3, Appli
7	392.5	31.3	3435	12 US-10-210-120-86	Sequence 86, Appli
8	392.5	31.3	3454	10 US-09-969-347-226	Sequence 226, App
9	392.5	31.3	3454	14 US-10-171-581-312	Sequence 312, App
10	371	29.6	1063	14 US-10-106-698-2068	Sequence 2068, Ap
11	371	29.6	1365	9 US-09-757-982-6	Sequence 6, Appli
12	371	29.6	2120	9 US-09-757-982-4	Sequence 838, App
13	371	29.6	2251	12 US-10-094-749-838	Sequence 36, Appli
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15	355	28.4	3111	13 US-10-014-882-1	Sequence 23, Appli
16	355	28.4	3518	13 US-10-014-882-3	Sequence 3, Appli
17	355	28.4	5549	12 US-10-354-358-23	Sequence 23, Appli
18	353.5	28.2	2440	14 US-10-153-668-435	Sequence 435, App
19	353.5	28.2	3365	14 US-10-153-668-323	Sequence 323, App
20	353.5	28.2	3428	14 US-10-153-668-437	Sequence 437, App
21	353.5	28.2	3761	12 US-09-814-353-20138	Sequence 20138, A
22	353.5	28.2	6378	12 US-10-252-157-482	Sequence 482, App
23	347	27.7	1428	10 US-09-938-842A-882	Sequence 882, App
24	345.5	27.6	1662	10 US-09-938-842A-1014	Sequence 1014, Ap
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29	335.5	26.8	3026	10 US-09-947-199-7	Sequence 7, Appli
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31	328.5	26.2	2211	10 US-09-938-842A-1577	Sequence 1577, Ap
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33	313.5	25.0	3286	10 US-09-904-389-1	Sequence 1, Appli
34	305.5	24.4	1774	11 US-09-866-050A-403	Sequence 403, App
35	305.5	24.4	1774	12 US-10-152-661-403	Sequence 403, App
36	305.5	24.4	2361	12 US-10-128-174-11	Sequence 11, Appli
37	305.5	24.4	2370	14 US-10-164-080-1	Sequence 1, Appli
38	305.5	24.4	2370	14 US-10-298-327-1	Sequence 1, Appli
39	305.5	24.4	3516	11 US-09-866-050A-257	Sequence 257, App
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43	304.5	24.3	5355	12 US-09-971-392-67	Sequence 67, Appli
44	304.5	24.3	5615	12 US-10-241-220-18	Sequence 18, Appli
45	304.5	24.1	3650	12 US-10-366-288-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-10-283-023-1
; Sequence 1, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Caroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
; FILE REFERENCE: MPI01-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283, 023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335, 044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-283-023-1

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Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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RESULT 2
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; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; diagnosis and treatment of hematological disorders using
; FILE REFERENCE: MPI01-239FIRM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1705
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1557)
US-10-283-023-3

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Db 526 TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTGG 585
Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 586 ATGGCACCCTGAAGTTTTTGAAGGTAGTAATTCACAGTGAATAATGTGACGCTTCAGCTGG 645
Qy 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db 646 GGTATTATCTTTGGGAGTGCATACGCTGCGAAACCCCTTTGATGAGATTGGTGGCCCA 705
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 706 GCCTTCCGAATCATGTGGCTGTTCAATAATGATGACTCATTGATGCGGTACTTTCAGAGGACAGAT 765
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerClnArgPro 200
Db 766 CCTAAGCCCATGTAGAGCCTGATGACTGTTGGTCTAAGATCCTTCCAGCGCCCT 825
Qy 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 826 TCAATGAGGAAATTTGTGAAATAATGACTCACTTGTATGCGGTACTTTCAGAGGACAGAT 885
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 886 GAGCCATTACAGTATCTTGTGCAG 909

RESULT 3
US-10-384-743-14
; Sequence 14, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
```



```
QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
DB GTAGAGCTTCGGCAGTTATCCGCTGGAACCATCTATATTTGTAAGCTTTATGAGCC 467
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
DB TGCCTTGAATCCAGTCTGCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATGTG 527
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
DB CTGCATGTGCTGGAACCATTTGCAATATATCTGCTGCCACGCAATGAGTTGGTGTTA 587
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
DB CAGTGTTCCTCCAGAGTAGTGGCTTATCTTACAGCATGCAACCCAAAGCGCTAATTCACAGG 647
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
DB GACCTGAAACACCACCAAACTTACTGCTGTTGTCAGGGGGACAGTTCTAAAAATTTGTGAT 707
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
DB TTTGTATACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGCTGCTTGG 767
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
DB ATGGCACCTGAAGTTTTTTGAGGTAGTAAATTACAGTGAAATGTGACGTCTTCAGCTGG 827
QY 141 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
DB GGTATATATCTTTGGGAAGTGATAACGGCTCGGAAACCTTTGATGAGATTGGTGGCCCA 887
QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleHisAsnLeu 180
DB GCTTTCGAAATCATGTGGCTGTTTCAATATGTACTCGACCACTCATGAAATAATTTA 947
QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
DB CCTAAGCCCATTTGAGAGCTGATGACTGTTGTTGGTCTTAAGATCCTTCCAGCGCCCT 1007
QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
DB TCAATGGAGGAAATGTTGAAATAATGACTCACTTGATGGGTACTTTCCAGGACAGAT 1067
QY 221 GluProLeuGlnTyrProCysGln 228
DB GAGCCATTACAGTATCTTGTGAC 1091
```

```
RESULT 7
US-10-210-120-86
; Sequence 86, Application US/10210120
; Publication No. US2003017536A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Sreekumar, Arun
; APPLICANT: Rubin, Mark A.
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-86
Alignment Scores:
```

```
Pred. No.: 9,11e-40 Length: 3435
Score: 292.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
DB: 12 Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-210-120-86 (1-3435)

QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
DB GAAGCCCGCTCTTTGGAGCCCTGCGAGCACCCCACTAATTCCTTTAGGGCGCCCTG 780
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
DB CTCAACCCCCACACCTCTGCTAGTGTGAGTATGCCCGGGTGTGCACTGAGCAGG 840
QY 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
DB GTGCTGGCAGGTGCGCGGTGCCACCTCAGTG-----CTGCTCACTGGGCT 888
QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
DB GTGAGGTGGCGCGGGCATGAACCTACCTACACATGATGCCCTGTGCCCATCATCCAC 948
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
DB CGGACCTCAAGTCCATCAACATCTGATCTCTGGAGGCCATCGAGAACCAACCTCGCA 1008
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
DB GACAGGTGCTCAAGATCACGAGCTTCGSCCTCGCCCGGAGTGCACAAAGACACCAG 1068
QY 112 ThrAsnAsnLysGlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyr 131
DB ATGAGCGCTGCGGGGACCTACGCTGATGCGCGGAGGTATCCGCTCTCTCCCTCTTC 1128
QY 132 SerGluLysCysAspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArg 151
DB TCCAAAAGCAGTGTGCTGAGGCTTCGGGTGCTGTGTGGAGCTCTGACGCGGGGAG 1188
QY 152 LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
DB GTCCCTTACCTGAGATC-----GACGCTTGGCCCGGTGCGGTATGCGCTATGAT 1242
QY 171 GlyThrArgProProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArg 190
DB AAGCTGACGCTGCCATTCCTCCAGCGTCCCGAGCCCTTTGCCGCTCTCTGGAGGAA 1302
QY 191 CysTrpSerLysAspProSerGlnArgProSerMetGluGluIleValLys 207
DB TGCTGGGACCCAGACCCCGGCGCCAGATTTCGGTATGATCTTTGAAG 1353
```

```
RESULT 8
US-09-969-347-226
; Sequence 226, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: Sets
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 226
; LENGTH: 3454
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-969-347-226

Alignment Scores:
Pred. No.: 9,18e-40 Length: 3454
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
DB: 14 Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-09-969-347-226 (1-3454)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 721 GAAGCCCGGCTCTTTGGAGCCCTGCAGACCCCAACATAATTCCTTAGGGGCGCTGC 780
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 781 CTCACCCCCACACACCTCTGCTAGTAGTGCACCTCAGCTG-----CTGGTCAACTGGCT 840
QY 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db 841 GTGCTGCAGGTGCGCGGGTGCACCTCAGCTG-----CTGGTCAACTGGCT 888
QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
Db 889 GTGAGGTGCGCGGGCATGAACCTACCTACAAATGATGCCCTGTGCCCATCATCCAC 948
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
Db 949 CGGGACCTCAAGTCCATCACTCTGATCTGGAGGCCATCGAGAACCAACCTCGCA 1008
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp----IleGlnThrHisMet 111
Db 1009 GACACGGTGTCTAAGATCAGGACTTCGGCTCGCGCGAGTGGCACAAGACCAACCAAG 1068
QY 112 ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyr 131
Db 1129 TCACAAAGCAGTGTCTGAGGCTTCGGGGTGTCTGTGGAGCTGTACGCGGGGAG 1188
QY 152 LysProPheAspGluIleGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
Db 1189 GTCCCTTACCGTGAGATC-----GACGCTTGGCGGTGCGGTATGCGGTATGAAAT 1242
QY 171 GlyThrArgProProLeuLysAsnLeuProLysProLysProLysProLysProLys 190
Db 1243 AAGTGACGTGGCCATTCCTCCACGTGCCCGGAGCCCTTTGGCCGCCCTCTCGAGGAA 1302
QY 191 CysTrpSerLysAspProSerGlnArgProSerMetGluGluIleValLys 207
Db 1303 TGCTGGGACCCAGACCCCGCGGCGCCAGATTTCGTAGCATCTTGAAG 1353

RESULT 10
US-10-106-698-2068/c
; Sequence 2068, Application US/10106698
; Publication No. US2003010960A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
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; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X90846
; DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-312

Alignment Scores:
Pred. No.: 9,18e-40 Length: 3454
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
DB: 14 Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-171-581-312 (1-3454)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 721 GAAGCCCGGCTCTTTGGAGCCCTGCAGACCCCAACATAATTCCTTAGGGGCGCTGC 780
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 781 CTCACCCCCACACACCTCTGCTAGTAGTGCAGCTG-----CTGGTCAACTGGCT 840
QY 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db 841 GTGCTGCAGGTGCGCGGGTGCACCTCAGCTG-----CTGGTCAACTGGCT 888
QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
Db 889 GTGAGGTGCGCGGGCATGAACCTACCTACAAATGATGCCCTGTGCCCATCATCCAC 948
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
Db 949 CGGGACCTCAAGTCCATCACTCTGATCTGGAGGCCATCGAGAACCAACCTCGCA 1008
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp----IleGlnThrHisMet 111
Db 1009 GACACGGTGTCTAAGATCAGGACTTCGGCTCGCGCGAGTGGCACAAGACCAACCAAG 1068
QY 112 ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyr 131
Db 1069 ATGAGCGCTCGGGGACCTACGCTGATGCGCGCGAGTATCCGCTCTCTCCCTCTTC 1128
QY 132 SerGluLysCysAspValPheSerTrpGlyIleLeuLeuTrpGluValIleThrArgArg 151
Db 1129 TCACAAAGCAGTGTCTGAGGCTTCGGGGTGTCTGTGGAGCTGTACGCGGGGAG 1188
QY 152 LysProPheAspGluIleGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
Db 1189 GTCCCTTACCGTGAGATC-----GACGCTTGGCGGTGCGGTATGCGGTATGAAAT 1242
QY 171 GlyThrArgProProLeuLysAsnLeuProLysProLysProLysProLysProLys 190
Db 1243 AAGTGACGTGGCCATTCCTCCACGTGCCCGGAGCCCTTTGGCCGCCCTCTCGAGGAA 1302
QY 191 CysTrpSerLysAspProSerGlnArgProSerMetGluGluIleValLys 207
Db 1303 TGCTGGGACCCAGACCCCGCGGCGCCAGATTTCGTAGCATCTTGAAG 1353

RESULT 10
US-10-106-698-2068/c
; Sequence 2068, Application US/10106698
; Publication No. US2003010960A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
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; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-11-03
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2068
; LENGTH: 1063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-2068

Alignment Scores:
Pred. No.: 1,03e-37 Length: 1063
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservativeness: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 14 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-10-106-698-2068 (1-1063)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnHisValLysLeuTyrGlyAlaCys 21
DB 737 GAGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 678

QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
DB 677 CTTGAACCTCCCAACTATGGCATTGTACAGAAATATGCTTCTCTGGGATCACTCTATGAT 618

QY 40 ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
DB 617 TACATTAAACAGTAACAGAAAGTGGAGAGATG-----GATATGGATCACTATATGACC 567

QY 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
DB 566 TGGCCACTGATGTAGCCAGGAAGTATGATTATACATATGGAGGCTCCTGTCAAGGTG 507

QY 78 IleHisArgAspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
DB 506 ATTCACAGAGACCTCAAGTCAAGAAACGTTGTATAGCTGCTGATGGA---GTATTGAAG 450

QY 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLys-----115
DB 449 ATCTGTGACTTTGGT---GCCTCTCGGTTCCATACCAACATACACACACATGCTCTTGGTT 393

QY 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
DB 392 GGAACCTTCCCATGGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGTCAAGAACTTGT 333

QY 136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
DB 332 GACACATATTCCTATGTGTGTGTCTCTGGGAGATGCTAAACAAGGAGGCTCCCTTTTAAA 273

QY 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
DB 272 GGTITGGAAGA-----TTACAAGTAGCTTGGCTTGTAGTGGAAAAAAGCAGAGATTA 219

QY 175 ProLeuLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
DB 218 ACCATTCAACAGAGTTGCCAGAAAGTTTGTCTGACTGTTTACATCAGTGTGGAGACT 159

QY 195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
DB 158 GATGCCAAGAAAGCGCCCATCATTTCAAGCAAAATCATTTCAATCTTG 114

RESULT 11
US-09-757-982-6
; Sequence 6, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
```

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; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)..(1411)
US-09-757-982-4

Alignment Scores:
Pred. No.: 2,73e-37 Length: 2120
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 9 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-757-982-4 (1-2120)

Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 203 GAGCAGAAATACCTCAGTCCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 262
Qy 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 263 CTGGAACCTCCCAACTAGTGCATTGTCACAGAAATATGCTCTCTGGGATCCTATGAT 322
Qy 40 ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
Db 323 TACATTAAACAGTAAACAGAGTGGAGAGATG-----GATATGGATCATTATGACC 373
Qy 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
Db 374 TGGCCCACTGATGTAGCCAAAGAGTAATGATTATATATGAGGCTCCTGTCAAGGTG 433
Qy 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
Db 434 ATTCACAGACCTCAAGTCAAGAAACGTTGTTATAGTCTGCTGATGGA---GTACTGAAG 490
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db 491 ATCTGTGACTTTGTT---GGCTCTCGGTTTCCATAACCATACACACACATGCTCCTGTT 547
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
Db 548 GGAACCTTCCCATGGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGTGTCAGAAACTGT 607
Qy 136 AspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db 608 GACACATATCTTCTATGTTGGTTCTCTGGAGATGCTAAACAGGAGGTCCTCCCTTTAA 667
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db 668 GGTTTGAAGA---TTTCAAGTACTTGGCTTGTAGTGGAAAAAACAAGACGAGATTA 721
Qy 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db 722 ACCATTCCACAGCAGTTGCCCCAGAGTTTCTGCTGAACCTGTTTACATCAGTGTGG 781
Qy 195 AspProSerGlnArgProSerMetGluIleValLysIleMet 209
Db 195 AspProSerGlnArgProSerMetGluIleValLysIleMet 209
```

Db 782 GATGCCAAGAAACGGCCATCATTTCAAGAAATCATTTCAATCTCTG 826

RESULT 13

```
US-10-094-749-838
; Sequence 838, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 2251
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-838

Alignment Scores:
Pred. No.: 2,98e-37 Length: 2251
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 12 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-10-094-749-838 (1-2251)

Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 358 GAGCAGAAATACCTCAGTCCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 417
Qy 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 418 CTGGAACCTCCCAACTAGTGCATTGTCACAGAAATATGCTCTCTGGGATCCTATGAT 477
Qy 40 ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
Db 478 TACATTAAACAGTAAACAGAGTGGAGAGATG-----GATATGGATCATTATGACC 528
Qy 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
Db 529 TGGCCCACTGATGTAGCCAAAGGAATGCAATTATTTACATATGGAGGCTCCTGTCAAGGTG 588
Qy 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
Db 589 ATTCACAGACCTCAAGTCAAGAAACGTTGTTATAGTCTGCTGATGGA---GTATTGAAG 645
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
```

Db 646 ATCTGTGACTTTGGT---GCCTCTGGTTCCATAACCAACACACATGCTTGGTT 702
QY 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
Db 703 GGAATCTTCCCATGATGGCTCCAGAGTATCCAGAGTCTCCCTGTGTGCAAGAACTTGT 762
QY 136 AspValPheSerTrpGlyLeuLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db 763 GACACATATCTCTATGTTGGTTCTCTGGGAGATGCTAACAGAGGAGGAGTCCCTTTAAA 822
QY 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db 823 GGTTTGGAGGA-----TTCAAGTAGCTTGGCTTGTAGTGGAAAAAAGAGAGATTA 876
QY 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db 877 ACCATCCAGAGTGGCCCAAGAGTTTGTCTGAACTGTTTACATCAGTGTGGGAAGCT 936
QY 195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db 937 GATGCCAAGAACGCCCATCATTCACGCAAAATCATTTCAATCTGT 981

RESULT 14

US-10-288-798-36
; Sequence 36, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Dannel B;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandira; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Valda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Prseti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 3538
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 55052990CB1
US-10-288-798-36

Alignment Scores:

Pred. No.: 9-48e-36 Length: 3538
Score: 361.50 Matches: 86
Percent Similarity: 55.45% Conservative: 36
Best Local Similarity: 39.09% Mismatches: 82
Query Match: 28.87% Indels: 17
DB: 12 Gaps: 5
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Db 571 GAGGCCAAGCTCTTCGCCATGCTGAGCACCACCATCATCTGCCCTAAGAGGGGTATGT 630
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsn 39
Db 631 CTGAAGAGGAGCCCAACCTCTGCTTGGTCATGGAGTTTGTCTGGTGGAGGACCTTTGAATAGA 690
QY 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db 691 GTGTTATCTGGGAAAAGGATTCCTCCCAACATC-----CTGGTGAATTTGGGCT 738
QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
Db 739 GTGCAGATTGCCAGAGGATGNACTTACTTGTATGAGGCAATTTGTTCCCATCATCCAC 798
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
Db 799 CGCGACCTTAAGTCCAGCAACATATTGATCTCCAGAAAGTGGAGATGGAGACCTGAGC 858
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
Db 859 AACAAAGATTCGAAGATCACTGATTTTGGCTGGCTCGGGAATGGCACCCAGACCAAG 918
QY 112 ThrAsnAsnLysGlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyr 131
Db 919 ATGAGTGGCGGAGGACCTGCTGTGATGGACCCAGAGTCATCGGGGCCTCCATGTTT 978
QY 132 SerGluLysCysAspValPheSerTrpGlyLeuIleLeuTrpGluValIleThrArgArg 151
Db 979 TCCAAAGGCAGTGTGTGGAGCTATGGGTGCTACTTTGGAGTTGCTGACTGCTGAG 1038
QY 152 LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaValHisAsnGly 171
Db 1039 GTGCCCTTTTCAGGCATTGCTGCTTAGCAGT-CGC---TTATGGAGTGGCCATGAACAA 1094
QY 172 ThrArgPro-ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCys 191
Db 1095 ACTCGCCCTTCTCTATCTCTTACGTGCCAGAACCTTTTCCCAAACTCATGGAAGACTG 1154
QY 191 sTrpSerLysAspProSerGlnArgProSerMetGluLeuValLysIleMetThr 210
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RESULT 15

US-10-014-882-1
; Sequence 1, Application US/10014882
; Publication No. US20020107384A1
; GENERAL INFORMATION:
; APPLICANT: Kieke, James
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. US20020107384A1el Human Kinase and Polynucleotides Encoding ti
; FILE REFERENCE: LEX-0279-USA
; CURRENT APPLICATION NUMBER: US/10/014,882
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,744
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3111
; TYPE: DNA

ORGANISM: homo sapiens
US-10-014-882-1

Alignment Scores:
Pred. No.: 5,45e-35 Length: 3111
Score: 355.00 Matches: 83
Percent Similarity: 53.48% Conservative: 40
Best Local Similarity: 36.09% Mismatches: 85
Query Match: 28.35% Indels: 22
DB: 13 Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-014-882-1 (1-3111)

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Db      511 GAGGCTCGGCTCTTCGGCATGCTCGCGCACCCCAACATCATCAGCTGCGCGGTGTGC 570

QY      22  LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db      571 CTGACGAGCGGCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 630

QY      40  ValLeuHisGlyAlaGluProLeuProTyrTyrThrAla----- 52
Db      631 GCGTGGCGCTGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 690

QY      53  -----AlaHisAlaMet---SerTyrCysLeuGlnCysSerGlnGlyValAlaTyr 68
Db      691 CGCATCCCTCCGCGACGTGCTGCTCACTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 750

QY      69  LeuHisSerMetGlnProLysAlaLeuIleHisArgAspLeuLysProProAsnLeuLeu 88
Db      751 CTGATCAGGAGGCGCTTCTGCTGCCCATCTGTCGCCCGCGCGCGCGCGCGCGCGCGCGCG 810

QY      89  LeuValAlaGly-----GlyThrValLeuLysIleCysAspPhe 101
Db      811 CTACTTCAGAGATAGACATGATGACATCTGCAATAAACTTTGAAGATTACAGATTTT 870

QY      102 GlyThrAlaCysAsp---IleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
Db      871 GGGTTGGCGAGGAATGGCACAGACACCACCAAAATGACACAGCAGCAGCAGCAGCAGCAGC 930

QY      121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db      931 ATGCCCCCGAAGTATCAAGTCTTCTGTTTCTAAGGGAACGACATCTGGAGCTAT 990

QY      141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db      991 GGAGTGCTGCTGTGGAACTGCTCACCGGAGAAGTCCCTATCGGGCATTGATGGCTC 1050

QY      161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db      1051 GCCGTGGCTTATGGGGTAGCAGTCAATAAATCACTTTG---CCCATTCATCCACCTGC 1107

QY      181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db      1108 CCTGAGCGCTTGGCAAGCTCATGAAGAATGCTGGCAAGACCCCTCATATTCTGTCCA 1167

QY      201 SerMetGluGluIleValIysIleMetThr 210
Db      1168 TCGTTTGCCTTAATTCGAACAGTTGACT 1197

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Search completed: December 4, 2003, 14:31:32
Job time : 467.851 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:28:31 ; Search time 8.72973 Seconds
(without alignments)
329.579 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPRLTQSTWHTQSSSS.....AEFYRLMSVDHGQSVVTAP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	504	2	US-08-752-891-2
2	359	100.0	504	2	US-08-752-891-6
3	359	100.0	504	2	US-09-144-178-2
4	359	100.0	504	2	US-09-144-178-6
5	359	100.0	504	3	US-09-406-854-2
6	359	100.0	504	3	US-09-406-854-6
7	359	100.0	504	4	US-09-529-279-2
8	359	100.0	504	4	US-10-158-895-2
9	359	100.0	513	4	US-09-529-279-4
10	359	100.0	513	4	US-10-158-895-4
11	359	100.0	517	4	US-09-529-279-11
12	359	100.0	517	4	US-10-158-895-11
13	77	21.4	16	4	US-09-529-279-41
14	77	21.4	16	4	US-10-158-895-41
15	67.5	18.8	852	2	US-07-070-060-3
16	67.5	18.8	852	3	US-09-357-746-3
17	66	18.4	16	4	US-09-529-279-40
18	66	18.4	16	4	US-10-158-895-40
19	65	18.1	335	4	US-09-252-991A-24494
20	64.5	18.0	244	4	US-09-461-325-463
21	63.5	17.7	240	4	US-09-152-060-100
22	63.5	17.7	335	4	US-09-152-060-64
23	63.5	17.7	391	3	US-08-706-216-6
24	60.5	16.9	854	2	US-09-070-060-4
25	60.5	16.9	854	3	US-09-357-746-4
26	60	16.7	1037	4	US-09-428-711A-21
27	58.5	16.3	1093	3	US-08-545-860D-55

28 58.5 16.3 1093 5 PCT-US94-04496-55 Sequence 55, Appl
29 57.5 16.0 421 4 US-09-322-478-6 Sequence 6, Appl
30 57.5 16.0 701 4 US-09-252-991A-23288 Sequence 23288, A
31 57.5 16.0 856 4 US-09-152-060-77 Sequence 77, Appl
32 56.5 15.7 922 4 US-09-116-473-4 Sequence 4, Appl
33 56.5 15.7 1385 2 US-08-687-399-7 Sequence 7, Appl
34 56 15.6 151 4 US-09-252-991A-31031 Sequence 31031, A
35 56 15.6 181 1 US-08-278-091-15 Sequence 15, Appl
36 56 15.6 181 1 US-08-483-859-15 Sequence 15, Appl
37 56 15.6 181 1 US-08-472-173-15 Sequence 15, Appl
38 56 15.6 181 2 US-08-482-816-15 Sequence 15, Appl
39 56 15.6 181 2 US-08-296-149-15 Sequence 15, Appl
40 56 15.6 181 2 US-08-801-439-15 Sequence 15, Appl
41 56 15.6 181 2 US-08-615-271-15 Sequence 15, Appl
42 56 15.6 181 3 US-09-074-660-15 Sequence 15, Appl
43 56 15.6 181 3 US-09-074-659-15 Sequence 15, Appl
44 56 15.6 181 3 US-09-106-468-15 Sequence 15, Appl
45 56 15.6 181 3 US-09-106-468-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-752-891-2
; Sequence 2, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-891-2

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 60
Db 437 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 496
QY 61 EQSVWTAP 68
Db 497 EQSVWTAP 504

RESULT 2
US-08-752-891-6
; Sequence 6, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-891-6

(8)

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 60
Db 437 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 496
QY 61 EQSVWTAP 68
Db 497 EQSVWTAP 504

RESULT 3
US-09-144-178-2
; Sequence 2, Application US/09144178

; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-144-178-2

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 60
Db 437 QSPFTLQSTNTHTQSSSSDGLFRSRPAHSLPPGEGDGRVPEYVDFAEFYRLWSVDHG 496
QY 61 EQSVWTAP 68
Db 497 EQSVWTAP 504

RESULT 4
US-09-144-178-6
; Sequence 6, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.

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; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-144-178-6

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPILTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 60
Db 437 QSPILTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 496

QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 5
US-09-406-854-2
; Sequence 2, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-406-854-2

Query Match 100.0%; Score 359; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPILTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 60
Db 437 QSPILTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 496

QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 6
US-09-406-854-6
; Sequence 6, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
```

RESULT 8
US-10-158-895-2
; Sequence 2, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278

RESULT 10

US-10-158-895-43

? Sequence 43, Application US/10158895

? Patent No. 6551840

? GENERAL INFORMATION:

? APPLICANT: ONO, KOICHIRO

? APPLICANT: OHTOMO, TOSHIHIKO


```

; APPLICANT:  TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER:  US/10/158,895
; CURRENT FILING DATE:  2002-06-03
; PRIOR APPLICATION NUMBER:  US/09/529,279
; PRIOR FILING DATE:  2000-04-11
; PRIOR APPLICATION NUMBER:  PCT/JP98/04796
; PRIOR FILING DATE:  1998-10-22
; PRIOR APPLICATION NUMBER:  JP 9/290188
; PRIOR FILING DATE:  1997-10-22
; NUMBER OF SEQ ID NOS:  48
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH:  513
; TYPE:  PRT
; ORGANISM:  Homo sapiens
; US-10-158-895-43

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Query Match      100.0%; Score 359; DB 4; Length 513;
Best Local Similarity 100.0%; Pred. No. 2.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 QSPYTLTQSNTHNQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDPFAEYRLWSVDHG 60
    |||||
Db 446 QSPYTLTQSNTHNQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDPFAEYRLWSVDHG 505
    |||||

Qy 61 EQSVVTAP 68
    |||||
Db 506 EQSVVTAP 513
    |||||

```

RESULT 11
 US-09-529-279-11
 ; Sequence 11, Application US/09529279
 ; Patent No. 6451617
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/09/529,279
 ; CURRENT FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatencIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-279-11

```

Query Match      100.0%; Score 359; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 2.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPTLTLLQSNTHNTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPVDFAEFYRLWSVDHG 60
    |||||
Db 437 QSPTLTLLQSNTHNTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPVDFAEFYRLWSVDHG 496
    |||||

QY 61 EQSVVTAP 68
    |||||
Db 497 EQSVVTAP 504
    |||||

```

RESULT 12
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840

```

: GENERAL INFORMATION:
: APPLICANT: ONO, KOICHIRO
: APPLICANT: OHTOMO, TOSHIHIKO
: APPLICANT: TSUCHIYA, MASAYUKI
: TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
: FILE REFERENCE: 053466/0278
: CURRENT APPLICATION NUMBER: US/10/158,895
: CURRENT FILING DATE: 2002-06-03
: PRIOR APPLICATION NUMBER: US/09/529,279
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: PCT/JP98/04796
: PRIOR FILING DATE: 1998-10-22
: PRIOR APPLICATION NUMBER: JP 9/290188
: PRIOR FILING DATE: 1997-10-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH: 517
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-158-895-11

Query Match      100.0%; Score 359; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 2.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1  QSPFLTLQSTNTHTQSSSSDGLFRSRPAHSIPGCGDGRVEPYVDFAEFYRLMSVDHG 60
Db      437 QSPFLTLQSTNTHTQSSSSDGLFRSRPAHSIPGCGDGRVEPYVDFAEFYRLMSVDHG 496

QY      61  EQSVVTAP 68
Db      497 EQSVVTAP 504

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RESULT 13
US-09-529-279-41
; Sequence 41, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-529-279-41

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Query Match      21.4%; Score 77; DB 4; Length 16;
Best Local Similarity 100.0%; Pred.No.0.0016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
US-10-158-895-41

; Sequence 41, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-158-895-41

Query Match 21.4%; Score 77; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPTLTQSTNTHTQ 15
Db 2 QSPTLTQSTNTHTQ 16

RESULT 15
US-09-070-060-3
; Sequence 3, Application US/09070060
; Patent No. 5976849
; GENERAL INFORMATION:
; APPLICANT: Hustad, Carolyn M.
; APPLICANT: Ghildyal, Namit
; TITLE OF INVENTION: Human E3 Ubiquitin Protein
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Pharmaceuticals, Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850-5437
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,060
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/073,839
; FILING DATE: 05-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Higgins, Patrick H
; REGISTRATION NUMBER: 39,709
; REFERENCE/DOCKET NUMBER: PHM.70312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302.886.4889
; TELEFAX: 302.886.8221
; TELEX:

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 852 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-070-060-3

Query Match 18.8%; Score 67.5; DB 2; Length 852;
Best Local Similarity 31.1%; Pred. No. 5.1;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;

QY 2 SPTLTQSTNTHTQSSSSSDG-----GLFRSRPAH-----SLPPGEDGRVEPYVDF 48
Db 232 SSTGSLPPPTNTNTSEGATSGLIILITISGGSGRPLNPVTOAPLPPGWEQRVD----- 286

QY 49 AEFYRLMSVDHGQ 62
Db 287 -QHGRVYVDHVEK 299

Search completed: December 4, 2003, 09:34:53
Job time : 8.72973 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:21:38 ; Search time 2450.23 Seconds
(without alignments)
6784.777 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 684
Sequence: 1 gtagagcttcggcaggtatc.....cattacagtatcctgtcag 684

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_man:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_png:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	90.9	1201	13 BX364931	BX364931 BX364931
2	586.4	85.7	2994	11 AK053911	AK053911 Mus muscu
3	583.2	85.3	2976	11 AK046565	AK046565 Mus muscu
4	581.6	85.0	1221	13 B0511353	B0511353 AGENCOURT

5	543.6	79.5	739	12	BI696710
6	543	79.4	1062	12	BM554120
7	530	77.5	600	14	CB112561
8	509.8	74.5	1087	9	AL525728
9	482.6	70.6	604	12	BM426610
10	472.6	69.1	542	10	AW960377
11	468.2	68.5	1118	9	AL550589
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13	446.4	65.3	910	10	BF780358
14	444.6	65.0	750	13	BU104161
15	433.6	63.4	590	14	CB583299
16	408	59.6	646	12	B0703883
17	407	59.5	686	10	BG548917
18	406.4	59.4	688	12	BJ062988
19	406.4	59.4	696	12	BJ074867
20	405.4	59.3	1006	13	BQ219348
21	399	58.3	771	12	BI093821
22	390.4	57.1	1016	9	AL520975
23	374.2	54.7	742	13	BU058580
24	372	54.4	668	13	BU259310
25	370.4	54.2	1157	14	CD508913
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27	327.2	47.8	1054	13	BQ067693
28	317	46.3	747	12	BI334774
29	309	45.2	760	12	BG773488
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34	290.8	42.5	745	12	BI767913
35	287.8	42.1	822	12	BI757369
36	286	41.8	560	2	HS0084713
37	269.2	39.4	820	14	CB995067
38	266.8	39.0	858	12	BG916821
39	264.6	37.8	1033	10	BE882182
40	258.6	37.8	588	13	BQ381175
41	257.8	37.7	538	13	BQ557823
42	257	37.6	894	14	CA792459
43	254.6	37.2	788	14	CD350811
44	251.8	36.8	1191	12	BM472107
45	247.8	36.2	707	13	BW233644

ALIGNMENTS

RESULT 1
BX364931
LOCUS
DEFINITION
BX364931 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI032YB01 5-PRIME, mRNA sequence.
ACCESSION
BX364931
VERSION
BX364931.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3613.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1008ZH01QPI&cluster=3613.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

BX364931 1201 bp mRNA linear EST 05-MAY-2003
BX364931 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI032YB01 5-PRIME, mRNA sequence.

BI696710 603347214
BM554120 AGENCOURT
CB112561 K-EST0154
AL525728 AL525728
BM426610 pgin.pk0
AW960377 EST372448
AL550589 AL550589
BU418819 603962410
BF780358 602103276
BU104161 603005894
CB583299 AMGNNUC.N
B0703883 B0703883
BG548917 602575750
BJ062988 BJ062988
BJ074867 BJ074867
BQ219348 AGENCOURT
BI093821 602860601
AL520975 AL520975
BU058580 UI-M-F00-
BU259310 603748590
CD508913 CDA93-E03
BQ386875 NISC mn20
BQ067693 AGENCOURT
BI334774 602999677
BG773488 602720209
BX473160 DKF2p6861
AV718168 AV718168
BJ035129 BJ035129
CA984799 AGENCOURT
BI767913 603061057
BI757369 603029591
BX491885 Homo sapi
CB995067 AGENCOURT
BG916821 602816079
BE882182 601505283
BQ381175 603582172
BQ557823 H4048E02-
CA792459 AGENCOURT
CD350811 UI-M-G10-
BM472107 AGENCOURT
BW233644 BW233644

Paraday Avenue Genoscope sequence ID : CSIAI008ZH01QP1.

FEATURES
Source Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI032YB01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 290 a 253 c 320 g 299 t 39 others
ORIGIN

Query Match 90.9%; Score 622; DB 13; Length 1201;
Best Local Similarity 96.9%; Pred. No. 1.8e-175;
Matches 663; Conservative 11; Mismatches 6; Indels 4; Gaps 4;
QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTCTAATATTTGTAAGCTTTATGAGCC 60
Db 446 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTCTAATATTTGTAAGCTTTATGAGCC 505
QY 61 TCGTTGAATCCAGTGTGTTGTGATGAATATGCTGAAGGGGCTCTTTATATATATG 120
Db 506 TCGTTGAATCCAGTGTGTTGTGATGAATATGCTGAAGGGGCTCTTTATATATATG 565
QY 121 CTGCATGTGCTGAACCATTCGATATATATCTGCTGCCACGCAATGATGTTGGTTT 180
Db 566 CTGCATGTGCTGAACCATTCGATATATATCTGCTGCCACGCAATGATGTTGGTTT 625
QY 181 CAGTGTTCACAGGAGTGCTTATCTTCACAGTGCACACCATTCACAGG 240
Db 626 CAGTGTTCACAGGAGTGCTTATCTTCACAGTGCACACCATTCACAGG 685
QY 241 GACCTGAACACCAACCTTACTGCTGTGTCAGGGGGACAGTCTTCAAAATTTGTGAT 300
Db 686 GACCTGAACACCAACCTTACTGCTGTGTCAGGGGGACAGTCTTCAAAATTTGTGAT 745
QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGAGTCTGCTTGG 360
Db 746 TTGTGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGAGTCTGCTTGG 805
QY 361 ATGGCACCTGAAGTTTGAAGTACTATACGATGAAAATGACGCTTTCAGCTGG 420
Db 806 ATGGCACCTGAAGTTTGAAGTACTATACGATGAAAATGACGCTTTCAGCTGG 865
QY 421 GGTATTATTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGATGAGTGTGGCCCA 480
Db 866 GGTATTATTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGATGAGTGTGGCCCA 925
QY 481 GCTTTCCGAATCATGTGGCTGTTTCAATATGTTACTCGACACCACTGATAAAAATT 540
Db 926 GCTTTCCGAATCATGTGGCTGTTTCAATATGTTACTCGACACCACTGATAAAAATT 985
QY 541 CCTAGGCCATTCAGAGCTGATGACTCGTGTGCTGCTTAAGATCTTCCAGGCCCT 600
Db 986 CCTAGGCCATTCAGAGCTGATGACTCGTGTGCTGCTTAAGATCTTCCAGGCCCT 1044
QY 601 TCAATGGAGGAATTTGAAATAATAGTCACTGTGATCGGATCTTCCAGGACAGAT 660
Db 1045 TCAATGGAGGAATTTGAAATAATG-MTCMTTGTATGGCGACTTTCMGGAG-AGAT 1102
QY 661 GAGCCATACAGTATCCTTGTCAG 684
Db 1103 GAGCC-WTAMAGTWCYTTKTRAG 1125

RESULT 2
AK053911
LOCUS AK053911 2994 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched

library, clone:EL30320K22 product:mitogen activated protein kinase kinase kinase 7, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK053911
GI:26343862
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS

Carninci, P. and Hayashizaki, Y.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

REFERENCE
AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuenli, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stauber, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bernaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K. P., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409 (6821), 685-690 (2001)

MEDLINE

21085660

PUBMED

11217851

REFERENCE
AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 409, 563-573 (2002)

REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
URL: http://Location/Qualifiers

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BASE COUNT

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Query Match

85.7%; Score 586.4; DB 11; Length 2994;

Best Local Similarity

91.1%; Pred. No. 1.7e-164;

Matches 623; Conservative

0; Mismatches 61; Indels 0; Gaps 0;

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368 GTGGAGCTCCGGCAGTGTCTCAGGTGACCATCTTAACTTGTATGGAGCC 427
61 TGCCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGGCTCTTTATATAATGTG 120
428 TGCCTGATCCAGTATGCTTGTGATGAATATGATGAGGGGGGGCTCATTTGATAATGTG 487
121 CTGATGTGTGTGAACCATTTGCTATATATCTGTCGCCACGCAATGAGTGTGTTTGA 180
488 CTGATGTGTGTGAACCATTTGCTTACTACTACCTGCTGCTCATGCCATGAGTGTGTTTGA 547
181 CAGTGTTCACAGGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTAATTCACAGG 240

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848 GCTTTGAGATCATGTGGGCTGTTTCAATATGTTGTTCTGACCCACTGATAAAAAATTTA 907
541 CCTAAGCCCATTCAGAGCCTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
908 CCTAAGCCCATTCAGAGCCTGATGACACGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 967
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661 GAGCCATTACAGTATCTTCTGTCAG 684
1028 GAGCCATTACAGTATCTTCTGTCAG 1051

RESULT 3

AK046565

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DEFINITION Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430101B05 product:mitogen activated protein kinase kinase 7, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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TITLE

JOURNAL

MEDLINE
PUBMED
REFERENCE
AUTHORS

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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Aehburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hune, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohseki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6921), 685-690 (2001)

21085660
11217851

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2976)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/

FEATURES
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ACCESSION BU511353
VERSION BU511353.1 GI:22817586
KEYWORDS EST.


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VERSION
BM554120.1 GI:18793446
KEYWORDS
SOURCE
EST.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
NIH-MGC http://mgi.cni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: f column: 18
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FEATURES
source

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cloning). Average insert size 1.3 kb, insert size range
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(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH MGC Library."
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ORIGIN

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Db 408 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTCTAATATTGTAAAGCTTTATGGAGCC 467
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QY 301 TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATAACAGGGGAGTGTCTGTGG 360
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QY 361 ATGGCAGCTGAGTTTGAAGGTAGTAAATACAGTGAATAATGACGCTCTTCAGCTGG 420
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QY 595 CGCCCTTCAATGGA-GGAAATTTGAAAAATTAATGACTCACTTG 636
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K-BST0154393 L6ChoCK0 Homo sapiens cDNA clone L6ChoCK0-4-G09 5',
mRNA sequence.
BM112561
ACCESSION
BM112561.1 GI:27938368
KEYWORDS
Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE Unpublished
JOURNAL
COMMENT
Genome Research Center
Contact: Kim YS
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: G column: 09
High quality sequence stop: 600.
Location/Qualifiers
1. .600
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L6ChoCK0-4-G09"
/sex="M"
/cell_line="Cho-CK"
/lab_host="Top10F"
/clone_lib="L6ChoCK0"
/notes="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transposition of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 164 a 113 c 154 g 169 t
ORIGIN
Query Match 77.5%; Score 530; DB 14; Length 600;
Best Local Similarity 100.0%; Pred. No. 5.5e-148;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATTGAAAGCTTTATGGAGCC 60
DB 71 GTAGAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATTGAAAGCTTTATGGAGCC 130
QY 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
DB 131 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 190
QY 121 CTGATCGGTGTGAACATTCGCAATATATATCTGCTGCCACGAATGAGTGTGTTA 180
DB 191 CTGATCGGTGTGAACATTCGCAATATATATCTGCTGCCACGAATGAGTGTGTTA 250
QY 181 CAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAAATTCACAGG 240
DB 251 CAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAAATTCACAGG 310
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTCAGGGGGACAGTTCTAAAAATTGTGAT 300
DB 311 GACCTGAAACCAACCAACTTACTGCTGTGTCAGGGGGACAGTTCTAAAAATTGTGAT 370
QY 301 TTTGCTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGAGTGTCTTGG 360

DB 371 TTGTGTCAGCCTGTGACATTCAGACACACATGACCAATAACAGAGGAGTGTCTTGG 430
QY 361 ATGGCAGCTGAGTGTGTTTGAAGGTAGTAAATACAGTGAAATAATGACGCTTTCAGCTGG 420
DB 431 ATGGCAGCTGAGTGTGTTTGAAGGTAGTAAATACAGTGAAATAATGACGCTTTCAGCTGG 490
QY 421 GGTATTATTCTTTGGGAAGTGATACAGGCTCGGAAACCTTTTGAATGAGATTGGTGGCCCA 480
DB 491 GGTATTATTCTTTGGGAAGTGATACAGGCTCGGAAACCTTTTGAATGAGATTGGTGGCCCA 550
QY 481 GCTTTCCGAATCATGCGGCTTTCATATGATGCTACGACCACTGAT 530
DB 551 GCTTTCCGAATCATGCGGCTTTCATATGATGCTACGACCACTGAT 600
RESULT 8
AL525728 1087 bp mRNA linear EST 23-MAY-2003
LOCUS AL525728 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CSODC013YE20 5-PRIME, mRNA sequence.
ACCESSION AL525728 GI:31063592
VERSION AL525728.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1087)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12789221.
Contact: Genoscope Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3613.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODC013BC10QPl&cluster=3613.r. Contact :
Peng Liang Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSODC013BC10QPl.
FEATURES
Location/Qualifiers
1. .1087
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC013YE20"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 267 a 247 c 289 g 265 t 19 others
ORIGIN
Query Match 74.5%; Score 509.8; DB 9; Length 1087;
Best Local Similarity 98.1%; Pred. No. 9.5e-142;
Matches 574; Conservative 4; Mismatches 1; Indels 6; Gaps 6;
QY 1 GTAGAGCTTCGGAG-TTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGC 59
DB 489 GTAGAGCTTCGGAGATTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGC 548
QY 60 CTGCTTGAATCCAGTGTCTTGTGATGGAATAT-CTGAAGGGGCTCTTATATAATG 118
DB 549 CTGCTTGAATCCAGTGTCTTGTGATGGAATATAGTGAAGGGGCTCTTATATAATG 608
QY 119 TGTGTCATGTTGCGAACCATTGCCATATATATCTGCTGCCACCAATGAGTTGGTGT 178

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Db      609  TGCTGCATGGTCTGAACCAATTCGCCATATATATCTGCTGCCCGCAGCAATGARTGGTGT 668
Qy      179  TACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACA 238
Db      669  TACAGTGTTCCTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACA 728
Qy      239  GGGACCTGAACACACAACTTACTGCTGTTGCGAGGGGGGACAGTCTTAAAAATTGTG 298
Db      729  GGGACCTGAACACCAAACTTACTGCTGTTGCGAGGGGGGACAGTCTTAAAAATTGTG 788
Qy      299  ATTTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGGGAGTGGCT 358
Db      789  ATTTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGGGAGTGGCT 848
Qy      359  GGATGCACTGAAGTGTGAGTGTGAGGTAGTAAATACAGTGAATAATGACGCTTCAGCT 418
Db      849  GGATGCACTGAAGTGTGAGTGTGAGGTAGTAAATACAGTGAATAATGACGCTTCAGCT 908
Qy      419  GGGGTATTATCTTTGGGAGTGAACCGCTCGGAAACCTTTGATGAGATTGGTGGCC 478
Db      909  GGGGTATTATCTTTGGGAGTGAAT-AMGCGTCGGAAA-CCTTTGTATGAGATTGGTGGCC 966
Qy      479  CAGCTTTCGCAATCATGTGGGCTG-TTCATATGTTACTCGACCAACCATGATAAAAAAT 537
Db      967  CAGCTTTCGCAATCATGTGGGCTGTTTCATATGTTACTCGACCAACCATGATAAAAAAT 1026
Qy      538  TTACTTAAGCCATTGAGAGCCTGATGACTCGTGTGTTGCTTAAA 582
Db      1027  TTACTTAAG-CCATTGAGAGCCTGATGACTCGTGTGTTGCTTAAA 1070

RESULT 9
BM426610
LOCUS
DEFINITION
  pgf2n.pk004.d15 Normalized Chicken Abdominal Fat Library (pgf2n)
  Gallus gallus cDNA clone pgf2n.pk004.d15 5' similar to
  emb|CAB87605.1 (A1121964) dU15414.1.4 (mitogen-activated protein
  kinase kinase kinase 7 (TGF-beta activated kinase 1d (TAK1))) [Homo
  sapiens], mRNA sequence.
ACCESSION
  BM426610
VERSION
  EST.
SOURCE
  BM426610.1 GI:18431087
  Gallus gallus (chicken)
  Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  1 (bases 1 to 604)
  Cogburn,L.A., Morgan,R. and Burnside,J.
  ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal
  Genome Project
  Unpublished
  Contact: Larry A. Cogburn
  University of Delaware
  Townsend Hall, Newark, DE 19717, USA
  Tel: 302-831-1335
  Fax: 302-831-2822
  Email: cogburn@udel.edu, www.Chickest.udel.edu.
FEATURES
  source
    1. '604
      /organism="Gallus gallus"
      /mol_type="mRNA"
      /strain="Commercial broiler, Ottawa Research Centre,
      leghorn"
      /db_xref="taxon:9031"
      /clone="pgf2n.pk004.d15"
      /sex="Male and Female"
      /tissue_type="Abdominal Fat"
      /dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9
      ,w16,1yr)"
      /lab_host="E. coli EMDH10B"
      /clone_lib="Normalized Chicken Abdominal Fat Library
      (pgf2n)"

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/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each developmental age
(across strains); Single pass sequencing from 5'-end"
BASE COUNT      167 a      125 c      140 g      167 t      5 others
ORIGIN
Query Match      70.6%; Score 482.6; DB 12; Length 604;
Best Local Similarity 87.6%; Pred. No. 9.8e-134;
Matches 524; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy      87  GGAATATGCTGAAGGGGCTCTTTATATATGCTGTCATGTCGTCACCAATGGCATA 146
Db      1  GGAATATGCTGAAGGGGCTCTCTGTACAAATGCTGTCATGTCGTCGTCGCTCA 60
Qy      147  TTATATGCTGTCGCCAGCAATGATTTGTTTACAGTGTTCCTCAAGGAGTGGCTATCT 206
Db      61  TTATATGCTGTCGCCAGCAATGATTTGTTTACAGTGTTCCTCAAGGAGTGGCATACT 120
Qy      207  TCACAGCATGCAACCCAAAGCGCTAATTCACAGGGACCTGAAACCAACCAACTTACTGCT 266
Db      121  TCACAGTATGAACCAAGAGCGCTAATTCACAGAGACCTGAAACCAACCAATTTGCTCT 180
Qy      267  GGTTCAGGGGGGACAGTTCTTAAATTTTGTGATTTTGTGTCAGCTGTGACATTCAGAC 326
Db      181  GGTAGCTGGGGGACAGTTCTTAAAGATCTGTGATTTTGTACAGCTGTGATATTCAAAC 240
Qy      327  ACACATGACCAATTAACAGGGGAGTCTGCTTGGATGGCACCTGAAGTTTGAAGGTAG 386
Db      241  ACACATGACCAACAAATAAGGGAGTGTCTTGGATGGCACCTGAAGTTTGAAGGTAG 300
Qy      387  TAATTACAGTGAATAATGTGAGCTCTTCAGCTGGGTATTATTCTTTGGAGTGATAAC 446
Db      301  CAATTACAGTGAATAATGTGAGCTTTTCAATTTGGGTATTATTCTTTGGAGTGATAAC 360
Qy      447  GGTTCGGAACCCCTTTGATGAGATTTGTGGCCAGCTTTCCGAATCATGTGGGCTTTCA 506
Db      361  CGGTAGGAACCCCTTTTGTGATGAGATTTGTGGTCCAGCTTTCCGCAATAATGTGGCAGTTCA 420
Qy      507  TAATGTTACTCGACCAACCACTGATATAAAATTTTACTTAAGCCCATGAGAGCTGATGAC 566
Db      421  CAATGGTACTCGACCAACCACTGATCAAAATTTTACTTAAGCCCATGAGAGTTAATGAC 480
Qy      567  TCGTTGTTGTTCTAAAGATCTTCCAGCGCCCTTCAATGGAGGAATTTGAAATAT 626
Db      481  CGCTGTTGTTCTCAAGATCTTCAACAGACCTTCCATGGAGGAATTTGTTAAATAT 540
Qy      627  GACTCACTGATGCGGTACTTTCCAGGAGCAGATGAGCCATTACAGTATCTCTTGTGAC 684
Db      541  GACACACTGATGCGGTACTTTCCNNNAGCTGATGAACCTCTGCAATATCTTGCNAG 598

RESULT 10
AW960377
LOCUS
DEFINITION
  EST372448 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION
  AW960377
VERSION
  AW960377.1 GI:8150061
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 542)
  Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
  ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
  Quackenbush,J.
  Assessment of gene expression patterns in a model of colon tumor
  metastasis using a 19,200 element cDNA microarray
  Unpublished
  Contact: John Quackenbush
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 3528

```

Fax: 301 838 0208
Email: johnq@cigr.org
Plate: 145
Seq primer: Reverse.

FEATURES

Location/Qualifiers

1..542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
/note="Vector: pBluescriptSKm"

149 a 102 c 136 g 155 t

BASE COUNT
ORIGIN

Query Match 69.1%; Score 472.6; DB 10; Length 542;

Best Local Similarity 99.0%; Pred. No. 9.3e-131;

Matches 486; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGCC 60

Db 51 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGCC 110

QY 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATGTG 120

Db 111 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATGTG 170

QY 121 CTGCAFTGCTGTAACCATTCGCAATATTAATGCTGCGCCACGCAATGAGTTGGTGTGA 180

Db 171 CTGCAFTGCTGTAACCATTCGCAATATTAATGCTGCGCCACGCAATGAGTTGGTGTGA 230

QY 181 CAGTGTCCCAAGGAGTGGCTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 240

Db 231 CAGTGTTCACCAAGGAGTGGCTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 290

QY 241 GACCTGAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGAT 300

Db 291 GACCTGAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGAT 350

QY 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGTGCTTGG 360

Db 351 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGTGCTTGG 410

QY 361 ATGGCACTGAAGTTTGTGAGTAGTAATACAGTGAAAATGTGACGTCCTCAGCTGG 420

Db 411 ATGGCACTGAAGTTTGTGAGTAGTAATACAGTGAAAATGTGACGTCCTCAGCTGG 470

QY 421 GGTATTATCTTTGGGAAGTGATAACCGCTC-GGAAACCCCTTTGATGAGATTGGTGGCCC 479

Db 471 GGTATTATCTTTGGGAAGTGATAACCGCTGCGGAACCCCTGTGATGAGATTGGTGGCCC 530

QY 480 AGCTTTCCGAA 490

Db 531 AACTTCCCAA 541

RESULT 11

AL550589

LOCUS

DEFINITION AL550589 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1058Y014 5-PRIME, mRNA sequence.

ACCESSION AL550589

VERSION AL550589.2 GI:31272406

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 15, 2001 this sequence version replaced gi:12887700.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 3613.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1058BH070P1&cluster=3613.r. Contact :

Peng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0D1058BH07Q1.

Location/Qualifiers

1..1118

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="CS0D1058Y014"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 276 a 227 c 292 g 274 t 49 others

ORIGIN

Query Match 68.5%; Score 468.2; DB 9; Length 1118;

Best Local Similarity 94.3%; Pred. No. 3.1e-129;

Matches 510; Conservative 7; Mismatches 20; Indels 4; Gaps 3;

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGCC 60

Db 454 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGCC 513

QY 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATGTG 120

Db 514 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATGTG 173

QY 121 CTGCAFTGCTGTAACCATTCGCAATATTAATGCTGCGCCACGCAATGAGTTGGTGTGA 180

Db 574 CTGCAFTGCTGTAACCATTCGCAATATTAATGCTGCGCCACGCAATGAGTTGGTGTGA 633

QY 181 CAGTGTTCCTCAAG-GAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAG 239

Db 634 CAGTGTTCCTCAAGAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAG 693

QY 240 GGACCTGAAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGA 299

Db 694 GGACCTGAAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGA 753

QY 300 TTTTGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 359

Db 754 TTTTGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 813

QY 360 GATGGCACCTGGAAGTTTTCAGAGTAGTAATACAGTGAAAATGTGACGTCCTTCAGCTG 419

Db 814 GATGGCACCTGGAAGTTTTCAGAGTAGTAATACAGTGAAAATGTGACGTCCTTCAGCTG 873

QY 420 GGGTATTATTTCTTTGGGAAGTGAACCGCTCGGAAACCCCTTTGATGAGATTGGTGGCCC 479

Db 874 GGGTATTATTTCTTTGGGAAGTGAAT-AMSCGTGCGAAACCCCTTTGATGAGATTGGTGGCCC- 931

QY 480 AGCTTTCCGAAATCATGTGGGCTGTTTATATGTTACTCGACCACTGATATAAAATTT 539

Db 932 -AGCTTTCSAATCATGTGGGCTGTTTATATGTTATCGACMACACTGATAAAAAATTCCT 990

540 A 540

991 A 991

RESULT 12

BU418819

LOCUS BU418819 839 bp mRNA linear EST 29-NOV-2002
 DEFINITION 603962410F1 CSEQRN09 Gallus gallus cdna clone CHEST939d3 5', mRNA
 sequence.
 ACCESSION BU418819
 VERSION BU418819.1 GI:25911490
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 839)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..839
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST939d3"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate
 cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQRN09"
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;
 Site 2: NotI; This normalized library was constructed from
 1 million independent clones. cDNA synthesis was initiated
 using an oligo(dT) primer, using methylated C in the first
 strand and synthesized reaction. Following this first strand
 reaction, double-stranded cDNA was blunted, ligated to
 NotI adapters, digested with EcoRI, size-selected, and
 cloned into the NotI and EcoRI compatible sites of a
 custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
 Bonaldo et al., Genome Research 6 (1996): 791, except that
 a significantly longer reannealing hybridization was
 used."

FEATURES

source
 BASE COUNT 237 a 182 c 205 g 215 t
 ORIGIN
 Query Match 65.5%; Score 448.2; DB 13; Length 839;
 Best Local Similarity 87.3%; Pred. No. 2.7e-123;
 Matches 514; Conservative 0; Mismatches 73; Indels 2; Gaps 2;
 QY 1 GTAGAGCTTCGACGTTATCCGGTGTGAACATCTCTATATGTAAAGCTTTATGAGCC 60
 DB 232 GTAGAGCTTCGACATCTGACGATTAACCATCTCCATATTTGTCAAGTTATGAGCC 291
 QY 61 TGCCTGAATCCAGTGTCTTCTGATGAATATGCTGAAGGGGCTCTTTATATATG 120
 DB 292 TGTCTAACCAGTGTGCTTGTATGAGTATGCTGAAGAGGTTCTGTACAAATGTG 351
 QY 121 CTGCAATGTGTGAACCAATGTCATATATATCTGCTGCCACGCAATGAGTTGTGTTA 180
 DB 352 CTGCATGTGTGTAACCTCTGCTCATTTATCTGCTGCACACGCAATGAGTTGTGTTA 411
 QY 181 CAGTGTTCACAGGAGTGGCTATCTTACAGCATGCAACCAAGCGCTAATTCACAGG 240

DB 412 CAGTGTTCACAGGAGTGGCATATCTTCAGATGAACCAAGGCCCTAATTCACAGA 471
 QY 241 GACCTGAACCAACCAAACTTACTGCTGTGGAGGGGGACAGTTCTTAAAAATTTGTGAT 300
 DB 472 GACCTGAACCAACCAAAATTTGCTTCTGTAGCTGGGGGACAGTTCTTAAAGATCTGTGAT 531
 QY 301 TTGTGTACAGCTGTGCACATTCAGACACATGACCAATTAACCAAGGGAGTGTGCTTGG 360
 DB 532 TTGTGTACAGCTGTGTATTTCAACACATGACCAACAATAAGGGAAGTGTGCTTGG 591
 QY 361 ATGGCACTCTGAAGTTTGAAGGTAGTAATTAAGTGAATAATGACGCTCTTCAGCTGG 420
 DB 592 ATGGCACTCTGAAGTTTGAAGGTAGTAATTAAGTGAATAATGACGCTCTTCAGCTGG 651
 QY 421 GGTATTAATCTTTGGGAAGTATAAGCGTGTGGAACCCCTTTGATGAGATT-GGTGGCCC 479
 DB 652 GGTATTAATCTTTGGGAGGTAATCACCCGTAGGAACCTTTTGAAGATTGGTGGTCC 711
 QY 480 AGCTTTCCGAATCATGTGGCTGTTTCATAATGTGCTACTCGACCACTGATAAAATTT 539
 DB 712 AGCTTTCCGAATTAATGTGGCAGTTCAATGTGCTACTCGACCACTGATAAAATTT 771
 QY 540 ACCTAAGCCCATTTGAGAGCT-GATGACTCGTTTGTGTCTAAAGATCC 587
 DB 772 ACCTAAGCCCATTTGAGAGTTTAAATGACCCGCTGTGTGTCACAGATCC 820

RESULT 13

BF780358
 LOCUS 602103276F1 NCI_CGAP_Kid14 Mus musculus cdna clone IMAGE:4221379
 DEFINITION 5', mRNA sequence.
 ACCESSION BF780358
 VERSION BF780358.1 GI:12085481
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 910)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM9806 row: h column: 20
 High quality sequence stop: 664.
 Location/Qualifiers
 1..910
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4221379"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Kid14"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP library. |"
 BASE COUNT 247 a 209 c 246 g 207 t
 ORIGIN
 Query Match 65.3%; Score 446.4; DB 10; Length 910;
 Best Local Similarity 89.7%; Pred. No. 9.8e-123;

FEATURES

source
 BASE COUNT 247 a 209 c 246 g 207 t
 ORIGIN
 Query Match 65.3%; Score 446.4; DB 10; Length 910;
 Best Local Similarity 89.7%; Pred. No. 9.8e-123;

ACCESSION CB583299
VERSION CB583299.1 GI:29528785
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 590)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00366 row: h column: 12.
FEATURES
source
1..590
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 /clone="nrhy5-00366-h12"
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 hypothalamus adult female Wistar rat avg. insert size 2.3
 kb fraction 6 and 7"
BASE COUNT 162 a 141 c 144 g 143 t
ORIGIN

Query Match 63.4%; Score 433.6; DB 14; Length 590;
Best Local Similarity 91.3%; Pred. No. 5.3e-119;
Matches 460; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 181 CAGTGTCCACAGGAGTGGCTTATCTTCACAGCATCCACCCAAAGCGCTAATTCACAGG 240
DB |||||||
2 CAGTGTCCACAGGAGTGGCTTACCTGCACAGCATGCCGCCAAAGCTCTCATTCATAGG 61

QY 241 GACCTGAACACCAACCTTACTGCTGGTTGACAGGGGGACAGTTCCTAAAAATTTGTGAT 300
DB |||||||
62 GACCTCAAGCCTCCAAACTTGTCTGGTTGACAGGGGGACAGTTCCTAAAAATTTGTGAT 121

QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGAGTGTCTGTGG 360
DB |||||||
122 TTGTGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGAGTGTCTGTGG 181

QY 361 ATGGCACCTGAAGTTTTCAGGTAGTAAATACAGTGAATAATGTGACGCTTCAGCTGG 420
DB |||||||
182 ATGGCACCGAAGTTTTCAGGTAGTAAATACAGTGAATAATGTGACGCTTCAGCTGG 241

QY 421 GGTATTATTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGATGAGATTGGTGGCCCA 480
DB |||||||
242 GGTATTATTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGATGAGATTGGTGGCCCA 301

QY 481 GCTTTCCGAATCATGTGGCTGTTTCAATATGTGATCTCGACACACCTGATATAAAATTTA 540
DB |||||||
302 GCTTTCCGAATCATGTGGCTGTTTCAATATGTGATCTCGACACACCTGATATAAAATTG 361

QY 541 CCTAAGCCCATTTGAGAGCTGATGACTGCTGCTGTGCTTAAGATCCTTCCAGCGCCCT 600
DB |||||||
362 CCTAAGCCCATTTGAGAGCTGATGATGACCCGCTGTTGGTCTAAGGACCCCTTCTCAGCGCCCT 421

QY 601 TCAATGGAGGAATTTGAAATAATGATCTACATTGATCGGCTACTTTCCAGGAGCAGAT 660
DB |||||||
422 TCAATGGAGGAATTTGAAATAATGATCTACATTGATCGGCTACTTTCCAGGAGCAGAT 481

QY 661 GAGCCATTACAGTATCCTTGTTCAG 684
DB |||||||
482 GAGCCGTTACAGTATCCTTGTTCAG 505

Search completed: December 4, 2003, 07:04:36
Job time : 2458.23 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 09:34:12 : Search time 118.541 Seconds
(without alignments)
1548.515 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPFLTQSTNTHNQSSSS.....AEFYRLMSVDHGEQSVVTP 68

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq 19Jun03 -QMT=fastcap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144@cgn 1 0 @runat 03122003 122509 23313 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 19Jun03:*

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14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	359	100.0	1515	21	AAZ48861 Human TAB1 coding
2	359	100.0	1560	18	AAT91175 Human TAB1 (TAK1 b
3	359	100.0	1560	18	AAT91178 Human TAB1 (TAK1 b
4	359	100.0	1560	20	AA556278 Human TAB1 encodin
5	359	100.0	1560	21	AAA39106 Human TAB-1 nucleo
6	359	100.0	1568	20	AA556310 Human TAB1 encodin
7	359	100.0	1569	20	AA556282 Human TAB1-FLAG en
8	359	100.0	3450	25	ABX34568 Human mdt cdna SE
9	359	100.0	16877	22	ABA20494 Human nervous syst
10	359	100.0	16877	22	AAL36984 Human musculoskele
11	359	100.0	16877	25	ABX59972 cDNA encoding nove
12	352	98.1	696	21	AAF15895 Human prostate can
13	76	21.2	519	24	ABN61139 Human cancer relat
14	75	20.9	14091	23	ABL11586 Drosophila melanog
15	74.5	20.8	990	23	AAS80813 DNA encoding novel
16	71.5	19.9	1108	14	AAQ49396 Class II AP endonu
17	71	19.8	996	24	ABK78928 Bacillus clausii g
18	70	19.5	3489	23	ABL28043 Drosophila melanog
19	70	19.5	19674	23	ABL28042 Human HT4SG84 seri
20	69.5	19.4	1492	22	AAH78731 Drosophila melanog
21	69.5	19.4	3820	23	ABL12378 Drosophila melanog
22	69.5	19.4	4877	23	ABL13708 Drosophila melanog
23	69.5	19.4	9507	22	AAL07097 Human reproductive
24	69.5	19.4	9507	25	ABZ73900 Secreted protein g
25	69.5	19.4	9507	25	ABZ67483 Human secreted pro
26	69	19.2	6743	23	AAS65172 DNA encoding novel
27	69	19.2	6743	23	AAS88306 DNA encoding novel
28	69	19.2	12409	22	AAS30238 DNA encoding rena
29	69	19.2	23580	22	AAK66230 Human immune/haema
30	69	19.2	23580	22	AAK83578 Human immune/haema
31	68.5	19.1	3068	22	AAS14723 Human phosphinosi
32	68.5	19.1	3082	22	AAS14724 Human phosphinosi
33	68.5	19.1	12094	23	AAS59536 Propionibacterium
34	68.5	19.1	16951	22	AAH48620 Human fascin DNA f
35	68.5	19.1	16951	22	AAH48622 Human foetal liver
36	68	18.9	273	22	ABA70748 Probe #15715 for g
37	68	18.9	273	22	ABA37249 Human bone marrow
38	68	18.9	273	22	AAK19001 Probe #15009 for g
39	68	18.9	273	22	AAK44951 Probe #19607 used
40	68	18.9	273	22	AAI25076 Probe #19607 used
41	68	18.9	273	22	AAI50921 Human liver single
42	68	18.9	273	23	ABS44616 Human genome-deriv
43	68	18.9	273	24	ABS19195 Human genomic DNA
44	68	18.9	8918	22	AAS26708 Human novel polynu
45	68	18.9	8918	25	ABX74057

ALIGNMENTS

RESULT 1

AAZ48861

ID AAZ48861 standard; cDNA; 1515 BP.

XX AAZ48861;

DT 24-MAR-2000 (first entry)

XX Human TAB1 coding sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
transforming growth factor-beta activated kinase 1; monocyte migration;
TAK1 binding protein 1; extracellular matrix protein production;
cell growth inhibitor; beta-amyloid protein deposition;
immunosuppression; Transforming growth factor-beta; ds.
XX Homo sapiens.

XX JPL1326328-A.
 PN XX
 XX 26-NOV-1999.
 PD XX
 XX 13-MAY-1998; 98JP-0130378.
 PF XX
 XX 13-MAY-1998; 98JP-0130378.
 PR XX
 XX (MATSU) MATSUMOTO K.
 PA WPI; 2000-078337/07.
 XX DR
 XX P-PSDB; AAY59450.
 PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein -
 XX
 XX Claim 2; Page 25-26; 43pp; Japanese.
 PS
 XX This sequence encodes the human TAB1 protein.
 CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.
 XX
 SQ Sequence 1515 BP; 323 A; 457 C; 463 G; 272 T; 0 other;

Alignment Scores:
 Pred. No.: 2,32e-35 Length: 1515
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AA248861 (1-1515)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 DB 1309 CAAAGCCGACCTTAACCCCTGCAGTCCACCAACACGACGACGAGCAGCTCCAGC 1368
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 1369 TCTGACGAGGAGCTTCCTCCGCTCCGCGCCGCGCCACCTCGCTCCGCGGAGAGCGGT 1428
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 DB 1429 CGTGTTCAGCCCTATGTGGACTTGTGAGTTTACCGCTCTCGAGCGTGGACCATGCC 1488
 QY 61 GluGlnSerValThrAlaPro 68
 DB 1489 GAGCAGAGCGTGGTGACAGCACCG 1512

RESULT 2
 AAT91175
 ID AAT91175 standard; cDNA; 1560 BP.
 XX
 AC AAT91175;
 XX
 XX 25-MAR-2003 (updated)
 DT 14-APR-1998 (first entry)
 DT
 XX Human TAB1 (TAK1 binding protein) cDNA.
 DE
 XX TAB1; TAK1 binding protein; transforming growth factor-beta;
 KW

KW signal transduction; human; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 30..1544
 FT /*tag= a
 FT variation 185
 FT /*tag= b
 FT /note= "another clone has adenine at position 185,
 FT with codon AGC (Ser) altered to AGA (Arg)"
 FT
 XX EP803571-A2.
 XX
 XX 29-OCT-1997.
 XX
 XX 24-APR-1997; 97EP-0302808.
 XX
 XX 20-NOV-1996; 96US-0752891.
 PR 24-APR-1996; 96JP-0126282.
 PR 28-OCT-1996; 96JP-0300856.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Matsumoto K, Nishida E;
 XX WPI; 1997-515318/48.
 DR P-PSDB; AAW26706.
 XX
 XX DNA encoding TAK1 binding protein TAB1 - member of transforming
 PT growth factor beta receptor signal production pathway, which
 PT activates TAK-1 kinase activity upon binding
 XX
 XX Claim 1; Page 17-19; 30pp; English.
 XX
 XX This cDNA clone codes for human TAB1 (see AAW26706), a novel member
 CC of the transforming growth factor-beta receptor signal transduction
 CC pathway, which activates TAK-1 kinase activity upon binding. To
 CC obtain the full-length TAB1 coding sequence, a human kidney cDNA
 CC library was screened using as a probe a partial TAB1 cDNA obtained
 CC from a yeast two-hybrid assay for proteins that interacted with
 CC TAK1. The 5' terminus was identified by 5'RACE. 2 Different
 CC clones were sequenced, with cytosine and adenine (see AAT91178) as
 CC the 185th nucleotide, respectively, and deposited as FERM BP-5599
 CC and FERM BP-5508, respectively. Also claimed are: isolated DNA
 CC encoding a protein modified by a substitution, deletion and/or
 CC addition of 1 or more amino acids of the 504-residue TAB1 sequence;
 CC (2) DNA which can hybridize with the 1560 bp nucleic acid sequence;
 CC (3) isolated DNA encoding a protein comprising amino acids 21-579
 CC or 437-504 of the 504 TAB1 sequence; (4) DNA encoding a fusion
 CC protein comprising an above protein or polypeptide; (5) expression
 CC vector comprising an above DNA; and (6) host cell, preferably a
 CC mammalian or yeast cell, transformed by the expression vector.
 CC Cells expressing TAB1 and TAK1 can be used to screen for TGF-beta
 CC signalling pathway inhibitors by contacting the cells with a test
 CC compound, and measuring the TAK1 kinase activity.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX SQ Sequence 1560 BP; 332 A; 469 C; 480 G; 279 T; 0 other;

Alignment Scores:
 Pred. No.: 2,41e-35 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAT91175 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 DB 1338 CAAAGCCGACCTTAACCCCTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 1398 TCTGACGAGGCCTTCCGCTCCGCGCCGCCCACTCGCTCCCGCTGGGAGACGGT 1457
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
 DB 1458 CGTGTGAGCCCTATGTGGACTTTCCTGAGTTTACCGCCCTCTGGAGGTGGACCATGGC 1517
 QY 61 GluGlnSerValThrAlaPro 68
 DB 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 3
 AAT91178
 ID AAT91178 standard; cDNA; 1560 BP.
 XX AC AAT91178;
 XX DT 25-MAR-2003 (updated)
 XX DT 14-APR-1998 (first entry)
 XX DE Human TAB1 (TAK1 binding protein) cDNA.
 XX KW TAB1; TAK1 binding protein; transforming growth factor-beta;
 XX KW signal transduction; human; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 30..1544
 XX FT /*tag= a
 XX FT 185
 XX FT /*tag= b
 XX FT /note= "another clone has cytosine at position 185,
 XX FT with codon AGA (Arg) altered to AGC (Ser)"
 XX PN EP803571-A2.
 XX PD 29-OCT-1997.
 XX PF 24-APR-1997; 97EP-0302808.
 XX PR 20-NOV-1996; 96US-0752891.
 XX PR 24-APR-1996; 96JP-0126282.
 XX PR 28-OCT-1996; 96JP-0300856.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Matsumoto K, Nishida E;
 XX DR WPI; 1997-515318/48.
 XX DR P-PSDB; AAW26707.
 XX PT DNA encoding TAK1 binding protein TAB1 - member of transforming
 XX PT growth factor beta receptor signal production pathway, which
 XX PT activates TAK-1 kinase activity upon binding
 XX PS Example 5; Page 19-21; 30pp; English.
 XX CC This cDNA clone codes for human TAB1 (see AAW26707), a novel member
 XX CC of the transforming growth factor-beta receptor signal transduction
 XX CC pathway, which activates TAK-1 kinase activity upon binding. To
 XX CC obtain the full-length TAB1 coding sequence, a human kidney cDNA
 XX CC library was screened using as a probe a partial TAB1 cDNA obtained
 XX CC from a yeast two-hybrid assay for proteins that interacted with
 XX CC TAK1. The 5' terminus was identified by 5'RACE. 2 Different
 XX CC clones were sequenced, with cytosine (see AAT91175) and adenine as
 XX CC the 185th nucleotide, respectively, and deposited as FERM BP-5599
 XX CC and FERM BP-5508, respectively. Also claimed are: isolated DNA
 XX CC encoding a protein modified by a substitution, deletion and/or
 XX CC addition of 1 or more amino acids of the 504-residue TAB1 sequence;
 XX CC (2) DNA which can hybridise with the 1560 bp nucleic acid sequence;

(3) isolated DNA encoding a protein comprising amino acids 21-579
 or 437-504 of the 504 TAB1 sequence; (4) DNA encoding a fusion
 protein comprising an above protein or polypeptide; (5) expression
 vector comprising an above DNA; and (6) host cell, preferably a
 mammalian or yeast cell, transformed by the expression vector.
 Cells expressing TAB1 and TAK1 can be used to screen for TGF-beta
 signalling pathway inhibitors by contacting the cells with a test
 compound, and measuring the TAK1 kinase activity.
 (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1560 BP; 333 A; 468 C; 480 G; 279 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.41e-35 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAT91178 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 DB 1338 CAAGAGCCGACCTTAACCTGAGTCCACCAACAGCACAGCAGCAGCAGCTCCAGC 1397
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 1398 TCTGACGAGGCCTTCCGCTCCGCGCCGCCCACTCGCTCCCGCTGGGAGACGGT 1457
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
 DB 1458 CGTGTGAGCCCTATGTGGACTTTCCTGAGTTTACCGCCCTCTGGAGGTGGACCATGGC 1517
 QY 61 GluGlnSerValThrAlaPro 68
 DB 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 4
 AAX56278
 ID AAX56278 standard; DNA; 1560 BP.
 XX AC AAX56278;
 XX DT 21-JUL-1999 (first entry)
 XX DE Human TAB1 encoding DNA.
 XX KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 XX KW transforming growth factor beta; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 30..1544
 XX FT /*tag= a
 XX PN WO9921010-A1.
 XX PD 29-APR-1999.
 XX PF 22-OCT-1998; 98WO-JP04796.
 XX PR 22-OCT-1997; 97JP-0290188.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ohtomo T, Ono K, Tsuchiya M;
 XX DR WPI; 1999-312645/26.
 XX DR P-PSDB; AAY09541.
 XX PT Screening for TGF-beta inhibitory substances, which are useful as

PT drugs for treatment of diseases relating to its disorder
 XX
 PS Example 1; Page 143-147; 195pp; Japanese.
 XX

CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors, or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes human TAB1.

SQ Sequence 1560 BP; 332 A; 469 C; 480 G; 279 T; 0 other;

Alignment Scores:
 Pred. No.: 2,41e-35 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAX56278 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 DB 1338 CAAAGCCGACCTTAACCTCTGAGTCACCAACAGCAGCAGCAGCAGCTCCAGC 1397
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 1398 TCTGACGGAGGCTCTTCGCTCCCGCCCGCCACCTCGCTCCCGCTGCGAGGACGT 1457
 QY 41 ArgValGluProThrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 DB 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGCG 1517
 QY 61 GluGlnSerValValThrAlaPro 68
 DB 1518 GAGCAGAGCGTGTGTGACAGCACCG 1541

RESULT 5
 AAA39106
 ID AAA39106 standard; DNA; 1560 BP.
 XX
 AC AAA39106;

XX 04-SEP-2000 (first entry)

DE Human TAB-1 nucleotide sequence SEQ ID NO.3.

KW Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;
 KW screening; signal transduction; inhibition; inflammatory cytokine;
 KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;
 KW antiinflammatory; suppression; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 30..1544
 CDS /*tag= a
 FT /*product= "TAB-1"

XX WO200023610-A1.

XX 27-APR-2000.

PD

XX 21-OCT-1999; 99WO-JP05817.
 XX
 PR 21-OCT-1998; 98JP-0299962.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;
 XX WPI; 2000-339707/29.
 DR P-PSDB; AAY91001.
 XX
 PT Method for screening inhibitors of TAK1 signal transduction for
 PT suppression of inflammatory cytokine production and use as
 PT antiinflammatory agents
 XX
 PS Disclosure; Page 85-90; 100pp; Japanese.

CC The present invention describes a method for screening compounds for
 CC inhibition of inflammatory cytokine signal transduction by contacting
 CC the sample with TAK1 and its receptor TAB1 and selecting for inhibition
 CC of TAK1/TAB1 binding. Also described is a method for screening compounds
 CC for inhibition of inflammatory cytokine signal transduction in which the
 CC inhibition of TAK1 phosphorylation is selected for; and drug
 CC compositions for the treatment of inflammatory disorders containing as
 CC active component an inflammatory cytokine signal transduction inhibitor.
 CC TAK1 is an essential component of the signalling process which results
 CC in release of inflammatory cytokines such as interleukin-1 (IL-1),
 CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used
 CC for the selection of effective antiinflammatory agents. The present
 CC sequence encodes human TAB-1, which is used in the exemplification of the
 CC present invention.

XX SQ Sequence 1560 BP; 332 A; 469 C; 480 G; 279 T; 0 other;

Alignment Scores:

Pred. No.: 2,41e-35 Length: 1560
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAA39106 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 DB 1338 CAAAGCCGACCTTAACCTCTGAGTCACCAACAGCAGCAGCAGCAGCTCCAGC 1397
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 1398 TCTGACGGAGGCTCTTCGCTCCCGCCCGCCACCTCGCTCCCGCTGCGAGGACGT 1457
 QY 41 ArgValGluProThrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 DB 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGCG 1517
 QY 61 GluGlnSerValValThrAlaPro 68
 DB 1518 GAGCAGAGCGTGTGTGACAGCACCG 1541

RESULT 6
 AAX56310
 ID AAX56310 standard; DNA; 1568 BP.
 XX
 AC AAX56310;

XX 21-JUL-1999 (first entry)

XX Human TAB1 encoding DNA SEQ ID NO:42.

XX Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta; ss.

```
XX OS Homo sapiens.
XX AC
XX FH Key Location/Qualifiers
XX FT 11..1552
XX FT CDS /*tag= a
XX XX
XX PN WO9921010-A1.
XX PD 29-APR-1999.
XX PF 22-OCT-1998; 98WO-JP04796.
XX PR 22-OCT-1997; 97JP-0290188.
XX XX (CHUS ) CHUGAI SEIYAKU KK.
XX FA Ohtomo T, Ono K, Tsuchiya M;
XX PI WPI; 1999-312645/26.
XX DR P-PSDB; AAY09550.
XX DR
XX FT Screening for TGF- beta inhibitory substances, which are useful as
XX FT drugs for treatment of diseases relating to its disorder
XX XX
XX PS Example 13; Page 182-186; 195pp; Japanese.
XX CC
XX CC A method has been developed for screening for substances which inhibit
XX CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
XX CC comprises: (a) contacting the polypeptide in the presence of a sample;
XX CC and (b) detecting the amount of bound polypeptide, in which the sample
XX CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
XX CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
XX CC indications e.g. as TGF-beta signal transduction inhibitors or
XX CC activators, or extracellular matrix protein production enhancement
XX CC inhibitors, or activators, or cell proliferation prevention inhibitors or
XX CC activators, or monocyte migration inhibitors or activators, or
XX CC physiological activity induction inhibitors or activators, or
XX CC immunosuppression inhibitors or activators, or amyloid beta protein
XX CC precipitation inhibitors or activators, and such substances can also be
XX CC inhibitors of the TAK1 polypeptide function, particularly kinase
XX CC activity. The present sequence encodes human TAB1.
XX SQ Sequence 1568 BP; 339 A; 472 C; 477 G; 280 T; 0 other;

Alignment Scores:
Pred. No.: 2.43e-35 Length: 1568
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAX56310 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 1346 CAAAGCCGACCTTAACCCCTGCAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1405
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
DB 1406 TCTGACGAGGCTCTTCGCTCCGCGCCGCGCCACTGCTCCCGCTGGCAGACCGT 1465
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
DB 1466 CGTGTGAGCCCTATGTGACCTTCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 1525
QY 61 GluGlnSerValValThrAlaPro 68
DB 1526 GAGCAGCGTGTGTGACAGCACCG 1549

RESULT 7
AAX56282
```

```
ID AAX56282 standard; DNA; 1569 BP.
XX XX
XX AC AAX56282;
XX XX
XX DT 21-JUL-1999 (first entry)
XX XX
XX DE Human TAB1-FLAG encoding DNA.
XX XX
XX KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
XX KW transforming growth factor beta; ss.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 7..1560
XX FT /*tag= a
XX XX
XX PN WO9921010-A1.
XX XX
XX PD 29-APR-1999.
XX XX
XX PF 22-OCT-1998; 98WO-JP04796.
XX PR 22-OCT-1997; 97JP-0290188.
XX XX
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX XX
XX PI Ohtomo T, Ono K, Tsuchiya M;
XX XX
XX DR WPI; 1999-312645/26.
XX DR P-PSDB; AAY09546.
XX XX
XX PT Screening for TGF- beta inhibitory substances, which are useful as
XX PT drugs for treatment of diseases relating to its disorder
XX XX
XX PS Example 1; Page 159-163; 195pp; Japanese.
XX XX
XX CC A method has been developed for screening for substances which inhibit
XX CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
XX CC comprises: (a) contacting the polypeptide in the presence of a sample;
XX CC and (b) detecting the amount of bound polypeptide, in which the sample
XX CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
XX CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
XX CC indications e.g. as TGF-beta signal transduction inhibitors or
XX CC activators, or extracellular matrix protein production enhancement
XX CC inhibitors, or activators, or cell proliferation prevention inhibitors or
XX CC activators, or monocyte migration inhibitors or activators, or
XX CC physiological activity induction inhibitors or activators, or
XX CC immunosuppression inhibitors or activators, or amyloid beta protein
XX CC precipitation inhibitors or activators, and such substances can also be
XX CC inhibitors of the TAK1 polypeptide function, particularly kinase
XX CC activity. The present sequence encodes TAB1-FLAG from an example of
XX CC the present invention.
XX SQ Sequence 1569 BP; 343 A; 466 C; 476 G; 284 T; 0 other;

Alignment Scores:
Pred. No.: 2.43e-35 Length: 1569
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAX56282 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 1315 CAAAGCCGACCTTAACCCCTGCAGTCCACCAACAGCAGCAGCAGCTCCAGC 1374
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
```

Db 1375 TCTGAGGAGGCTCTTCGCTCCGCGCCGCGCACTCGCTCCGCTCGGAGGACGGT 1434
 Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 |||||
 Db 1435 CGTGTTCAGCCCTATGTGGACTTTGTCTGAGTTTACCGCTCTCTGGAGCGTGGACCATGGC 1494
 Qy 61 GluGlnSerValValThrAlaPro 68
 |||||
 Db 1495 GAGCAGAGCGTGTGTGACGACCG 1518

RESULT 8
 ABX34568
 ID ABX34568 standard; cDNA; 3450 BP.
 XX AC ABX34568;
 XX 13-FEB-2003 (first entry)
 XX Human mddt cDNA SEQ ID 129.
 XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis; gene; ss.
 XX OS Homo sapiens.
 XX

XX W0200279449-A2.
 XX 10-OCT-2002.
 XX

XX 27-MAR-2002; 2002WO-US09944.
 XX

XX 28-MAR-2001; 2001US-279619P.
 XX 29-MAR-2001; 2001US-280067P.
 XX 29-MAR-2001; 2001US-280068P.
 XX 16-MAY-2001; 2001US-291280P.
 XX 17-MAY-2001; 2001US-291829P.
 XX 17-MAY-2001; 2001US-291849P.
 XX 19-JUN-2001; 2001US-299428P.
 XX 20-JUN-2001; 2001US-299776P.
 XX 20-JUN-2001; 2001US-300001P.
 XX

(INCY-) INCYTE GENOMICS INC.
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 XX Daugherty SC, Dam TC, Liu IF, Nguyen DA, Kleefeld Y, Gerstin EH;
 XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 XX Flores V, Marwaha R, Lo A, Lan RV, Urashka MF;
 XX WPI: 2003-058431/05.
 XX P-PSDB; ABU11578.
 XX

XX New purified disease detection and treatment molecule proteins and
 XX polynucleotides, useful for diagnosing, treating or preventing cancers
 XX (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 XX or hepatitis -
 XX

XX Claim 1; SEQ ID NO 129; 339pp + Sequence Listing; English.
 XX

XX This invention describes a novel disease detection and treatment molecule
 XX polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 XX osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 XX antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 XX and the polypeptides of the invention can be used for gene therapy,
 XX protein replacement therapy and are useful for treating a variety of
 XX diseases or conditions. These polypeptides or polynucleotides are
 XX particularly useful for diagnosing, treating or preventing cell

CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 3450 BP; 711 A; 1039 C; 1042 G; 658 T; 0 other;
 XX

Alignment Scores:
 Pred. No.: 6.86e-35 Length: 3450
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x ABX34568 (1-3450)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 |||||
 Db 1345 CAAGCCGACCTTACCTTGAGTCCACCAACGACGACGACGACGACGACGACG 1404

Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 |||||
 Db 1405 TCTGAGGAGGCTCTTCGCTCCGCGCCGCGCACTCGCTCCGCTCGGAGGACGGT 1464

Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 |||||
 Db 1465 CGTGTTCAGCCCTATGTGGACTTTGTCTGAGTTTACCGCTCTCTGGAGGACCATGGC 1524

Qy 61 GluGlnSerValValThrAlaPro 68
 |||||
 Db 1525 GAGCAGAGCGTGTGTGACGACCG 1548

RESULT 9
 ABA20494
 ID ABA20494 standard; DNA; 16877 BP.
 XX AC ABA20494;
 XX 23-JAN-2002 (first entry)
 XX

Human nervous system related polynucleotide SEQ ID NO 12825.
 XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
 XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 XX antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
 XX antithematic; hepatotropic; cerebroprotective; antiinflammatory;
 XX antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX OS Homo sapiens.
 XX

XX W0200159063-A2.
 XX 16-AUG-2001.
 XX

XX 17-JAN-2001; 2001WO-US01334.
 XX

XX 31-JAN-2000; 2000US-0179065.
 XX 04-FEB-2000; 2000US-0180628.
 XX 24-FEB-2000; 2000US-0184664.
 XX 02-MAR-2000; 2000US-0186350.
 XX 16-MAR-2000; 2000US-0189874.
 XX 17-MAR-2000; 2000US-0190076.
 XX 18-APR-2000; 2000US-0198123.
 XX 19-MAY-2000; 2000US-0205515.
 XX 07-JUN-2000; 2000US-0209467.
 XX

PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0215647.
PR 07-JUL-2000; 2000US-0215680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 324 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12825; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABA14678-ABA18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 16877 BP; 3563 A; 4508 C; 4516 G; 4290 T; 0 other;

Alignment Scores:
 Pred. No.: 5,57e-34 Length: 16877
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x ABA20494 (1-16877)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 15011 CAAAGCCGACCTTAACTCCGCTGACCTCCACCAACAGCAGCAGCAGCTCCAGC 15070
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 15071 TCTGACGAGGCGCTTCCGCTCCGCGCCGCCACCTCGCTCCGCGCTGCGAGACGGT 15130
 QY 41 ArgValGluProTrpValAspPheAlaGluPheTrpArgLeuTrpSerValAspHisGly 60
 Db 15131 CGTCTGAGCGCTATGTGACTTTGCTGAGTTTACCGCCTCTCGAGCGTGGACCATGGC 15190
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 15191 GAGCAGACGCGTGGTACAGCACCG 15214

RESULT 10
 AAL36984
 ID AAL36984 standard; DNA; 16877 BP.
 AC AAL36984;
 XX
 XX 08-JAN-2002 (first entry)
 XX
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3349.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200155367-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01338.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.

20-OCT-2000; 2000US-0241221.
 20-OCT-2000; 2000US-0241785.
 20-OCT-2000; 2000US-0241786.
 20-OCT-2000; 2000US-0241787.
 20-OCT-2000; 2000US-0241808.
 20-OCT-2000; 2000US-0241809.
 20-OCT-2000; 2000US-0241826.
 01-NOV-2000; 2000US-0244617.
 08-NOV-2000; 2000US-0246474.
 08-NOV-2000; 2000US-0246475.
 08-NOV-2000; 2000US-0246476.
 08-NOV-2000; 2000US-0246477.
 08-NOV-2000; 2000US-0246478.
 08-NOV-2000; 2000US-0246523.
 08-NOV-2000; 2000US-0246524.
 08-NOV-2000; 2000US-0246525.
 08-NOV-2000; 2000US-0246526.
 08-NOV-2000; 2000US-0246527.
 08-NOV-2000; 2000US-0246528.
 08-NOV-2000; 2000US-0246532.
 08-NOV-2000; 2000US-0246609.
 08-NOV-2000; 2000US-0246610.
 08-NOV-2000; 2000US-0246611.
 08-NOV-2000; 2000US-0246613.
 17-NOV-2000; 2000US-0249207.
 17-NOV-2000; 2000US-0249208.
 17-NOV-2000; 2000US-0249209.
 17-NOV-2000; 2000US-0249210.
 17-NOV-2000; 2000US-0249211.
 17-NOV-2000; 2000US-0249212.
 17-NOV-2000; 2000US-0249213.
 17-NOV-2000; 2000US-0249214.
 17-NOV-2000; 2000US-0249215.
 17-NOV-2000; 2000US-0249216.
 17-NOV-2000; 2000US-0249217.
 17-NOV-2000; 2000US-0249218.
 17-NOV-2000; 2000US-0249244.
 17-NOV-2000; 2000US-0249245.
 17-NOV-2000; 2000US-0249264.
 17-NOV-2000; 2000US-0249265.
 17-NOV-2000; 2000US-0249297.
 17-NOV-2000; 2000US-0249299.
 17-NOV-2000; 2000US-0249300.
 01-DEC-2000; 2000US-0250160.
 01-DEC-2000; 2000US-0250391.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 05-DEC-2000; 2000US-0256719.
 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251868.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-02559678.
 (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 DR
 PT Isolated polypeptide for treating, preventing and/ or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 XX
 PS Example 2; SEQ ID NO 3349; 781pp + Sequence Listing; English.
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by

CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 16877 BP; 3563 A; 4508 C; 4516 G; 4290 T; 0 other;

Alignment Scores:
 Pred. No.: 5.57e-34 Length: 16877
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAL36984 (1-16877)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrThrLeuHisThrGlnSerSerSerSer 20
 DB 15011 CAAGCCCGACCTTAACTGCTGAGTCCACCAACGACACGACGAGCAGCTCCAGC 15070
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 DB 15071 TCTGACGGAGGCTCTTCCGCTCCCGCCGCCACTCGCTCCGCTCCGCGAGCGGT 15130
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 DB 15131 CGTGTGAGCCCTATGTGGACTTTCTGAGTTTACCGCTCTGAGCGCTGGACCATGTC 15190
 QY 61 GluGlnSerValValThrAlapro 68
 DB 15191 GAGCAGCGGTGGTACAGCACCG 15214

RESULT 11
 ABX59972
 ID ABX59972 standard; cDNA; 16877 BP.
 XX
 AC ABX59972;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE cDNA encoding novel human musculoskeletal system antigen #2316.
 XX
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height;
 KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biorhythm; circadian rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 XX nutritional component.
 OS Homo sapiens.

XX
FN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
XX
PF 17-JAN-2001; 2001US-0764877.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-225759P.
PR 30-AUG-2000; 2000US-226868P.
PR 01-SEP-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-228928P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-128199/12.
XX
XX Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer -
XX
XX Disclosure; SEQ ID NO 3349; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence encoding musculoskeletal system associated polypeptides useful
XX
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid; stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms,
CC cardiac rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.
XX
SQ Sequence 16877 BP; 3563 A; 4508 C; 4516 G; 4290 T; 0 other;

Alignment Scores:
Pred. No.: 5,57e-34 Length: 16877
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x ABX59972 (1-16877)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 15011 CAAAGCCCGACCTTACCTGACGTCCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 15070

Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluaspGly 40
Db 15071 TCTGACGAGGCGCTCTTCGCTCCCGCGCGCCGACCTCGCTCCCGCGCGAGACGGT 15130

Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 15131 CGTGTGAGCCCTAAGTGAGACTTTGAGTTTACGCCCTCTGGAGCGTGGACCATGGC 15190

Qy 61 GluGlnSerValValThrAlaPro 68
Db 15191 GAGCAGAGCGTGTGTGACAGCACCG 15214

RESULT 12
AAF15895
ID AAF15895 standard; cDNA; 696 BP.
XX
XX AAF15895;
AC AAF15895;
XX
XX 13-MAR-2001 (first entry)
DT
XX
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:330.
DE
XX
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW

KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
XX 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
DR P-PsDB; AAB56692.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 1; Page 837; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 696 BP; 143 A; 237 C; 187 G; 120 T; 9 other;

Alignment Scores:
Pred. No.: 6,34e-35 Length: 696
Score: 352.00 Matches: 67
Percent Similarity: 98.53% Conservative: 0
Best Local Similarity: 98.53% Mismatches: 1
Query Match: 98.05% Indels: 0
DB: 21 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AAF15895 (1-696)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 49 CAAAGCCGACCTTAACCCCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 108
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 109 TCTRACGAGGAGGCTCTCCGCTCCGGGCGGCGCCACCTCGCTCCGCGGAGACGGT 168
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 169 CGTGTGTAGCCCTATGTGACATTTCTGAGTTTACCCTCTGGAGCGTGACCATGGC 228
QY 61 GluGlnSerValValThAlaPro 68
Db 229 GAGCAGAGCGTGGTGACAGCACCG 252

RESULT 13
ABN61139/c
ID ABN61139 standard; cDNA; 519 BP.
XX
XX AC ABN61139;
XX
XX DT 28-JUN-2002 (first entry)
XX
DE Human cancer related polynucleotide SEQ ID NO 1106.
XX
XX Human; cytostatic; gene expression; gene mapping; tissue profiling;
KW gene therapy; cancer; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200214500-A2.
XX
XX PD 21-FEB-2002.
XX
XX PF 16-AUG-2001; 2001WO-US25840.
XX
XX PR 16-AUG-2000; 2000US-226326P.
XX
XX PA (CHIR) CHIRON CORP.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;
PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
XX
XX WPI; 2002-241905/29.
XX
XX New nucleic acid for producing a polypeptide, detecting differentially
PT expressed genes correlated with a cancerous state of a mammalian cell,
PT and inhibiting tumor growth -
XX
XX Claim 1; SEQ ID NO 1106; 883pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
CC with cytostatic activity. The polynucleotide is used to produce a
CC polypeptide, to detect differentially expressed genes correlated with a
CC cancerous state of a mammalian cell and to inhibit tumour growth. The
CC polynucleotide is used as a probe in mapping and tissue profiling. The
CC encoded polypeptide and antibodies to the polypeptide can also be used
CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
CC gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 519 BP; 152 A; 118 C; 114 G; 135 T; 0 other;

Alignment Scores:
Pred. No.: 2.59 Length: 519
Score: 76.00 Matches: 22
Percent Similarity: 49.23% Conservative: 10
Best Local Similarity: 33.85% Mismatches: 25
Query Match: 21.17% Indels: 8
DB: 24 Gaps: 3

US-09-830-144-4_COPY_437_504 (1-68) x ABN61139 (1-519)
QY 5 LeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerAspGlyGly 24
Db 368 CTCCTCCATCAGAAAGTCAGAAACACTGACTGAGCAGAGTCATCATGTG- ----GGCTGC 315
QY 25 LeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGlyArgValGluPro 44
Db 314 AGATTCTCAAGGCTCTCTCTGCACAGCTCTGCGCCCTGGAGTAGTGGGAGGCGCATTC 255
QY 45 --TyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGlyGlnSer 63
Db 254 AACAGTCTCTCTTCCCC-----TGGAGTGGGGAAGGAGGTATCATGAGT 210

QY	64 ValValThralaPro 68	64 ValValThralaPro 68	64 ValValThralaPro 68
Db	209 CTCAATCTAATTCCT 195	209 CTCAATCTAATTCCT 195	209 CTCAATCTAATTCCT 195
QY	RESULT 14	RESULT 14	RESULT 14
Db	ABL11586	ABL11586	ABL11586
QY	ABL11586 standard; cDNA; 14091 BP.	ABL11586 standard; cDNA; 14091 BP.	ABL11586 standard; cDNA; 14091 BP.
Db	ABL11586;	ABL11586;	ABL11586;
QY	26-MAR-2002 (first entry)	26-MAR-2002 (first entry)	26-MAR-2002 (first entry)
Db	Drosophila melanogaster expressed polynucleotide SEQ ID NO 29240.	Drosophila melanogaster expressed polynucleotide SEQ ID NO 29240.	Drosophila melanogaster expressed polynucleotide SEQ ID NO 29240.
QY	Drosophila; developmental biology; cell signalling; insecticide;	Drosophila; developmental biology; cell signalling; insecticide;	Drosophila; developmental biology; cell signalling; insecticide;
Db	pharmaceutical; gene; ss.	pharmaceutical; gene; ss.	pharmaceutical; gene; ss.
QY	Drosophila melanogaster.	Drosophila melanogaster.	Drosophila melanogaster.
Db	WO200171042-A2.	WO200171042-A2.	WO200171042-A2.
QY	27-SEP-2001.	27-SEP-2001.	27-SEP-2001.
Db	23-MAR-2001; 2001WO-US09231.	23-MAR-2001; 2001WO-US09231.	23-MAR-2001; 2001WO-US09231.
QY	23-MAR-2000; 2000US-191637P.	23-MAR-2000; 2000US-191637P.	23-MAR-2000; 2000US-191637P.
Db	11-JUL-2000; 2000US-0614150.	11-JUL-2000; 2000US-0614150.	11-JUL-2000; 2000US-0614150.
QY	(PEKE) PE CORP NY.	(PEKE) PE CORP NY.	(PEKE) PE CORP NY.
Db	Venter JC, Adams M, Li PWD, Myers EW;	Venter JC, Adams M, Li PWD, Myers EW;	Venter JC, Adams M, Li PWD, Myers EW;
QY	WPI; 2001-656860/75.	WPI; 2001-656860/75.	WPI; 2001-656860/75.
Db	P-PSDB; ABB67483.	P-PSDB; ABB67483.	P-PSDB; ABB67483.
QY	New isolated nucleic acid detection reagent for detecting 1000 or more	New isolated nucleic acid detection reagent for detecting 1000 or more	New isolated nucleic acid detection reagent for detecting 1000 or more
Db	genes from Drosophila and for elucidating cell signalling and cell-cell	genes from Drosophila and for elucidating cell signalling and cell-cell	genes from Drosophila and for elucidating cell signalling and cell-cell
QY	interactions -	interactions -	interactions -
Db	Claim 1; SEQ ID NO 29240; 21pp + Sequence Listing; English.	Claim 1; SEQ ID NO 29240; 21pp + Sequence Listing; English.	Claim 1; SEQ ID NO 29240; 21pp + Sequence Listing; English.
QY	The invention relates to an isolated nucleic acid detection reagent	The invention relates to an isolated nucleic acid detection reagent	The invention relates to an isolated nucleic acid detection reagent
Db	capable of detecting 1000 or more genes from Drosophila. The invention is	capable of detecting 1000 or more genes from Drosophila. The invention is	capable of detecting 1000 or more genes from Drosophila. The invention is
QY	useful in developmental biology and in elucidating cell signalling and	useful in developmental biology and in elucidating cell signalling and	useful in developmental biology and in elucidating cell signalling and
Db	cell-cell interactions in higher eukaryotes for the development of	cell-cell interactions in higher eukaryotes for the development of	cell-cell interactions in higher eukaryotes for the development of
QY	insecticides, therapeutics and pharmaceutical drugs. The invention	insecticides, therapeutics and pharmaceutical drugs. The invention	insecticides, therapeutics and pharmaceutical drugs. The invention
Db	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
QY	sequences (ABL01840-ABL16175) and the encoded proteins	sequences (ABL01840-ABL16175) and the encoded proteins	sequences (ABL01840-ABL16175) and the encoded proteins
Db	(ABB57737-ABB72072).	(ABB57737-ABB72072).	(ABB57737-ABB72072).
QY	The sequence data for this patent did not form part of the printed	The sequence data for this patent did not form part of the printed	The sequence data for this patent did not form part of the printed
Db	specification, but was obtained in electronic format directly from WIPO	specification, but was obtained in electronic format directly from WIPO	specification, but was obtained in electronic format directly from WIPO
QY	at ftp.wipo.int/pub/published_pct_sequences.	at ftp.wipo.int/pub/published_pct_sequences.	at ftp.wipo.int/pub/published_pct_sequences.
Db	Sequence 14091 BP; 3932 A; 3192 C; 3264 G; 3703 T; 0 other;	Sequence 14091 BP; 3932 A; 3192 C; 3264 G; 3703 T; 0 other;	Sequence 14091 BP; 3932 A; 3192 C; 3264 G; 3703 T; 0 other;
QY	Alignment Scores:	Alignment Scores:	Alignment Scores:
Db	Pred. No.: 270 Length: 14091	Pred. No.: 270 Length: 14091	Pred. No.: 270 Length: 14091
QY	Score: 75.00 Matches: 25	Score: 75.00 Matches: 25	Score: 75.00 Matches: 25
Db	Percent Similarity: 44.44% Conservative: 7	Percent Similarity: 44.44% Conservative: 7	Percent Similarity: 44.44% Conservative: 7
QY	Best Local Similarity: 34.72% Mismatches: 15	Best Local Similarity: 34.72% Mismatches: 15	Best Local Similarity: 34.72% Mismatches: 15
Db	Query Match: 20.89% Indels: 2	Query Match: 20.89% Indels: 2	Query Match: 20.89% Indels: 2
QY	DB: 23 Gaps: 2	DB: 23 Gaps: 2	DB: 23 Gaps: 2
Db	US-09-830-144-4_COPY_437_504 (1-68) x ABL11586 (1-14091)	US-09-830-144-4_COPY_437_504 (1-68) x ABL11586 (1-14091)	US-09-830-144-4_COPY_437_504 (1-68) x ABL11586 (1-14091)
QY	2 SerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 21	2 SerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 21	2 SerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 21
Db	9399 TCCCGAACGAGCTCACTGGCACAACACGCGTCACTACGCGGACGAGC 8998	9399 TCCCGAACGAGCTCACTGGCACAACACGCGTCACTACGCGGACGAGC 8998	9399 TCCCGAACGAGCTCACTGGCACAACACGCGTCACTACGCGGACGAGC 8998
QY	22 AspGlyClyLeuPheArgSerArgProAlaHisSerLeuProProGly----- 37	22 AspGlyClyLeuPheArgSerArgProAlaHisSerLeuProProGly----- 37	22 AspGlyClyLeuPheArgSerArgProAlaHisSerLeuProProGly----- 37
Db	8999 CGGGGATCAACCGTTT-----CGGCGGACACATCACTTCCTCCGCGAGTGGCCCTGCAGC 9052	8999 CGGGGATCAACCGTTT-----CGGCGGACACATCACTTCCTCCGCGAGTGGCCCTGCAGC 9052	8999 CGGGGATCAACCGTTT-----CGGCGGACACATCACTTCCTCCGCGAGTGGCCCTGCAGC 9052

Percent Similarity:	38.96%	Conservative:	8
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DB:	23	Gaps:	2

US-09-830-144-4_COPY_437_504 (1-68) x AAS80813 (1-990)

2	SerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer	21
412	CGGCCACACCGCGATCTGCGGACCCGCTGCCACCCACAGTCTCTCGCAGCTCA	471
22	AspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly---	40
472	GATGG-----AGGAACAGTGGCCCCCAGTCTCGGAAAGTAACCATGGCCGC	522
41	-----ArgValGluProTyr	45
523	CCTCATGGCAGCTCACCTGTTTTGGGGTATTTATTTCGCATCTGCAGATGAGAGGAAC	582
46	ValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGlyGluGln	62
	::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
583	ATTCCAGAAATGTGAAGACTTTCAGAACCTGGACCTCGGCTGGTTCGTGAGAGAG	633

Search completed: December 4, 2003, 09:53:46
Job time : 129.541 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 4, 2003, 09:34:57 : Search time 1463.84 Seconds
(without alignments)
1900.384 Million cell updates/sec
Title: US-09-830-144-4_COPY_437_504
Perfect score: 359
Sequence: 1 QSPTLTLQSTWTHQSSSSS.....AEFYRLMSVDHGQSVVTP 68

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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Database :

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41: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	359	100.0	1515	6	E31041 Method for
2	359	100.0	1560	6	AR058299 Sequence
3	359	100.0	1560	6	AR058302 Sequence
4	359	100.0	1560	6	AR088273 Sequence
5	359	100.0	1560	6	AR088276 Sequence
6	359	100.0	1560	6	AR116881 Sequence
7	359	100.0	1560	6	AR116884 Sequence
8	359	100.0	1560	6	AR231191 Sequence
9	359	100.0	1560	6	AR231192 Sequence
10	359	100.0	1560	6	E14752 Human mRNA
11	359	100.0	1568	6	AR231223 Sequence
12	359	100.0	1568	6	AR308004 Sequence
13	359	100.0	1569	6	AR231195 Sequence
14	359	100.0	1569	6	AR307976 Sequence
15	359	100.0	3096	9	HSU499215
16	359	100.0	3253	9	BC050554
17	359	100.0	3290	9	BC038582 Homo sapi
18	359	100.0	69660	9	HS407F17
19	359	100.0	171718	2	AC141444
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21	356	99.2	2943	10	BC041110
22	356	99.2	2944	10	BC027054
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ALIGNMENTS

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LOCUS E31041 1515 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for screening substance inhibiting binding to XIAP.
ACCESSION E31041
VERSION E31041.1 GI:13017306
KEYWORDS JP 199326328-A/1.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 1515)
AUTHORS Kunihiro, M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 199326328-A 1 26-NOV-1999;
COMMENT KUNIHIRO MATSUMOTO
OS Unidentified
PN JP 199326328-A/1
PD 26-NOV-1999
PP 13-MAY-1999 JP 1998130378
PR KUNIHIRO MATSUMOTO
PI GOIN33/536, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
PC A61K39/395,
PC A61K45/00, A61K45/00, C07K7/06, C07K14/47, PC
G01N33/536,
PC
G01N33/536, G01N33/536//C12N15/09, C12P21/08, A61K37/02, A61K37/02, PC
A61K37/02,
PC A61K37/02, A61K37/24, C12N15/00
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CC Topology: Linear;
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/db_xref="taxon:32644"
BASE COUNT 323 a 457 c 463 g 272 t
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Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1369 TCTGACGAGCGCTTTCGCTCCGCGCCGCCACCTCGCTCCGCTGGAGGAGCGGT 1428
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1429 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 1488
Qy 61 GluGlnSerValValThrAlaPro 68
Db 1489 GAGCAGAGCGTGTGACAGCACC 1512
RESULT 2
LOCUS AR058299 1560 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5837819.
ACCESSION AR058299
VERSION AR058299.1 GI:5983876
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Matsumoto, K. and Nishida, E.
TITLE TAB1 protein
JOURNAL Patent: US 5837819-A 1 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..1560
/organism="unknown"
BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN
Alignment Scores:
Pred. No.: 3,4e-30 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x AR058299 (1-1560)
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Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGCGCTTTCGCTCCGCGCCGCCACCTCGCTCCGCTGGAGGAGCGGT 1457
Qy 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 1517
Qy 61 GluGlnSerValValThrAlaPro 68
Db 1518 GAGCAGAGCGTGTGACAGCACC 1541
RESULT 3
LOCUS AR058302 1560 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5837819.
ACCESSION AR058302
VERSION AR058302.1 GI:5983879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Matsumoto, K. and Nishida, E.
TITLE TAB1 protein
JOURNAL Patent: US 5837819-A 5 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..1560
/organism="unknown"
BASE COUNT 333 a 468 c 480 g 279 t
ORIGIN
Alignment Scores:
Pred. No.: 3,4e-30 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x AR058302 (1-1560)
Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
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QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGCTCTTCCGCTCCGCGCCGCCACTCGCTCCGCTCGCGAGACGGT 1457

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 1517

QY 61 GluGlnSerValValThraPro 68
Db 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 4
LOCUS AR088273 1560 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5989862.
ACCESSION AR088273
VERSION AR088273.1 GI:10015036
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Matsuoto,K. and Nishida,E.
TITLE Tabi protein and DNA coding therefor
JOURNAL Patent: US 5989862-A 1 23-NOV-1999;
FEATURES
Location/Qualifiers
source 1..1560
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BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN

Alignment Scores:
Pred. No.: 3,4e-30 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AR088273 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
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QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGCTCTTCCGCTCCGCGCCGCCACTCGCTCCGCTCGCGAGACGGT 1457

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 1517

QY 61 GluGlnSerValValThraPro 68
Db 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 5
LOCUS AR088276 1560 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5989862.
ACCESSION AR088276
VERSION AR088276.1 GI:10015039
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Matsuoto,K. and Nishida,E.
TITLE Tabi protein and DNA coding therefor
JOURNAL Patent: US 5989862-A 5 23-NOV-1999;
FEATURES
Location/Qualifiers

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BASE COUNT 333 a 468 c 480 g 279 t
ORIGIN

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Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AR088276 (1-1560)

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QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGCTCTTCCGCTCCGCGCCGCCACTCGCTCCGCTCGCGAGACGGT 1457

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
Db 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 1517

QY 61 GluGlnSerValValThraPro 68
Db 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 6
LOCUS AR116881 1560 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6140042.
ACCESSION AR116881
VERSION AR116881.1 GI:14097787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Matsuoto,K. and Nishida,E.
TITLE Tabi protein and DNA coding therefor
JOURNAL Patent: US 6140042-A 1 31-OCT-2000;
FEATURES
Location/Qualifiers
source 1..1560
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BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN

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Pred. No.: 3,4e-30 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AR116881 (1-1560)

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QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
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Alignment Scores:
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Score:          359.00
Length:         1560
Matches:        68

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LOCUS	1560 bp	DNA	linear	PAT 28-JUL-1999
E14752				
DEFINITION Human mRNA for the TAB1 protein.				
E14752				

LOCUS	1560 bp	DNA	linear	PAT 28-JUL-1999
E14752				
DEFINITION Human mRNA for the TAB1 protein.				
E14752				


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ACCESSION E14752
VERSION E14752.1 GI:5709435
KEYWORDS JP 1998004976-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Matsumoto, K. and Nishida, E.
TITLE TAB1 PROTEIN AND DNA CODING THE SAME
JOURNAL Patent: JP 1998004976-A 1 13-JAN-1998;
UNO NAOO
COMMENT OS Homo sapiens (human)
PN JP 1998004976-A/1
PD 13-JAN-1998
PE 28-OCT-1996 JP 1996300856
PR 24-APR-1996 JP 96P 126282
PT MATSUMOTO KUNIHICO, NISHIDA EISUKE
PC C12N15/09, C07H21/04, C07K14/47, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, G01N33/53, (C12N1/19, C12R1:865), (C12N1/21, C12R1:19),
PC (C12N5/10),
PC C12R1:91', (C12P21/02, C12R1:865), (C12P21/02, C12R1:91); CC
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FT unsure 185
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Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 1338 CAAAGCCGACCTTAACCTGAGTCCACCAACGACGACGACGAGCTCCAGC 1397
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 1398 TCTGACGAGGCGCTTTCGCTCCGCGCCGCCACCTCGTCCGCTGGCGAGCGGT 1457
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517
QY 61 GlnGlnSerValValThrAlaPro 68
Db 1518 GAGCAGACGCGTGGTGACAGCACCG 1541
RESULT 11
LOCUS AR231223
DEFINITION Sequence 42 from patent US 6451617.
ACCESSION AR231223

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VERSION AR231223.1 GI:27272111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1568)
AUTHORS Ono, K., Ohtomo, T. and Tsuchiya, M.
TITLE Method of screening TGF-beta. inhibitory substances
JOURNAL Patent: US 6451617-A 42 17-SEP-2002;
FEATURES
source Location/Qualifiers
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BASE COUNT 339 a 472 c 477 g 280 t
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Pred. No.: 3,42e-30 Length: 1568
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 1406 TCTGACGAGGCGCTTTCGCTCCGCGCCGCCACCTCGTCCGCTGGCGAGCGGT 1465
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 1466 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
QY 61 GlnGlnSerValValThrAlaPro 68
Db 1526 GAGCAGACGCGTGGTGACAGCACCG 1549
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LOCUS AR2308004
DEFINITION Sequence 42 from patent US 6551840.
ACCESSION AR2308004
VERSION AR2308004.1 GI:31698761
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1568)
AUTHORS Ono, K., Ohtomo, T. and Tsuchiya, M.
TITLE Method of screening TGF-beta. inhibitory substances
JOURNAL Patent: US 6551840-A 42 22-APR-2003;
FEATURES
source Location/Qualifiers
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BASE COUNT 339 a 472 c 477 g 280 t
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Pred. No.: 3,42e-30 Length: 1568
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x AR308004 (1-1568)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20

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Db 1346 CAAAGCCGACCTTAACCTCGAGTCCACACGACGAGCAGGCTCCAGC 1405
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1406 TCTGACGGAGGCTCTTCCTCCGCGCCGCCACCTCGCTCCGCTCGCGAGGACGGT 1465
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1466 CGTGTGAGCCCTATCTGGACTTTGTGAGTTTACCGCTCTGGAGCGTGGACCAAGGC 1525
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 1526 GAGCAGAGCGTGGTGACGACCG 1549

RESULT 13
 AR2311195
 LOCUS AR2311195 1569 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 10 from patent US 6451617.
 ACCESSION AR2311195
 VERSION AR2311195.1 GI:27272083
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1569)
 AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
 TITLE Method of screening TGF-.beta. inhibitory substances
 JOURNAL Patent: US 6451617-A 10 17-SEP-2002;
 FEATURES
 source Location/Qualifiers
 1..1569 /organism="unknown"
 BASE COUNT 343 a 466 c 476 g 284 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3,42e-30 Length: 1569
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
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US-09-830-144-4_COPY_437_504 (1-68) x AR2311195 (1-1569)

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 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1375 TCTGACGGAGGCTCTTCCTCCGCGCCGCCACCTCGCTCCGCTCGCGAGGACGGT 1434
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1435 CGTGTGAGCCCTATCTGGACTTTGTGAGTTTACCGCTCTGGAGCGTGGACCAAGGC 1494
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 1495 GAGCAGAGCGTGGTGACGACCG 1518

RESULT 14
 AR307976
 LOCUS AR307976 1569 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 10 from patent US 6551840.
 ACCESSION AR307976
 VERSION AR307976.1 GI:31698733
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1569)
 AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
 TITLE Method of screening TGF-.beta.-inhibiting substances

JOURNAL Patent: US 6551840-A 10 22-APR-2003;
 FEATURES
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 ORIGIN

Alignment Scores:
 Pred. No.: 3,42e-30 Length: 1569
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AR307976 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 1315 CAAAGCCGACCTTAACCTCGAGTCCACACGACGAGCAGGCTCCAGC 1374
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 1375 TCTGACGGAGGCTCTTCCTCCGCGCCGCCACCTCGCTCCGCTCGCGAGGACGGT 1434
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 1435 CGTGTGAGCCCTATCTGGACTTTGTGAGTTTACCGCTCTGGAGCGTGGACCAAGGC 1494
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 1495 GAGCAGAGCGTGGTGACGACCG 1518

RESULT 15
 HSU49928
 LOCUS HSU49928 3096 bp mRNA linear PRI 06-APR-1998
 DEFINITION Homo sapiens TAK1 binding protein (TAK1) mRNA, complete cds.
 ACCESSION U49928
 VERSION U49928.1 GI:1401125
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3096)
 AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Shibuya,H., Yamaguchi,K., Shirakabe,K., Tonegawa,A., Gotoh,Y.,
 Ueno,N., Irie,K., Nishida,E. and Matsumoto,K.
 TITLE an activator of the TAK1 MAPKKK in TGF-beta signal transduction

JOURNAL Science 272 (5265), 1179-1182 (1996)

MEDLINE 96216294

PUBMED 8638164

REFERENCE 2 (bases 1 to 3096)

AUTHORS Shibuya,H.

TITLE Direct Submission

JOURNAL Submitted (25-FEB-1996) Hiroshi Shibuya, Faculty of Pharmaceutical Sciences, Hokkaido University, Nishi 6-chome, Kita 12, Kita-ku, Sapporo, Hokkaido 060, Japan

FEATURES
 source Location/Qualifiers
 1..3096 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1..3096 /gene="TAK1"
 21..1535 /gene="TAK1"
 /note="activator for TAK1"
 /codon_start=1
 /product="TAK1 binding protein"
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 /translation="MAAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGT"



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ETSGGAMAVAVLNNKLYAVNGTNRALLCKSTVDGLVTLQNLVDHTTENEDELFRLL
SOLGLDAGIKKQVGIICGESITRIGDYKVKYGTIDIDLSSAASKSPIIAEPEIHGAQ
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KKIHSDTFASGGERARFCPRHEDMTLLVRNFGYPLGEMSQPTSPAPAGGRVYPSV
PYSSAQSTSKTSVTLVMPSCQMVNGAHSASTIDEATPTLTNOSPULTLOSTNHT
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BASE COUNT 642 a 936 c 952 g 566 t
ORIGIN

Alignment Scores:
Pred. No.: 6.83e-30 Length: 3096
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x HSU49928 (1-3096)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1329 CAAGCCCGACCTTAACCTTGAGTCCACCAACGACACGACGAGCAGCTCCAGC 1388
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1389 TCTGACGAGGCGCTCTTCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGT 1448
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1449 CGTGTGAGCCCTATGTGACCTTGTGAGTTTACCGCCTCTGGAGCGTGGACCATGGC 1508
QY 61 GluGlnSerValValThrAlaPro 68
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1509 GAGCAGCGGTGGTGACGACCG 1532

Search completed: December 4, 2003, 11:40:02
Job time : 1469.84 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:09:50 ; Search time 6.66216 Seconds
(without alignments)
479.997 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPFLTLQSTNTHTQSSSS.....AEFYRLWSVDHGQSQSVTP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	359	100.0	504	1	TAB1_HUMAN	Q15750 homo sapien
2	63.5	17.7	243	1	IM17_ARATH	Q98P35 arabidopsis
3	63.5	17.7	824	1	AD08_HUMAN	P78125 homo sapien
4	62	17.3	541	1	N057_YEAST	P48837 saccharomyc
5	61	17.0	1119	1	ALS3_CANAL	O74623 candida alb
6	61	17.0	1511	1	PRR5_YEAST	P33302 saccharomyc
7	60	16.7	226	1	ORAZ_MOUSE	P54369 mus musculu
8	60	16.7	1260	1	ALS1_CANAL	P46590 candida alb
9	59	16.4	329	1	CAHX_FLAPR	P46281 flaveria pr
10	59	16.4	330	1	CAH1_FLALI	P46512 flaveria li
11	59	16.4	330	1	CAHX_FLAPR	P46511 flaveria br
12	59	16.4	399	1	PRS3_SHEEP	O97967 ovis aries
13	58.5	16.3	608	1	FLR1_MOUSE	Q98501 mus musculu
14	58.5	16.3	1093	1	AF17_HUMAN	P55198 homo sapien
15	58.5	16.3	1099	1	PLC1_CANAL	O13433 candida alb
16	58.5	16.3	3256	1	K167_HUMAN	P46013 homo sapien
17	58	16.2	142	1	YNEK_BACSU	P45711 bacillus su
18	58	16.2	276	1	CAPB_DROME	P48603 drosophila
19	58	16.2	532	1	SPG7_DICDI	P22698 dictyosteli
20	57.5	16.0	232	1	HXB4_XENLA	O30770 xenopus lae
21	57.5	16.0	396	1	CSA_HUMAN	Q13216 homo sapien
22	57.5	16.0	686	1	VILL_HUMAN	O15195 homo sapien
23	57	15.9	461	1	KEM2_MOUSE	Q9K187 mus musculu
24	57	15.9	937	1	NU98_HUMAN	P52948 homo sapien
25	57	15.9	1377	1	NEO1_RAT	P27603 rattus norv
26	57	15.9	1461	1	NEO1_HUMAN	Q92859 homo sapien
27	56.5	15.7	276	1	PSBS_LYCES	P54773 lycopersico
28	56.5	15.7	283	1	PANC_BACHD	Q9Kc86 bacillus ha
29	56.5	15.7	343	1	DHSO_BACHD	Q9Z900 bacillus ha
30	56.5	15.7	457	1	CUSC_ECOLI	P77211 escherichia
31	56.5	15.7	459	1	MCE1_YEAST	Q01159 saccharomyc
32	56.5	15.7	463	1	PLSB_CARTI	Q42713 carthamus t
33	56.5	15.7	922	1	NRP1_RAT	Q9QWJ9 rattus norv

RESULT 1

ID	TAB1_HUMAN	STANDARD;	PRT;	504 AA.
AC	Q15750;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Mitogen-activated protein kinase kinase 7 interacting protein 1			
DE	(TAK1-binding protein 1).			
GN	MAP3K7IP1 OR TAB1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=96216294; PubMed=8638164;			
RA	Shibuya H., Yamaguchi K., Shirakabe K., Tonegawa A., Gotoh Y.,			
RA	Ueno N., Irie K., Nishida E., Matsumoto K.;			
RT	"TAB1: an activator of the TAK1 MAPKKK in TGF-beta signal			
RT	transduction.";			
RL	Science 272:1179-1184 (1996).			
[2]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=20057165; PubMed=10591208;			
EX	Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Grahame D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	Mcclay J.N., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,			
RA	Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spragun L., Steward C.A., Sulston J.E., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,			
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,			
RA	Shintani A., Shibuya K., Sasaki T., Asakawa S., Kudoh J.,			
RA	Roe B.A., Chen F., Chu L., Crabtree J., Aoki N., Mitsuana S.,			
RA	Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Do T.,			
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,			
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,			
RA	Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,			
RA	Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,			

ALIGNMENTS

014786 homo sapien
P54674 dictyosteli
Q99212 homo sapien
P00776 streptomyce
O43597 homo sapien
Q39836 glycine max
Q60320 homo sapien
P08138 homo sapien
Q8ncw0 homo sapien
P22814 drosophila
Q92275 schizophylli
Q9rl60 mus musculu

34 56.5 15.7 923 1 NRPI_HUMAN
35 56.5 15.7 1858 1 P3K2_DICDI
36 56 15.6 237 1 TG12_HUMAN
37 56 15.6 297 1 PRTA_STRGR
38 56 15.6 315 1 SPY2_HUMAN
39 56 15.6 325 1 GBLP_SOYEN
40 56 15.6 405 1 Y574_HUMAN
41 56 15.6 427 1 TRI6_HUMAN
42 56 15.6 462 1 KRM2_HUMAN
43 56 15.6 509 1 RUNT_DROME
44 56 15.6 639 1 BARI_SCHCO
45 56 15.6 652 1 FXO1_MOUSE

RA	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Schect P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J., Rana I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.
RT	"The DNA sequence of human chromosome 22."
RL	Nature 402:489-495(1999)
CC	-1- FUNCTION: MAY BE AN IMPORTANT SIGNALING INTERMEDIATE BETWEEN TGFB RECEPTORS AND MAP3K7/TAK1.
CC	-1- SUBUNIT: Interacts with MAP3K7 and with BIRC7.
CC	-1- TISSUE SPECIFICITY: Ubiquitous.
CC	-1- SIMILARITY: Contains 1 PP2C-like domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC	-----
EMBL	U49928; AAC12660.1; -
DR	EMBL; Z83845; CAB55304.1; -
DR	Genew; HGNC:18157; MAP3K7IP1.
DR	MM, 602615; -
DR	GO: 0008047; F:enzyme activator activity; TAS.
DR	GO: 0005515; F:protein binding activity; TAS.
DR	GO: 0000185; P:activation of MAPKK; TAS.
DR	InterPro: IPR001932; PP2C-like.
DR	Pfam: PF00481; PP2C; 1.
DR	SMART; SM00332; PP2CC; 1.
FT	DOMAIN 64 368
FT	DOMAIN 452 457
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Query Match	100.0%; Score 359; DB 1; Length 504;
Best Local Similarity	100.0%; Pred. No. 7.7e-34;
Matches	68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	437 QSPTLTQSTNTHTQSSSSDGLFRSPAHSPPGDDGRVEPYVDFAEFYRLWSVDHG 496
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Db	497 EQSVVTAP 504
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AC	Q9SP35; Q9ZUS5;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Mitochondrial import inner membrane translocase subunit TIM17.
GN	TIM17 OR A12G37410 OR F3G5.20.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;
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RN	SEQUENCE FROM N.A.
RA	Miernyk J.A., Coop N.E.;
RP	"A component of the Arabidopsis thaliana mitochondrial inner membrane protein translocase, atTIM17."
RT	

RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]	
RN	SEQUENCE FROM N.A.
RC	STRAIN=cv. Columbia;
RX	MEDLINE=20083487; PubMed=10617197;
RA	Lin X., Kaul S., Rounsley S.D., Shear T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead C.M., Koo H.L., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Van Aken S., Moffat K.S., Cronin L.A., Shen M., Pai G., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."
RL	Nature 402:761-768(1999).
CC	-1- FUNCTION: COMPONENT OF THE PREPROTEIN IMPORT MACHINERY OF THE MITOCHONDRIAL INNER MEMBRANE. INTEGRAL PART OF A PROTEIN-CONDUCTING CHANNEL OF THE MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
CC	-1- SUBUNIT: FORMS PART OF THE TIM23 RECEPTOR COMPLEX THAT CONSISTS OF AT LEAST 3 DIFFERENT PROTEINS; TIM17, TIM23 AND TIM44 (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
CC	-1- SIMILARITY: BELONGS TO THE TIM17/TIM22/TIM23 FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC	-----
EMBL	AF16847; AAF03749.1; -
DR	EMBL; AC005896; AAC98060.1; -
DR	PIR; D84792; D84792.
DR	InterPro: IPR000087; Collagen.
DR	InterPro: IPR003397; Tim17_Tim22.
DR	Pfam; PF02466; Tim17; 1.
KW	Transport; Protein transport; Translocation; Mitochondrion;
KW	Inner membrane; Transmembrane.
FT	TRANSMEM 15 35
FT	TRANSMEM 63 83
FT	TRANSMEM 117 137
FT	CONFLICT 116 116 A -> T (IN REF. 1).
FT	CONFLICT 219 219 Q -> H (IN REF. 1).
SQ	SEQUENCE 243 AA; 25571 MW; 199285297F58BD51 CRC64;
Query Match	17.7%; Score 63.5; DB 1; Length 243;
Best Local Similarity	39.0%; Pred. No. 3.6;
Matches	16; Conservative 6; Mismatches 18; Indels 1; Gaps 1;
Qy	8 QSTNTHTQSSSSDGLFRSPAHSPPGDDGRVEPYVDF 48
Db	193 QNQTASSSSSSSWFGGLF-DKKKEVQPGSEKTEVLESF 232
RESULT 3	
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ID	AD08_HUMAN
AC	P78325;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	ADAM 8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 8) (Cell surface antigen MS2) (CD156a antigen) (CD156).
GN	ADAM8 OR MS2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
OX	NCBI_TaxID=9606;

FT	DOMAIN	76	223	9 X 4 AA REPEATS OF G-L-F-G.
FT	DOMAIN	26	31	POLY-ASN.
FT	DOMAIN	127	130	POLY-THR.
FT	DOMAIN	217	220	POLY-GLY.
FT	DOMAIN	258	266	POLY-GLN.
FT	DOMAIN	277	280	POLY-GLN.
FT	DOMAIN	398	425	COILED COIL (POTENTIAL).
SQ	SEQUENCE	541 AA;	57498 MW;	B292ADF7B1D7E83C CRC64;
Query Match				
Best Local Similarity 17.3%; Score 62; DB 1; Length 541;				
Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;				
QY	8 QSTNTHQSSSSSDGGLFRSRPA	31		
Db	60 QATNFGSNQSSSTGGGLFGNKPA	83		
RESULT 5				
AL53-CANAL	STANDARD;	PRT;	1119 AA.	
AC	074623;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Agglutinin-like protein 3 precursor.			
GN	ALS3.			
OS	Candida albicans (Yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.			
OX	NCBI_TaxID=5476;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=11161;			
RX	MEDLINE=98309840; PubMed=9644209;			
RA	Hover L.L., Payne T.L., Bell M., Myers A.M., Scherer S.;			
RT	"Candida albicans ALS3 and insights into the nature of the ALS gene family";			
RL	Curr. Genet. 33:451-459(1998).			
CC	- - FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.			
CC	- - PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U87956; AAC39486.1; -			
KW	Cell adhesion; Glycoprotein;			
FT	SIGNAL	1	17	Repeat; Signal.
FT	CHAIN	18	1119	POTENTIAL.
FT	DOMAIN	433	792	AGGLUTININ-LIKE PROTEIN 3.
FT	REPEAT	433	468	10 X 36 AA TANDEM REPEATS.
FT	REPEAT	469	504	1-1.
FT	REPEAT	505	540	1-2.
FT	REPEAT	541	576	1-3.
FT	REPEAT	577	612	1-4.
FT	REPEAT	613	648	1-5.
FT	REPEAT	649	684	1-6.
FT	REPEAT	685	720	1-7.
FT	REPEAT	721	756	1-8.
FT	REPEAT	757	792	1-9.
FT	REPEAT	793	829	1-10.
FT	DOMAIN	399	404	POLY-THR.
FT	DOMAIN	450	455	POLY-THR.
FT	DOMAIN	557	563	POLY-THR.
FT	DOMAIN	593	597	POLY-THR.
FT	DOMAIN	630	635	POLY-THR.
FT	DOMAIN	666	671	POLY-THR.
FT	DOMAIN	702	707	POLY-THR.
FT	DOMAIN	738	743	POLY-THR.

FT	DOMAIN	774	777	POLY-THR.
FT	DOMAIN	1044	1047	POLY-THR.
FT	CARBOHYD	471	471	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	543	543	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	579	579	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	651	651	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	687	687	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	723	723	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	759	759	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	845	845	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	987	987	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1050	1050	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1061	1061	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1119 AA;	119927 MW;	6A3FB3FC8C879A71 CRC64;
Query Match				
Best Local Similarity 23.8%; Pred. No. 44;				
Matches 24; Conservative 13; Mismatches 28; Indels 36; Gaps 4;				
QY	1 QSPTLTLOSTNTHQSSSSS	-----SDGGLFRSRPAHSL	-----	34
Db	720 EPNHVTITTEYWSQSYATTTT	APPGETDTVLIREPNNHTVTTEYWSQSYATTTTII	779	
QY	35 -PEGEDGRV	-----EPYVDFAEFYRLWSVDHGQSVVTAP	68	
Db	780 APGETDTVLIREPNNHTVTTEY	---WSQSYTTATTVTAP	817	
RESULT 6				
PDR5 YEAST	STANDARD;	PRT;	1511 AA.	
ID	PDR5 YEAST			
AC	P33302;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Suppressor of toxicity of sporidesmin.			
GN	PDR5 OR STS1 OR YDR1 OR LEM1 OR YOR153W.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=AB320;			
RX	MEDLINE=94140838; PubMed=9307980;			
RA	Bissinger P.H., Kuchler K.;			
RT	"Molecular cloning and expression of the Saccharomyces cerevisiae			
RT	STS1 gene product. A yeast ABC transporter conferring mycotoxin			
RT	resistance.";			
RL	J. Biol. Chem. 269:4180-4186 (1994).			
CC	[2]			
CC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	MEDLINE=94124579; PubMed=8294477;			
RA	Balzi E., Wang M., Leterme S., van Dyck L., Goffeau A.;			
RT	"PDR5, a novel yeast multidrug resistance conferring transporter			
RT	controlled by the transcription regulator PDR1.";			
RL	J. Biol. Chem. 269:2206-2214 (1994).			
CC	[3]			
CC	SEQUENCE FROM N.A.			
RC	STRAIN=AH22;			
RX	MEDLINE=95188264; PubMed=7882421;			
RA	Hirata D., Yano K., Miyahara K., Miyakawa T.;			
RT	"Saccharomyces cerevisiae YDR1, which encodes a member of the ATP-			
RT	binding cassette (ABC) superfamily, is required for multidrug			
RT	resistance.";			
RL	Curr. Genet. 26:285-294 (1994).			
CC	[4]			
CC	SEQUENCE FROM N.A.			
RC	STRAIN=S288C / FY1678;			
RA	Ayadi A., Bordonne R., Camasses A., Madania A., Poch O.,			
RA	Tarasov I.A., Winsor B., Martin R.P.;			
RT	"Analysis of a 35600 bp region on the right arm of Saccharomycetes			

cerevisiae chromosome XV.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: TRANSPORTER, WHOSE PHYSIOLOGICAL FUNCTION IS NOT YET
CC ESTABLISHED. CONFERS RESISTANCE TO THE CHEMICALS CYCLOHEXIMIDE
CC AND SULFOMETHURON METHYL. EXHIBITS NUCLEOSIDE TRIPHOSPHATASE
CC ACTIVITY.
CC !- SUBCELLULAR LOCATION: Integral membrane protein.
CC !- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
CC !- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 61.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X74113; CAA52212.1; -
CC EMBL; L19922; AAB53769.1; -
CC EMBL; D28548; BAA05547.1; ALT_INIT.
CC EMBL; U55020; AAC49639.1; -
CC EMBL; Z75061; CAA99359.1; -
CC PIR; A53151; A53151.
CC SGD; S0005679; PDR5.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR005285; PDR.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC_transporter; 2.
CC SMART; SM00382; AAA; 2.
CC TIGRfams; TIGR00956; 3a01205; 1.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
CC ATP-binding; Transmembrane; Glycoprotein; Transport.
CC DOMAIN 1 517 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 518 542 POTENTIAL.
CC TRANSMEM 559 579 POTENTIAL.
CC TRANSMEM 612 628 POTENTIAL.
CC TRANSMEM 632 650 POTENTIAL.
CC TRANSMEM 666 685 POTENTIAL.
CC TRANSMEM 775 793 POTENTIAL.
CC DOMAIN 794 1237 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 1238 1260 POTENTIAL.
CC TRANSMEM 1292 1313 POTENTIAL.
CC TRANSMEM 1325 1349 POTENTIAL.
CC TRANSMEM 1355 1379 POTENTIAL.
CC TRANSMEM 1389 1407 POTENTIAL.
CC TRANSMEM 1477 1499 POTENTIAL.
CC DOMAIN 1500 1511 CYTOPLASMIC (POTENTIAL).
CC NP_BIND 905 912 ATP (POTENTIAL).
CC DOMAIN 784 787 POLY-PHE.
CC CONFLICT 171 171 N -> L (IN REF. 3).
CC CONFLICT 190 190 V -> I (IN REF. 3).
CC CONFLICT 214 214 D -> T (IN REF. 3).
CC CONFLICT 308 308 G -> V (IN REF. 3).
CC CONFLICT 340 345 MISSING (IN REF. 3).
CC CONFLICT 476 476 R -> H (IN REF. 3).
CC CONFLICT 648 648 MISSING (IN REF. 3).
CC CONFLICT 770 770 D -> H (IN REF. 3).
CC SEQUENCE 1511 AA; 170437 MW; 4540DC0BF04744BA CRC64;
Query Match 17.0%; Score 61; DB 1; Length 1511;
Best Local Similarity 38.8%; Pred. No. 64;
Matches 19; Conservative 6; Mismatches 16; Indels 8; Gaps 3;
QY 4 TLTLQSTNTHQTSSSSSDG-GLFRS-----RPAHSLP--PGDGRVPEP 44
DB 49 TLTAQSMQNSTQAPNKSQAQSFSSGVEGVNPIFSDPEAPGYDPKLD 97

RESULT 7
OAZ_MOUSE
ID OAZ_MOUSE STANDARD; PRT; 226 AA.
AC P54369; O08610;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ornithine decarboxylase antizyme (ODC-AZ).
GN OAZ1 OR OAZ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9808944; PubMed=9428668;
RA Nilsson J., Koskinen S., Persson K., Grahn B., Holm I.;
RT "Polyamines regulate both transcription and translation of the gene
RT encoding ornithine decarboxylase antizyme in mouse.";
RT Eur. J. Biochem. 250:223-231(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Svj;
RL Kankare K., Uusi-Oukari M., Janne O.A.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: BINDS TO, AND DESTABILIZES, ORNITHINE DECARBOXYLASE
CC WHICH IS THEN DEGRADED. ALSO INHIBITS CELLULAR UPTAKE OF
CC POLYAMINES BY INACTIVATING THE POLYAMINE UPTAKE TRANSPORTER.
CC !- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC FOR SER-67 AND ASP-68. AN AUTOREGULATORY MECHANISM ENABLES
CC MODULATION OF FRAMESHIFTING ACCORDING TO THE CELLULAR
CC CONCENTRATION OF POLYAMINES.
CC !- SIMILARITY: BELONGS TO THE ODC ANTIZYME FAMILY.
CC
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CC
CC EMBL; U52822; AAB96329.1; -
CC EMBL; U52823; AAB96330.1; -
CC EMBL; U84291; AAC53307.1; -
CC MGD; MGI:109433; Oaz1.
CC InterPro; IPR002993; ODC_AZ.
CC Pfam; PF02100; ODC_AZ; 1.
CC ProDom; PD007483; ODC_AZ; 1.
CC PROSITE; PS01337; ODC_AZ; 1.
CC RIBOSOMAL frameshift.
CC FT INIT MET 0 0 BY SIMILARITY.
CC FT CONFLICT 68 68 D -> C (IN REF. 1: AAB96330).
CC SEQUENCE 226 AA; 25002 MW; C58D8D6B730318F6 CRC64;
Query Match 16.7%; Score 60; DB 1; Length 226;
Best Local Similarity 31.7%; Pred. No. 8.4;
Matches 19; Conservative 8; Mismatches 23; Indels 10; Gaps 2;
QY 1 QSTP-----LTLOSTNTHQTSSSSSDGGLFRSRAHSLPPGDGRVPEYVDPAE 50
DB 104 EEPSTNDKTRVLSTQTLTEAKQVTRAVWSGGGLYELPAGLPPEGSKDSFAALLFAE 163
RESULT 8
ALSL1_CANAL
ID ALSL1_CANAL STANDARD; PRT; 1260 AA.
AC P46590;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Agglutinin-like protein 1 precursor.
GN ALSL1.

OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11651 / B792;
RA MEDLINE=95272392; PubMed=7752895;
RX Hoyer L.L., Scherer S., Shatzman A.R., Livi G.P.;
RT "Candida albicans ALS1: domains related to a Saccharomyces cerevisiae
RT sexual agglutinin separated by a repeating motif.",
RL Mol. Microbiol. 15:39-54(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
CC -!- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).
CC -!- SIMILARITY: TO YEAST SAG1.
CC
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CC
CC -----
CC EMBL; L25902; AAC41649.2;
CC Cell adhesion; Glycoprotein; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 17
FT SIGNAL 18 1260
FT DOMAIN 433 792
FT REPEAT 433 468
FT REPEAT 469 504
FT REPEAT 505 540
FT REPEAT 541 576
FT REPEAT 577 612
FT REPEAT 613 648
FT REPEAT 649 684
FT REPEAT 685 720
FT REPEAT 721 756
FT REPEAT 757 792
FT DOMAIN 983 1152
FT REPEAT 1092 1152
FT REPEAT 1092 1152
FT DOMAIN 399 404
FT DOMAIN 408 418
FT DOMAIN 450 455
FT DOMAIN 486 491
FT DOMAIN 522 527
FT DOMAIN 558 563
FT DOMAIN 594 599
FT DOMAIN 630 635
FT DOMAIN 666 671
FT DOMAIN 702 707
FT DOMAIN 738 743
FT DOMAIN 774 779
FT DOMAIN 874 877
FT CARBOHYD 471 471
FT CARBOHYD 579 579
FT CARBOHYD 615 615
FT CARBOHYD 687 687
FT CARBOHYD 723 723
FT CARBOHYD 820 820
FT CARBOHYD 886 886
FT CARBOHYD 918 918
FT CARBOHYD 973 973
FT CARBOHYD 1045 1045
FT CARBOHYD 1068 1068
SQ SEQUENCE 1260 AA; 132641 MW; 763D1063A2354C24 CRC64;

Query Match 16.7%; Score 60; DB 1; Length 1260;
Best Local Similarity 24.2%; Pred. No. 67;
Matches 23; Conservative 9; Mismatches 35; Indels 28; Gaps 3;

2 SPTLTL-----QSTNTHQSSSSSDGGLFRSRPAHSL-----PP 36

Db 651 NPVTITTEYSQSYATTTTITAPPGBTDTVLIREPNNHTVTTTEYSQSYATTTTAPP 710
QY 37 GEDGRV---EPYVDFAEFRLWSVDHGEQSVVTAP 68
Db 711 GETDTVLIREPNNHTVTTTTEYSQSYATTTTAP 745

RESULT 9
CAHX FLAPR STANDARD; PRT; 329 AA.
ID CAHX FLAPR STANDARD; PRT; 329 AA.
AC P46281;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase).
OS Flaveria pringlei.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=4226;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=96046753; PubMed=7579185;
RA Ludwig M., Burnell J.N.;
RT "Molecular comparison of carbonic anhydrase from Flaveria species
RT demonstrating different photosynthetic pathways.",
RL Plant Mol. Biol. 29:353-365(1995).
CC -!- FUNCTION: Reversible hydration of carbon dioxide.
CC -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC -!- SUBUNIT: Homohexamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- DOMAIN: POSSESSES A TRANSIT-LIKE PEPTIDE, BUT IT IS PROPOSED THAT
CC THIS PEPTIDE IS NOT REMOVED AND THAT THEREFORE THE ENZYME STAYS
CC IN THE CYTOPLASM INSTEAD OF GOING TO THE CHLOROPLAST
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PLANT AND PROKARYOTIC CARBONIC
CC ANHYDRASE FAMILY.
CC
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CC
CC -----
CC EMBL; U19737; AAA86992.1;
CC FIR; S61884; S61884.
CC Interpro; IPR001765; Prok_Coanhd.
CC Pfam; PF00484; Pro_CA; 1.
CC PROSITE; PS00704; PROK_CO2_ANHYDRASE_1; 1.
CC PROSITE; PS00705; PROK_CO2_ANHYDRASE_2; 1.
CC Lyase; Zinc. 1 108 CHLOROPLAST TRANSIT PEPTIDE-LIKE.
FT DOMAIN 23 26 POLY-SER.
FT DOMAIN 40 46 POLY-SER.
SQ SEQUENCE 329 AA; 35486 MW; B18E656B1E84C34B CRC64;

Query Match 16.4%; Score 59; DB 1; Length 329;
Best Local Similarity 27.0%; Pred. No. 17;
Matches 20; Conservative 13; Mismatches 33; Indels 8; Gaps 2;

QY 1 QSPITLTQSTNTHQSSSSSDGGLFRSRPAHSLPP-----GEDGRVYVDFAFYR 53
Db 28 RSGVLSARFTCNSSSSSSSSTPPSLIRNEPFAAPAIITPNWTEDGN-ESYEIDAALK 86

QY 54 LWSVDHGEQSVVTA 67
Db 87 KMLIEKGELEFVAA 100

[illegible]

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RC TISSUE=Pituitary;
RX MEDLINE=99367324; PubMed=10425452;
RA Whitley J.C., Moore C., Giraud A.S., Shulkes A.;
RT "Molecular cloning, genomic organization and selective expression of
RT bombesin receptor subtype 3 in the sheep hypothalamus and
RT pituitary.";
RL J. Mol. Endocrinol. 23:107-116(1999).
CC -!- FUNCTION: ROLE IN SPERM CELL DIVISION, MATURATION, OR FUNCTION.
CC THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS.
CC THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AF108210; AAD19642.1; -.
CC EMBL; AF108209; AAD19639.1; -.
CC EMBL; AF108207; AAD19639.1; JOINED.
CC EMBL; AF108208; AAD19639.1; JOINED.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 41
FT TRANSMEM 42 63
FT DOMAIN 64 82
FT TRANSMEM 83 103
FT DOMAIN 104 121
FT TRANSMEM 122 143
FT DOMAIN 144 163
FT TRANSMEM 164 184
FT DOMAIN 185 220
FT TRANSMEM 221 241
FT DOMAIN 242 272
FT TRANSMEM 273 293
FT DOMAIN 294 313
FT TRANSMEM 314 333
FT DOMAIN 334 399
FT CARBOHYD 10 10
FT CARBOHYD 18 18
FT CARBOHYD 29 29
FT DISULFID 120 203
SQ SEQUENCE 399 AA; 44373 MW; B48DD27197AED2EB CRC64;

Query Match 16.4%; Score 59; DB 1; Length 399;
Best Local Similarity 34.7%; Pred. No. 22;
Matches 17; Conservative 4; Mismatches 28; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTQSSSSSDGGLFRSPAHSLPPGDDGRVEPYVDFA 49
DB 7 QSPNQTLISTNDTESSSVVPDSTNKRRTGDSNPGIEALCAIYIYA 55

RESULT 13
PRLR MOUSE
ID_PRLR MOUSE STANDARD; PRT; 608 AA.
AC Q08501; P15212; P15213; Q62099;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DR Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM PRL-R3).
RP STRAIN=C3H; TISSUE=Mammary gland;
RX MEDLINE=94085788; PubMed=8262385;
RA Moore R.C., Oka T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RT long-form prolactin receptor.";
RL Gene 134:263-265(1993).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM PRL-R3).
RP STRAIN=Swiss Webster; TISSUE=Liver;
RX MEDLINE=93307149; PubMed=8319571;
RA Clarke D.L., Linzer D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RT mouse ovary.";
RL Endocrinology 133:224-232(1993).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM PRL-R3).
RP Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RA Sasaki M.;
RX Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM PRL-R3).
RP STRAIN=BALB/c; TISSUE=Mammary gland;
RX Ebery M., Pezet A., Nandi S., Kelly P.A.;
RA Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORMS PRL-R2 AND PRL-R1).
RP STRAIN=Swiss Webster; TISSUE=Liver;
RX MEDLINE=89261824; PubMed=2725531;
RA Davis J.A., Linzer D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse
RT liver.";
RL Mol. Endocrinol. 3:674-680(1989).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=PRL-R3;
CC IsoId=Q08501-1; Sequence=Displayed;
CC Name=PRL-R1;
CC IsoId=Q08501-2; Sequence=VSP_001723, VSP_001724;
CC Name=PRL-R2;
CC IsoId=Q08501-3; Sequence=VSP_001721, VSP_001722;
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L13593; AAC37641.1; -.
CC EMBL; L14811; AAA02686.1; -.
CC EMBL; D10214; BAA01066.1; -.
CC EMBL; X73372; CAA51789.1; -.
CC EMBL; M23859; AAA33977.1; -.
CC EMBL; M22958; AAA39976.1; -.
CC PIR; I53269; I53269.
CC PIR; I77524; I77524.
CC PIR; I77525; I77525.
CC HSSP; P16471; 1BP3.
CC MGD; MGI:97763; Prlr.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 2.

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DR SMART; SMO0060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 608
FT DOMAIN 20 229
FT TRANSMEM 230 253
FT DOMAIN 254 608
FT DOMAIN 254 608
FT DOMAIN 119 222
FT DISULFID 31 41
FT DISULFID 70 81
FT CARBOHYD 54 54
FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT VARSPLIC 281 292
FT VARSPLIC 293 608
FT VARSPLIC 281 303
FT VARSPLIC 304 608
FT CONFLICT 558 558
FT SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;

Query Match 16.3%; Score 58.5; DB 1; Length 608;
Best Local Similarity 24.7%; Pred. No. 41;
Matches 18; Conservative 12; Mismatches 24; Indels 19; Gaps 2;

QY 2 SPTLTQSTNTHNTOSSSSSDGLFRSPAHSLLPGEDGRVEYVDFAEFRLWSVDHGCQSVVTAP 68
Db 388 TPNNQNTNCHTDSKSTT-----WPLPPGQHTRRSPYHSIADVCKLAGSGDGT 437

QY 57 ----VDHGCQSV 65
Db 438 LDSFLDKAEENVL 450

QY 57 ----VDHGCQSV 65
Db 438 LDSFLDKAEENVL 450

RESULT 14
AF17 HUMAN
ID AF17 HUMAN STANDARD; PRT; 1093 AA.
AC P55198;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE AF-17 protein.
GN MLLT6 OR AF17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9436695; PubMed=8058765;
RA Prasad R., Leshkowitz D., Gu Y., Alder H., Nakamura T., Saito H.,
RA Ruebner K., Berger R., Croce C.M., Canaanani E.;
RA "Leucine-zipper dimerization motif encoded by the AF17 gene fused to
RL AL1-1 (ML1) in acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8107-8111(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY A CHROMOSOMAL
CC TRANSLOCATION T(11;17)(Q23;Q21) THAT INVOLVES MLLT6 AND MLL/HEX.
CC THE RESULT IS A ROGUE ACTIVATOR PROTEIN.
CC -!- SIMILARITY: Contains 2 PHD-type zinc fingers.
CC -!- SIMILARITY: HIGH, TO AF10.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/AF17.html".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
```

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U07932; AAA21145.1; -
CC F1R; I38533; I38533.
CC Genew; HGNC:7138; MLLT6.
CC MIM; 600328; -
CC GO; GO:0007048; P:oncogenesis; TAS.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
CC InterPro; IPR001965; Znf_PHD.
CC Pfam; PF00628; PHD; 1.
CC SMART; SMO0249; PHD; 2.
CC PROSITE; PS01359; ZF_PHD 1; 1.
CC PROSITE; PS00016; ZF_PHD 2; 2.
KW Nuclear protein; Zinc-finger; Repeat; Chromosomal translocation;
KW Proto-oncogene.
FT ZN_FING 5 57
FT ZN_FING 51 68
FT ZN_FING 117 180
FT DOMAIN 190 211
FT DOMAIN 275 282
FT DOMAIN 326 338
FT DOMAIN 729 764
FT DOMAIN 822 829
FT DOMAIN 834 862
FT DOMAIN 935 984
FT DOMAIN 1040 1051
FT DOMAIN 1069 1080
FT SITE 551 551
SQ SEQUENCE 1093 AA; 112021 MW; F60042A6D3BF579E CRC64;

Query Match 16.3%; Score 58.5; DB 1; Length 1093;
Best Local Similarity 36.4%; Pred. No. 84;
Matches 20; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 14 TQSSSSDGLFRSPAHSLLPGEDGRVEYVDFAEFRLWSVDHGCQSVVTAP 68
Db 330 SSSSSSSSGGPF--QPAVS-----SLQSSPDSAPPKLEQPEEDKYKPTAP 375

RESULT 15
PLC1 CANAL
ID PLC1 CANAL STANDARD; PRT; 1099 AA.
AC O13433;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1
DE (EC 3.1.4.11) (Phosphoinositide phospholipase C) (PLC-1)
DE (Phospholipase C-1).
GN PLC1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=132A;
RX MEDLINE=98129081; PubMed=9467900;
RA Bennett D.E., McCreary C.E., Coleman D.C.;
RA "Genetic characterization of a phospholipase C gene from Candida
RT albicans: presence of homologous sequences in Candida species other
RT than Candida albicans.";
RL Microbiology 144:55-72(1998).
CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
```

```

CC  -!- CATALYTIC ACTIVITY: 1-phosphatidy1-d-myo-inositol 4,5-
CC      bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC      diacylglycerol.
CC  -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC      PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC  -!- SIMILARITY: Contains 1 C2 domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; Y13975; CAA74308.1; -.
CC  PIR; T18257; T18257.
CC  RSP; F10688; 1DJX.
CC  InterPro; IPR000008; C2.
CC  InterPro; IPR001192; PI_PLC.
CC  InterPro; IPR000909; PI_PLC_Xdom.
CC  InterPro; IPR001711; PI_PLC_Y.
CC  Pfam; PF00168; C2; 1.
CC  Pfam; PF00388; PI_PLC-X; 1.
CC  Pfam; PF00387; PI_PLC-Y; 1.
CC  PRINTS; PR00390; PHEPLIPASEC.
CC  ProDom; PD001202; PI_PLC_Y; 1.
CC  SMART; SMC0239; C2; 1.
CC  SMART; SMC0148; PLCYC; 1.
CC  SMART; SMC0149; PLCYC; 1.
CC  PROSITE; PS50004; C2 DOMAIN 2; FALSE NEG.
CC  PROSITE; PS50007; PIPLC X DOMAIN; 1.
CC  PROSITE; PS50008; PIPLC Y DOMAIN; 1.
CC  Hydrolase; lipid degradation; Transducer.
CC  DOMAIN 566 726 DOMAIN X.
CC  DOMAIN 794 912 DOMAIN Y.
CC  DOMAIN 938 1066 C2 DOMAIN.
CC  ACT_SITE 579 579 BY SIMILARITY.
CC  ACT_SITE 642 642 BY SIMILARITY.
CC  DOMAIN 90 102 POLY-SER.
CC  DOMAIN 239 243 POLY-THR.
CC  DOMAIN 517 520 POLY-ASP.
CC  DOMAIN 619 623 POLY-THR.
CC  DOMAIN 629 632 POLY-ASP.
CC  DOMAIN 743 760 POLY-THR.
CC  DOMAIN 918 921 POLY-SER.
CC  SEQUENCE 1099 AA; 124591 MW; D54D687D53A2829B CRC64;

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Query Match      16.3%; Score 58.5; DB 1; Length 1099;
Best Local Similarity 28.1%; Pred. No. 84;
Matches 16; Conservative 12; Mismatches 20; Indels 9; Gaps 3;

QY 1 QSPFTLTQSTNTHQTQSSSSSDGGLFRSR----PAHSLP--PGEDGR---VEPYVDF 48
Db 912 RKPTLKSSSNVDRTSLTTNSKTIRNFELISGHQLPKPKDDYKDQAINPYISF 968

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Search completed: December 4, 2003, 09:30:50
Job time : 8.66216 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:33:11 ; Search time 21.1351 Seconds
(without alignments)
598.382 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPTLTQSTNTHWTQSSSS.....AEFYRLMSVDHGQSVVTAP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdb:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdb:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdb:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	359	100.0	504	12	US-10-384-743-2
2	359	100.0	504	14	US-10-123-427-2
3	359	100.0	504	14	US-10-123-427-6
4	359	100.0	504	14	US-10-158-895-2
5	359	100.0	513	12	US-10-384-743-3
6	359	100.0	513	14	US-10-158-895-43
7	359	100.0	517	12	US-10-384-743-11
8	359	100.0	517	14	US-10-158-895-11
9	352	98.1	84	10	US-09-925-300-1270
10	77	21.4	16	12	US-10-384-743-41
11	77	21.4	16	14	US-10-158-895-41
12	69.5	19.4	199	10	US-09-941-831-21
13	67.5	18.8	739	12	US-10-374-979-89
14	67.5	18.8	739	15	US-10-097-534-10
15	67.5	18.8	752	11	US-09-919-039-235

16	66	18.4	16	12	US-10-384-743-40	Sequence 40, Appl
17	66	18.4	16	14	US-10-158-895-40	Sequence 40, Appl
18	65.5	18.2	498	14	US-10-037-667-5	Sequence 5, Appl
19	64.5	18.0	244	15	US-10-012-542-463	Sequence 463, App
20	63.5	17.7	240	9	US-09-853-161-100	Sequence 100, App
21	63.5	17.7	240	9	US-09-852-659A-100	Sequence 100, App
22	63.5	17.7	240	10	US-09-852-797-100	Sequence 100, App
23	63.5	17.7	335	9	US-09-853-161-64	Sequence 64, Appl
24	63.5	17.7	335	9	US-09-852-659A-64	Sequence 64, Appl
25	63.5	17.7	335	10	US-09-852-797-64	Sequence 64, Appl
26	63.5	17.7	824	12	US-10-210-951-58	Sequence 58, Appl
27	63.5	17.7	824	12	US-10-211-884-58	Sequence 58, Appl
28	63.5	17.7	824	15	US-10-226-844-1	Sequence 1, Appl
29	63.5	17.7	946	15	US-10-156-761-14486	Sequence 14486, A
30	63	17.5	850	9	US-09-915-181A-3	Sequence 3, Appl
31	62	17.3	141	12	US-10-029-386-30357	Sequence 30357, A
32	62	17.3	734	15	US-10-040-862-10463	Sequence 10463, A
33	61	17.0	322	9	US-09-764-853-606	Sequence 606, Appl
34	61	17.0	1119	15	US-10-245-802-12	Sequence 12, Appl
35	61	17.0	1511	10	US-09-801-368-250	Sequence 250, App
36	60	16.7	402	15	US-10-156-761-8505	Sequence 8505, Ap
37	60	16.7	1260	15	US-10-245-802-8	Sequence 8, Appl
38	58.5	16.3	235	9	US-09-799-777-43	Sequence 43, Appl
39	58.5	16.3	515	12	US-10-094-466-16	Sequence 16, Appl
40	58.5	16.3	3256	10	US-09-919-172-98	Sequence 98, Appl
41	58.5	16.3	3256	11	US-09-919-039-21	Sequence 21, Appl
42	58	16.2	692	15	US-10-156-761-12598	Sequence 12598, A
43	58	16.2	1047	15	US-10-245-802-22	Sequence 22, Appl
44	57.5	16.0	367	15	US-10-106-698-5815	Sequence 5815, Ap
45	57.5	16.0	394	9	US-09-815-242-10233	Sequence 10233, A

ALIGNMENTS

RESULT 1

US-10-384-743-2
; Sequence 2, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JF98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-2

Query Match 100.0%; Score 359; DB 12; Length 504;

Best Local Similarity 100.0%; Pred. No. 1.6e-34;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPTLTQSTNTHWTQSSSSDGLFRSPAHSLPPDGDGRVPEYVDFAEYRLMSVDHG 60

Db 437 QSPTLTQSTNTHWTQSSSSDGLFRSPAHSLPPDGDGRVPEYVDFAEYRLMSVDHG 496

Qy 61 BQSVVTAP 68

Db 497 BQSVVTAP 504

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RESULT 2
US-10-123-427-2
; Sequence 2, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/123,427
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-123-427-2
Query Match 100.0%; Score 359; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QSPILTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEYRLMSVDHG 60
Db 437 QSPILTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEYRLMSVDHG 496
Qy 61 EQSVVTAP 68
Db 497 EQSVVTAP 504
RESULT 3
US-10-123-427-6
; Sequence 6, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
```

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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/123,427
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-123-427-6
Query Match 100.0%; Score 359; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QSPILTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEYRLMSVDHG 60
Db 437 QSPILTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEYRLMSVDHG 496
Qy 61 EQSVVTAP 68
Db 497 EQSVVTAP 504
RESULT 4
US-10-158-995-2
; Sequence 2, Application US/10158995
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
```



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; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-2

Query Match      100.0%; Score 359; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
Db 437 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496

QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 5
US-10-384-743-43
; Sequence 43, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-43

Query Match      100.0%; Score 359; DB 12; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
Db 446 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 505

QY 61 EQSVVTAP 68
Db 506 EQSVVTAP 513

RESULT 6
US-10-158-895-43
; Sequence 43, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
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; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Query Match      100.0%; Score 359; DB 14; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.6e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
Db 446 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 505

QY 61 EQSVVTAP 68
Db 506 EQSVVTAP 513

RESULT 7
US-10-384-743-11
; Sequence 11, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-11

Query Match      100.0%; Score 359; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
Db 437 QSPITLQSTNTHTCSSSSDGGFLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496

QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 8
US-10-158-895-11
; Sequence 11, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
```

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; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-158-895-11

Query Match      100.0%; Score 359; DB 14; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPTLTQSTNTHQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLWSVDHG 60
Db 437 QSPTLTQSTNTHQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLWSVDHG 496

Qy 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 9
US-09-925-300-1270
; Sequence 1270, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1270
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1270

Query Match      98.1%; Score 352; DB 10; Length 84;
Best Local Similarity 98.5%; Pred. No. 1.3e-34;
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSPTLTQSTNTHQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLWSVDHG 60
Db 17 QSPTLTQSTNTHQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLWSVDHG 76

Qy 61 EQSVVTAP 68
Db 77 EQSVVTAP 84

RESULT 10
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US-10-384-743-41
; Sequence 41, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-384-743-41

Query Match      21.4%; Score 77; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPTLTQSTNTHQ 15
Db 2 QSPTLTQSTNTHQ 16

RESULT 11
US-10-158-895-41
; Sequence 41, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-158-895-41

Query Match      21.4%; Score 77; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPTLTQSTNTHQ 15
Db 2 QSPTLTQSTNTHQ 16
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RESULT 12
US-09-941-831-21
; Sequence 21, Application US/09941831
; Patent No. US20020160493A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: PT049p1
; CURRENT APPLICATION NUMBER: US/09/941,831
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US01/06256
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/186,350
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-941-831-21

Query Match 19.4%; Score 69.5; DB 10; Length 199;
Best Local Similarity 41.9%; Pred. No. 2.2;
Matches 18; Conservative 3; Mismatches 17; Indels 5; Gaps 1;

QY 1 QSPTLTQSTNTHQTSSSSSDG-----LFRSRPAHSLPPGE 38
Db 119 QSPTLTLDQTRIHSSRDAFSSISGCKFTAVKRMADKLPVGQ 161

RESULT 13
US-10-374-979-89
; Sequence 89, Application US/10374979
; Publication No. US20030219793A1
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-021
; CURRENT APPLICATION NUMBER: US/10/374,979
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 09/544,398
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 89
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-979-89

Query Match 18.8%; Score 67.5; DB 12; Length 739;
Best Local Similarity 31.1%; Pred. No. 18;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;

QY 2 SPTLTQSTNTHQTSSSSSDG-----GLFRSRPAH-----SLPPGEDGRVEPYVDF 48
Db 119 SSTGSLPPTNTNTNTSEGATSLIPLTISGSGRPLNVTQAPLPFGWEQRVD----- 173
QY 49 AEFYRLMSVDHGEQ 62
Db 174 -QHGRVYVDHVEK 186

RESULT 14
US-10-097-534-10
; Sequence 10, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; TITLE OF INVENTION: MATURATION
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-534-10

Query Match 18.8%; Score 67.5; DB 15; Length 739;
Best Local Similarity 31.1%; Pred. No. 18;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;
QY 2 SPTLTQSTNTHQTSSSSSDG-----GLFRSRPAH-----SLPPGEDGRVEPYVDF 48
Db 119 SSTGSLPPTNTNTNTSEGATSLIPLTISGSGRPLNVTQAPLPFGWEQRVD----- 173
QY 49 AEFYRLMSVDHGEQ 62
Db 174 -QHGRVYVDHVEK 186

RESULT 15
US-09-919-039-235
; Sequence 235, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 235
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1989186CD1
US-09-919-039-235

Query Match 18.8%; Score 67.5; DB 11; Length 752;
Best Local Similarity 31.1%; Pred. No. 19;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;
QY 2 SPTLTQSTNTHQTSSSSSDG-----GLFRSRPAH-----SLPPGEDGRVEPYVDF 48
Db 132 SSTGSLPPTNTNTNTSEGATSLIPLTISGSGRPLNVTQAPLPFGWEQRVD----- 186
QY 49 AEFYRLMSVDHGEQ 62

Db 187 : |:: ||| |:
-QHGRVYVDHVEK 199

Search completed: December 4, 2003, 09:44:39
Job time : 21.1351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:23:11 ; Search time 39.2838 Seconds
(without alignments)
558.155 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252
Sequence: 1 VELRQLSRVNHPIVKLYG.....MTHLMRYFPGADEPLQYPCQ 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1252	100.0	567	2 JC5957	transforming growth
2	1252	100.0	579	2 JC5955	transforming growth
3	1252	100.0	606	2 JC5956	transforming growth
4	392.5	31.3	954	1 S68178	mixed-lineage prot
5	374	29.9	407	2 G84635	probable protein k
6	373	29.8	412	2 T10671	protein kinase hom
7	363.5	29.0	394	2 JU0229	mixed-lineage prot
8	362	28.9	1338	2 T18287	protein-tyrosine k
9	356	28.4	462	2 S29851	protein kinase 6 (
10	355.5	28.4	370	2 T46150	protein kinase ATM
11	353.5	28.2	668	2 JC2363	protein kinase (EC
12	353.5	28.2	888	2 A55318	serine/threonine p
13	351.5	28.1	888	2 JC5399	dual leucine zippe
14	350	28.0	546	2 D84555	probable protein k
15	348	27.8	391	2 T48115	protein kinase ATM
16	347	27.7	475	2 T12955	probable protein k
17	346	27.6	328	2 T16747	hypothetical prote
18	346	27.6	1030	2 F96763	hypothetical prote
19	345.5	27.6	553	2 T04683	hypothetical prote
20	345.5	27.6	847	1 A53800	mixed-lineage prot
21	344	27.5	390	2 T01451	protein kinase hom
22	341	27.2	410	2 B35670	protein-tyrosine k
23	340	27.2	387	2 T22511	hypothetical prote
24	336	26.8	356	2 S61766	protein kinase ATM
25	329.5	26.3	357	2 C84856	probable protein k
26	328.5	26.3	545	2 T05675	hypothetical prote
27	328.5	26.2	377	2 T46149	protein kinase ATM
28	328.5	26.2	736	2 T05137	protein kinase hom
29	324	25.9	982	2 T06576	probable protein k

ALIGNMENTS

RESULT 1

JC5957
transforming growth factor-beta activated kinase (EC 2.7.-.-) 1c - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Mar-2000
C:Accession: JC5957
R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
Biochem. Biophys. Res. Commun. 243, 545-549, 1998
A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-indu
A:Reference number: JC5955; MUID:98153801; PMID:9480845
A:Accession: JC5957
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-567 <SAK>
A:Cross-references: DDBJ:AB009358
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: phosphotransferase

Query Match 100.0%; Score 1252; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 4e-73;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VELRQLSRVNHPIVKLYGACLNIPVCLVMEYAEAGSLYNVLHGAPLPYYTAAHMSWCL 60
DB 76 VELRQLSRVNHPIVKLYGACLNIPVCLVMEYAEAGSLYNVLHGAPLPYYTAAHMSWCL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLLVAGGTVLKICDFTGACDIQTHMTNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLLVAGGTVLKICDFTGACDIQTHMTNNKGSAAW 195
QY 121 MAPEVFGSNYSKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPLIKNL 180
DB 196 MAPEVFGSNYSKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPLIKNL 255
QY 181 KPPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFFGADPELQYPCQ 228
DB 256 KPPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFFGADPELQYPCQ 303

RESULT 2

JC5955
transforming growth factor-beta activated kinase (EC 2.7.-.-) 1a - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5955
R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
Biochem. Biophys. Res. Commun. 243, 545-549, 1998
A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-indu
A:Reference number: JC5955; MUID:98153801; PMID:9480845
A:Accession: JC5955
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-579 <SAK>
A;Cross-references: DDBJ:AB009356; NID:g2924623; PIDN:BAA25025.1; PID:g2924624
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: phosphotransferase

Query Match 100.0%; Score 1252; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 60
DB 76 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNKGSAAW 195

QY 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPDDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPDDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPQRSMEIIVKIMTHLMRYFFGADPELQYPCQ 228
DB 256 PKPIESLMTRCWSKDPQRSMEIIVKIMTHLMRYFFGADPELQYPCQ 303

RESULT 3
JC5956
transforming growth factor-beta activated kinase (EC 2.7.1.-) 1b - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5956
R;Sakurai, H.; Shigenori, N.; Hasegawa, K.; Saito, T.
Biochem. Biophys. Res. Commun. 243, 545-549 (1998)
A;Title: TGF-beta-activated kinase 1 stimulates Ser/Thr phosphorylation by an NF-kappaB-ind
A;Reference number: JC5955; MUID:98153801; PMID:9480845
A;Accession: JC5956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-606 <SAK>
A;Cross-references: DDBJ:AB009357; NID:g2924625; PIDN:BAA25026.1; PID:g2924626
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: phosphotransferase

Query Match 100.0%; Score 1252; DB 2; Length 606;
Best Local Similarity 100.0%; Pred. No. 4.3e-73;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 60
DB 76 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNKGSAAW 195

QY 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPDDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPDDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPQRSMEIIVKIMTHLMRYFFGADPELQYPCQ 228
DB 256 PKPIESLMTRCWSKDPQRSMEIIVKIMTHLMRYFFGADPELQYPCQ 303

RESULT 4
S68178
mixed-lineage protein kinase 2 (EC 2.7.1.-) - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C;Accession: S68178; S32468
R;Dorow, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simps
Eur. J. Biochem. 234, 492-500, 1995

A;Title: Complete nucleotide sequence, expression, and chromosomal localisation of huma
A;Reference number: S68178; MUID:96128179; PMID:8536694
A;Accession: S68178
A;Molecule type: mRNA
A;Residues: 1-954 <DOR>
A;Cross-references: EMBL:X90846; NID:g971419; PIDN:CAA62351.1; PID:g971420
R;Kato, H.; Hirai, M.; Sugimura, T.; Terada, M.
Oncogene 10, 1447-1451, 1995
A;Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase
A;Reference number: I38044; MUID:95249256; PMID:7731697
A;Accession: I38044
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
A;Cross-references: EMBL:Z48615; NID:g758592; PIDN:CAA88531.1; PID:g758593
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
A;Title: Identification of a new family of human epithelial protein kinases containing
A;Reference number: S32467; MUID:93238756; PMID:8477742
A;Accession: S32468
A;Molecule type: mRNA
A;Residues: 244-464, 'AQAAGRRQHPQALWL' <DO2>
C;Genetics:
A;Gene: GDB:MLK2; GDB:MST
A;Cross-references: GDB:362654; GDB:624810; OMIM:600137
A;Map position: 19q13.1-19q13.2
C;Superfamily: mixed-lineage protein kinase 2; protein kinase homolog; SH3 homology
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
F;23-76/Domain: SH3 homology <SH3>
F;96-364/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif
F;384-405/Region: leucine zipper motif
F;419-440/Region: leucine zipper motif
F;449-463/Region: basic
F;125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 31.3%; Score 392.5; DB 1; Length 954;
Best Local Similarity 40.6%; Pred. No. 5.4e-18;
Matches 88; Conservative 35; Mismatches 77; Indels 17; Gaps 6;

QY 2 ELRQLSRVNHPIVLYGACLP--VCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 59
DB 145 EARLFGALQHPNIALRGACLP--VCLVMEYAEAGSLYVNLHGAEPPLPYTAHAHMSWCL 200

QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLV-----AGTVLKICDFGTACDIQTHTM 111
DB 201 VQVARGMNYLHNDAPVPIIHRDLKSNILILEAENHNLDATVTKITDFGLAREWHKTK 260

QY 112 TNKKGSAWNAPEVFGSNYSKCDVFSWGIIILWEVITRRKPDDEIGGPAFRIMWAV-HN 170
DB 261 MSAGTYAWNAPEVIRLSFKSDVMSFGVLLWELLTGEVYREL--DALAVAYGVAMN 318

QY 171 GTRPPLIKNLPKPIESLMTRCWSKDPQRSMEIIVK 207
DB 319 KLTLPIPTCTCFEPPARLLEECWDPDHPGRDPFGSILK 355

RESULT 5
G84635
probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: G84635
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>

A;Cross-references: GB:AE002093; NID:G4337195; PIDN:AA18109.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2G24360
A;Map position: 2
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 29.9%; Score 374; DB 2; Length 407;
Best Local Similarity 39.4%; Pred. No. 3.9e-17;
Matches 86; Conservative 40; Mismatches 70; Indels 22; Gaps 9;

QY 2 ELRQLSRVNHPIVLYGACLNVP--CLVMEYAEAGSGLYNVL-----HGAELPYPYTAHA 55
Db EVSMLANLKHPIVFIAGACIKPMWCIIVTEYAKGVSQFLTRQNRAPVPLK-----A 229
QY 56 MSWCLQCSQGVAYLHSMQPKALIHRLKPPNLLVAGGTVLKICDGTGTA-CDIQTH-MTN 113
Db VQKALDVARGWAYVHG---RNFIHRLKSDNLLISADKSI-KIADFGVARIQTEGWTTP 285
QY 114 NKGSAAMWAPVFEFGSNYSEKCDVFSWGIILWEVITRRKPFDEIGG--PAPRIMWAVHG 171
Db ETGTYRWMAPEMIQHRAYNQKVDVYSGIVLWELITGLLPFQNTAVQAFAV---VNRG 342
QY 172 TRPPLIKNLKPISLMTKRCWKDPSQSPSMEEIVKIM 209
Db VRPTVPNDCLPVLSDIMTRCWDANPEVRPCFVEVVKLL 380

RESULT 6

TI0671
protein kinase homolog F6E21.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C;Accession: TI0671
R;Byan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: TI0671
A;Molecule type: DNA
A;Residues: 1-412 <BEV>
A;Cross-references: ENBL:AL049914; GSPDB:GN00062; ATSP:F6E21.90
A;Experimental source: cultivar Columbia; BAC clone F6E21
C;Genetics:
A;Gene: ATSP:F6E21.90
A;Map position: 4
A;Introns: 300/2
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;135-392/Domain: protein kinase homology <KIN>

Query Match 29.8%; Score 373; DB 2; Length 412;
Best Local Similarity 39.9%; Pred. No. 4.6e-17;
Matches 87; Conservative 39; Mismatches 70; Indels 22; Gaps 9;

QY 2 ELRQLSRVNHPIVLYGACLNVP--CLVMEYAEAGSGLYNVL-----HGAELPYPYTAHA 55
Db 180 EVSMLANLKHPIVFIAGACIKPMWCIIVTEYAKGVSQFLTRQNRAPVPLK-----A 234
QY 56 MSWCLQCSQGVAYLHSMQPKALIHRLKPPNLLVAGGTVLKICDGTGTA-CDIQTH-MTN 113
Db 235 VQKALDVARGWAYVHE---RNFIHRLKSDNLLISADKSI-KIADFGVARIQTEGWTTP 290
QY 114 NKGSAAMWAPVFEFGSNYSEKCDVFSWGIILWEVITRRKPFDEIGG--PAPRIMWAVHG 171
Db 291 ETGTYRWMAPEMIQHRPYTKVDVYSGIVLWELITGLLPFQNTAVQAFAV---VNRG 347
QY 172 TRPPLIKNLKPISLMTKRCWKDPSQSPSMEEIVKIM 209
Db 348 VRPTVPNDCLPVLGEIMTRCWDADPEVRPCFPAEIVNLL 385

RESULT 7

JU0229
mixed-lineage protein kinase 1 - human
C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: S32467; JU0229
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
A;Title: Identification of a new family of human epithelial protein kinases containing t
A;Reference number: S32467; MUID:93238756; PMID:8477742
A;Accession: S32467
A;Molecule type: mRNA
A;Residues: 1-394 <DO2>

C;Genetics:
A;Gene: GDB:MLK1
A;Cross-references: GDB:141921; OMIM:600136
A;Map position: 14q24.3-14q31
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F;1-269/Domain: protein kinase homology <KIN>
F;1-268/Domain: catalytic <CAT>
F;9-17/Region: protein kinase ATP-binding motif
F;289-310/Region: leucine zipper motif
F;324-345/Region: leucine zipper motif
F;354-368/Region: basic

Query Match 29.0%; Score 363.5; DB 2; Length 394;
Best Local Similarity 37.7%; Pred. No. 1.8e-16;
Matches 83; Conservative 36; Mismatches 84; Indels 17; Gaps 6;

QY 2 ELRQLSRVNHPIVLYGACLNVP--CLVMEYAEAGSGLYNVLHGAELPYPYTAHAHMSWC 59
Db 50 EAKLFAMLKHPNIIALRGVCLKEPNLCVMEFARGGPLNVLGSKRIPPDI-----LVNWA 105
QY 60 LQCSQGVAYLHSMQPKALIHRLKPPNLLV-----AGTVLKI CDFTGACD-IQTHM 111
Db 106 VQIARGMNYLHDEAIVPIIHRDLKSSNLIILQKVENGLSNKLIKITDFGLAREWHRTTK 165
QY 112 TNNKGSAAWMAPEVFEFGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAV-HN 170
Db 166 MSAAGTYAWMAPEVIRASMFSGSDVWSYGVLNELLTGEVFFRGIDG--LRVAYGVAMN 223
QY 171 GTRPPLIKNLKPISLMTKRCWKDPSQSPSMEEIVKIMT 210
Db 224 KLALPPISTCPEPAFLKMECDWPNPHSRPSTNILDQLT 263

RESULT 8

TI8287
protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C;Accession: TI8287
R;Adler, K.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z18856
A;Accession: TI8287
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1338 <ADL>
A;Cross-references: EMBL:U64830; NID:G1468982; PID:G1468983; PIDN:AA04999.1
C;Genetics:
A;Introns: 1181/3
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 28.9%; Score 362; DB 2; Length 1338;
Best Local Similarity 38.1%; Pred. No. 6.4e-16;
Matches 80; Conservative 41; Mismatches 73; Indels 16; Gaps 6;

QY 2 ELRQLSRVNHPIVLYGACLNVPCLVMEYAEAGSGLYNVLH-----GAELPYPYTAHMS 57
Db 1100 EVSLSLKSHENPVVTFMGARIDPPCIFTEYLGQSGSLVDLHIQIKLNPLMVMYKWIHDL- 1158
QY 58 WCLQCSQGVAYLHSMQPKALIHRLKPPNLLVAGGTVLKICDFTGACDIQTHMT-NNKG 116
Db 1159 -----SLGMEHLHSIQ---MLHRDLTSKNILLDFEKNI-KIADFGLATTLSDMTLSGIT 1209

QY 177 IKNLKPPIESLMTRCWSKDPQSPQSPMEIVKIMTHL 212
 Db 332 PSSCPDGFKILLRQCWNKSPRNPSPFRQ---ILLHL 364
 RESULT 12
 A55318
 serine/threonine protein kinase (EC 2.7.1.1) DLK - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Sep-1999
 C:Accession: A55318
 R:Holzman, L.B.; Merritt, S.E.; Fan, G.
 J. Biol. Chem. 269, 30808-30817, 1994
 A:Title: Identification, molecular cloning, and characterization of dual leucine zipper
 s.
 A:Reference number: A55318; MUID:95074107; PMID:7983011
 A:Accession: A55318
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-888 <HOL>
 A:Cross-references: GB:U14636; NID:g602677; PIDN:AA57280.1; PID:g602678
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; leucine zipper; phosphotransferase
 F:156-404/Domain: protein kinase homology <KIN>
 F:164-172/Region: protein kinase ATP-binding motif

Query Match 28.2%; Score 353.5; DB 2; Length 888;
 Best Local Similarity 34.7%; Pred. No. 1.6e-15;
 Matches 75; Conservative 43; Mismatches 81; Indels 17; Gaps 8;
 QY 2 ELRQLSRVNHNPVIVKLYGACLNLP--VCLVMEYAEAGSLYNVLHGAEPPLPYTAHAMSWC 59
 Db 194 DIKHLRLKLPNIITFGVGTQAPCYCIMFECAQGLYEVLRAGRPV---TPSLLDVWS 250
 QY 60 LQCSOGVAYLHSMQPKALIHRLDKPPLLVLVAGGTVLKICDFGTACDIQTHMTNNK--GS 117
 Db 251 MGIAAGMYLHLK---IIHRDLKSPN-MLITYDDVVKISDFGTSKLSKTSKMSFAGT 306
 QY 118 AAWAPEVIRNEPVSEKVDIWSFGVLLWELLTGTETPKYKDVDSA--IIWGVGNSLSLHPV 364
 Db 307 VAWAPEVIRNEPVSEKVDIWSFGVLLWELLTGTETPKYKDVDSA--IIWGVGNSLSLHPV 364
 QY 177 IKNLKPPIESLMTRCWSKDPQSPQSPMEIVKIMTHL 212
 Db 365 PSSCPDGFKILLRQCWNKSPRNPSPFRQ---ILLHL 397
 RESULT 13
 JC5399
 dual leucine zipper kinase (EC 2.7.1.1) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 28-May-1999
 C:Accession: JC5399
 R:Matsu, N.; Sarkar, G.; Shuto, T.; Marrs, J.; Bronk, J.T.; Mizuno, K.; Bolander, M.E.
 Biochem. Biophys. Res. Commun. 229, 571-576, 1996
 A:Title: Identification of a dual leucine zipper kinase involved in rat fracture repair.
 A:Reference number: JC5399; MUID:97127443; PMID:8954939
 A:Accession: JC5399
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-888 <MAT>
 C:Comment: This enzyme is involved in regulating cell function in the musculoskeletal system
 C:Genetics:
 A:Gene: rDLK
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; phosphotransferase
 F:54-75/Region: glycine-rich
 F:156-454/Domain: kinase catalytic #status predicted <CAT>
 F:156-404/Domain: protein kinase homology <KIN>
 F:164-172/Region: protein kinase ATP-binding motif
 F:421-449/Region: leucine zipper motif
 F:472-500/Region: leucine zipper motif

F:557-888/Region: glycine-serine-proline rich #status predicted

Query Match 28.1%; Score 351.5; DB 2; Length 888;
 Best Local Similarity 34.3%; Pred. No. 2.1e-15;
 Matches 74; Conservative 44; Mismatches 81; Indels 17; Gaps 8;
 QY 2 ELRQLSRVNHNPVIVKLYGACLNLP--VCLVMEYAEAGSLYNVLHGAEPPLPYTAHAMSWC 59
 Db 194 DIKHLRLKLPNIITFGVGTQAPCYCIMFECAQGLYEVLRAGRPV---TPSLLDVWS 250
 QY 60 LQCSOGVAYLHSMQPKALIHRLDKPPLLVLVAGGTVLKICDFGTACDIQTHMTNNK--GS 117
 Db 251 MGIAAGMYLHLK---IIHRDLKSPN-MLITYDDVVKISDFGTSKLSKTSKMSFAGT 306
 QY 118 AAWAPEVIRNEPVSEKVDIWSFGVLLWELLTGTETPKYKDVDSA--IIWGVGNSLSLHPV 364
 Db 307 VAWAPEVIRNEPVSEKVDIWSFGVLLWELLTGTETPKYKDVDSA--IIWGVGNSLSLHPV 364
 QY 177 IKNLKPPIESLMTRCWSKDPQSPQSPMEIVKIMTHL 212
 Db 365 PSSCPDGFKILLRQCWNKSPRNPSPFRQ---ILLHL 397

RESULT 14

D84555
 probable protein kinase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: D84555
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nuss, D.; Nierman, W.C.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: D84555
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-546 <STO>
 A:Cross-references: GB:AR002093; NID:96598802; PIDN:AAB80785.2; GSPDB:GNO0139
 C:Genetics:
 A:Gene: At2g17700
 A:Map position: 2

Query Match 28.0%; Score 350; DB 2; Length 546;
 Best Local Similarity 36.3%; Pred. No. 1.7e-15;
 Matches 81; Conservative 41; Mismatches 83; Indels 18; Gaps 8;

QY 3 LRQLS-----RVNHPNIVKLYGACLN--PVCILVMEYAEAGSLYNVLHGAEPPLPYTA 53
 Db 325 LREFSQEVFIMRKVRHKNVQFLGACTRSPCLCTVTEFMARGSIYDFLHKQKCA--FKLQ 382
 QY 54 HAWSCLQCSOGVAYLHSMQPKALIHRLDKPPLLVLVAGGTVLKICDFGTACDIQTHM 111
 Db 383 TLLKVALDVAKGMYLHQ---NNIIHRDLKTPANLMDHGLV-KVADFGVARVQIESGM 438
 QY 112 TNKGSAAWMAPEVFEKSNYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMWVHNG 171
 Db 439 TAETGTVRWMAPEVIEHKPNHKAQVFSYALVWELLTGTIDIPYAF-LTPLOAAGVGVQKG 497
 QY 172 TRPLIKNLPKPIESLMTRCWSKDPQSPQSPMEIVKIMTHL 214
 Db 498 LRPKPKTPKPKVKGGLERQWHDQDEQRPLFEIEMLQIQIMK 540

RESULT 15

T48115
 protein kinase ATMRL1 (EC 2.7.1.1) [imported] - Arabidopsis thaliana
 N:Alternate names: protein F16M2.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2001
 C:Accession: T48115; T51942
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.

submitted to the Protein Sequence Database, April 2000

A;Reference number: Z24459
A;Accession: T48115
A;Molecule type: DNA
A;Residues: 1-391 <RIE>
A;Cross-references: EMBL:AL138648; NID:g7523397; PIDN:CA886427.1; PID:g7523408
A;Experimental source: cultivar Columbia; BAC clone F16M2
R;Ichimura, K.; Mizoguchi, T.; Shinozaki, K.
Plant Sci. 130, 171-179, 1997
A;Title: AtMRK1, an Arabidopsis protein kinase related to mammal mixed-lineage kinases
A;Reference number: Z24427
A;Accession: T51942
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-391 <ICH>
A;Cross-references: EMBL:AB006810; NID:g2351096; PIDN:BAA22079.1; PID:g2351097
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 3
A;Introns: 109/1; 149/3; 220/2; 278/3; 323/3
A;Note: F16M2.110
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase

Query Match 27.8%; Score 348; DB 2; Length 391;
Best Local Similarity 33.7%; Pred. No. 1.7e-15;
Matches 82; Conservative 35; Mismatches 76; Indels 50; Gaps 8;
QY 2 ELQLSRVNHPNIVKLYGACL-----NPVCLVMEYAEAGSGLY 38
DB 135 EVAVWQKLDHPNVTKEFGASNGTSDLRIPAGDTGGRNGAHPARACCVVEYVAGGTLK 194
QY 39 NVLHGAELPYTYA-----AHAMSWCLOCSQGVAVLHMQPKALHRLKPNLLVAGGT 94
DB 195 KFL-----IKRYAKLPKDVQIALDLARGLSYLHS---KATVHRDVKSENMLLPNK 246
QY 95 VLKICDFGTA--CDIOTHTNNKSAWMAPEVFEKSNYSEKCDVFSWGIILWEVITRR 151
DB 247 -LKIADFGVARVEAQNQDMTGETGTGLYMAPEVLEKPYNRKCDVYSFGVCLWEIYCCD 305
QY 152 KP-----FDEIGGPAFRIMMAVHNGTRPPLIKNLPKPIESLMTKCSKDPQSPRESMEIIV 206
DB 306 MPYADCGFAEISHA-----VVHRLRPEIKKCPHAVANIMKRCWDPNDRPMEBEVV 359
QY 207 KIM 209
DB 360 KLL 362

Search completed: December 4, 2003, 09:34:04
Job time : 40.2838 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:08:45 ; Search time 77.7973 Seconds
(without alignments)
465.179 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELRQLSRVNHPIVILKLYGA.....MTHLMRYFPGADPELPQYPCQ 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 19Jun03.*

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19: /SIDSL/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	100.0	567	20 AAY28998	Human TGF-beta act
2	1252	100.0	579	18 AAW27092	Mouse transforming
3	1252	100.0	579	18 AAW27093	Human transforming
4	1252	100.0	579	20 AAY28996	Human TGF-beta act
5	1252	100.0	579	20 AAY09542	Human TAK1 protein
6	1252	100.0	579	21 AAY91000	Human TAK-1 protei
7	1252	100.0	579	23 ABB85033	Pain regulated pro
8	1252	100.0	590	20 AAY09547	Human TAK1-6xHis p
9	1252	100.0	606	20 AAY28997	Human TGF-beta act

10	700	55.9	678	22	ABB58061	Drosophila melanog
11	414	33.1	252	22	AB860985	Drosophila melanog
12	374	29.9	367	21	AA32053	Arabidopsis thalia
13	374	29.9	369	21	AA32052	Arabidopsis thalia
14	374	29.9	407	21	AA32051	Arabidopsis thalia
15	373	29.8	369	21	AA32172	Arabidopsis thalia
16	373	29.8	374	21	AA32171	Arabidopsis thalia
17	373	29.8	412	21	AA32170	Arabidopsis thalia
18	371	29.6	349	22	AA375571	Human colon cancer
19	371	29.6	455	21	AA18657	A human regulator
20	371	29.6	455	21	AA18657	A human regulator
21	371	29.6	455	21	AA18657	A human regulator
22	371	29.6	455	21	AA18657	A human regulator
23	371	29.6	455	21	AA18657	A human regulator
24	371	29.6	455	21	AA18657	A human regulator
25	371	29.6	455	21	AA18657	A human regulator
26	363.5	29.0	394	24	AA37648	Human protein kin
27	363.5	29.0	1020	22	AB58999	Drosophila melanog
28	359.5	28.7	1024	23	AB98408	Human NOV7, a mixe
29	355.5	28.4	1021	23	ABP61000	Novel human protei
30	355	28.4	719	22	AB85513	Human protein kin
31	355	28.4	1036	23	AB80923	Novel human protei
32	355	28.4	1036	24	AB99779	Amino acid sequenc
33	355	28.4	1036	24	AA32028	Human kinase and p
34	353.5	28.2	859	16	AA82886	Human leucine zipp
35	353.5	28.2	859	18	AAW31227	Human leucine-zipp
36	353.5	28.2	859	24	AB99744	Polypeptide sequen
37	352.5	28.2	888	23	AB57049	Mouse ischaemic co
38	351.5	28.1	977	22	AB71694	Drosophila melanog
39	350	28.0	589	21	AA45984	Arabidopsis thalia
40	350	28.0	732	21	AA45983	Arabidopsis thalia
41	350	28.0	760	21	AA45982	Arabidopsis thalia
42	349.5	27.9	1046	22	AAE11775	Human kinase (PKIN
43	349.5	27.9	1097	23	AAE21717	Human PKIN-12 prot
44	348	27.8	319	21	AA325601	Arabidopsis thalia
45	348	27.8	341	21	AA325600	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AA28998
ID AAY28998 standard; Protein; 567 AA.

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX AC AAY28998;

XX PT Nuclear factor kappa B activation inhibitors, useful as preventives
 XX for, e.g. autoimmune diseases
 XX PS Examples; Page 43-46; 49pp; Japanese.
 XX CC The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the amino acid sequence of human TAK1C
 CC (hTAK1C) protein.

SQ Sequence 567 AA;
 Query Match 100.0%; Score 1252; DB 20; Length 567;
 Best Local Similarity 100.0%; Pred. No. 3e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VELRLSRVNHNPVIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 60
 DB 76 VELRLSRVNHNPVIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 135
 QY 61 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDPGTACDIQTHTMTNKGSAW 120
 DB 136 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDPGTACDIQTHTMTNKGSAW 195
 QY 121 MAPEVEGGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 DB 196 MAPEVEGGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255

RESULT 2
 AAW27092
 ID AAW27092 standard; Protein; 579 AA.
 AC AAW27092;
 XX 19-NOV-1997 (first entry)
 DT Mouse transforming growth factor-beta activated kinase TAK-1.
 DE TGF-beta; signal transduction; TGF-beta activated kinase; BMP;
 KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;
 KW protein kinase.
 XX Mus musculus.
 OS
 XX JP09163990-A.
 XX 24-JUN-1997.
 PD 27-SEP-1996; 96JP-0256747.
 PF 24-JUL-1996; 96US-0685625.
 PR 29-SEP-1995; 95JP-0253549.
 XX (CHUS) CHUGAI PHARM CO LTD.
 PA (UENO/) UENO N.
 XX WPI; 1997-380171/35.
 DR N-PSDB; AAT85094.
 XX DNA encoding transforming growth factor-beta-activated kinase, TAK-1
 PT - useful for studying the TGF-beta signal transduction system
 XX

PS Claim 14; Page 10-12; 20pp; Japanese.
 XX The present sequence represents mouse transforming growth factor-beta
 CC (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the
 CC TAK-1 protein which is involved in the TGF-beta family signal
 CC transmission system. TAK-1, also known as activator of MAPK Kinase
 CC (AMK-1), is an enzyme which is activated by TGF-beta and bone
 CC morphogenetic protein (BMP) and activates MAPK kinase by
 CC phosphorylation.
 XX SQ Sequence 579 AA;
 Query Match 100.0%; Score 1252; DB 18; Length 579;
 Best Local Similarity 100.0%; Pred. No. 1e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRLSRVNHNPVIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 60
 DB 76 VELRLSRVNHNPVIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPPLPYTTAAHMSWCL 135
 QY 61 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDPGTACDIQTHTMTNKGSAW 120
 DB 136 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDPGTACDIQTHTMTNKGSAW 195
 QY 121 MAPEVEGGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 DB 196 MAPEVEGGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
 QY 181 PKPESLMTRCWSKDPQSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 228
 DB 256 PKPESLMTRCWSKDPQSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 303

RESULT 3
 AAW27093
 ID AAW27093 standard; Protein; 579 AA.
 AC AAW27093;
 XX 19-NOV-1997 (first entry)
 DT Human transforming growth factor-beta activated kinase TAK-1.
 DE TGF-beta; signal transduction; TGF-beta activated kinase; BMP;
 KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;
 KW protein kinase.
 XX Homo sapiens.
 OS
 XX JP09163990-A.
 XX 24-JUN-1997.
 PD 27-SEP-1996; 96JP-0256747.
 PF 24-JUL-1996; 96US-0685625.
 PR 29-SEP-1995; 95JP-0253549.
 XX (CHUS) CHUGAI PHARM CO LTD.
 PA (UENO/) UENO N.
 XX WPI; 1997-380171/35.
 DR N-PSDB; AAT85095.
 XX DNA encoding transforming growth factor-beta-activated kinase, TAK-1
 PT - useful for studying the TGF-beta signal transduction system
 XX

PS Claim 15; Page 13-15; 20pp; Japanese.
 XX The present sequence represents human transforming growth factor-beta
 CC (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the
 CC TAK-1 protein which is involved in the TGF-beta family signal
 CC transmission system. TAK-1, also known as activator of MAPK Kinase
 CC

XX PT - useful for studying the TGF-beta signal transduction system
 XX

CC (AMK-1), is an enzyme which is activated by TGF-beta and bone
 CC morphogenetic protein (BMP) and activates MAPK kinase by
 CC phosphorylation.

XX Sequence 579 AA;
 SQ Query Match 100.0%; Score 1252; DB 18; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VELRQLSRVNHPIVVKLYGACLNVPVCLVMEYAEGSLYNVLHGAPLPYPTAAHAMSACL 60
 Db 76 VELRQLSRVNHPIVVKLYGACLNVPVCLVMEYAEGSLYNVLHGAPLPYPTAAHAMSACL 135
 QY 61 QCSQGVAVLHSMQPKALHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120
 Db 136 QCSQGVAVLHSMQPKALHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 195
 QY 121 MAPEVFECSNYSEKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 Db 196 MAPEVFECSNYSEKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
 QY 181 PKPIESLMTRCWSKDPSPQSPSMEIEIVKIMTHLMRYFPGADBPLOYPQ 228
 Db 256 PKPIESLMTRCWSKDPSPQSPSMEIEIVKIMTHLMRYFPGADBPLOYPQ 303

RESULT 4
 AAY28996
 ID AAY28996 standard; Protein; 579 AA.
 AC AAY28996;
 XX 29-OCT-1999 (first entry)
 DT Human TGF-beta activated kinase (TAK) 1a amino acid sequence.
 DE
 XX Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
 KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
 KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
 KW endotoxin shock; septicemia; human; hTAK1a.
 XX Homo sapiens.
 OS
 XX WO9940202-A1.
 PN 12-AUG-1999.
 PD 02-FEB-1999; 99WO-JP00422.
 PF 30-OCT-1998; 98JP-0309316.
 PR 06-FEB-1998; 98JP-0026003.
 XX (TANA) TANABE SEIYAKU CO.
 FA Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 PI WPI; 1999-494298/41.
 DR N-ESDB; AAX99696.
 XX Nuclear factor kappa B activation inhibitors, useful as preventives
 PT for, e.g. autoimmune diseases
 PT Examples; Page 35-39; 49pp; Japanese.
 PS

XX The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the amino acid sequence of human TAK1a

CC (hTAK1a) protein.
 XX Sequence 579 AA;
 SQ Query Match 100.0%; Score 1252; DB 20; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VELRQLSRVNHPIVVKLYGACLNVPVCLVMEYAEGSLYNVLHGAPLPYPTAAHAMSACL 60
 Db 76 VELRQLSRVNHPIVVKLYGACLNVPVCLVMEYAEGSLYNVLHGAPLPYPTAAHAMSACL 135
 QY 61 QCSQGVAVLHSMQPKALHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120
 Db 136 QCSQGVAVLHSMQPKALHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 195
 QY 121 MAPEVFECSNYSEKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 Db 196 MAPEVFECSNYSEKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
 QY 181 PKPIESLMTRCWSKDPSPQSPSMEIEIVKIMTHLMRYFPGADBPLOYPQ 228
 Db 256 PKPIESLMTRCWSKDPSPQSPSMEIEIVKIMTHLMRYFPGADBPLOYPQ 303

RESULT 5
 AAY09542
 ID AAY09542 standard; Protein; 579 AA.
 AC AAY09542;
 XX 21-JUL-1999 (first entry)
 DT Human TAK1 protein.
 DE
 XX Human; TAK1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta.
 XX Homo sapiens.
 OS

Key Location/Qualifiers
 CDS 183..1922
 /*tag= a
 WO9921010-A1.
 29-APR-1999.
 22-OCT-1998; 98WO-JP04796.
 22-OCT-1997; 97JP-0290188.
 (CHUS) CHUGAI SEIYAKU KK.
 Ohtomo T, Ono K, Tsuchiya M;
 WPI; 1999-312645/26.
 N-ESDB; AAX56279.
 Screening for TGF-beta inhibitory substances, which are useful as
 drugs for treatment of diseases relating to its disorder
 Claim 4; Page 155-157; 195pp; Japanese.

A method has been developed for screening for substances which inhibit
 the binding of TAK1 polypeptide to TAK1 polypeptide. The method
 comprises: (a) contacting the polypeptide in the presence of a sample;
 and (b) detecting the amount of bound polypeptide, in which the sample
 can be pre-mixed with TAK1 or TAK1 polypeptide first. The transforming
 growth factor (TGF)-beta inhibitory substances can be used in drugs for
 indications e.g. as TGF-beta signal transduction inhibitors or
 activators, or extracellular matrix protein production enhancement
 inhibitors or activators, or cell proliferation prevention inhibitors or

CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence represents human TAK1.
 XX
 SQ Sequence 579 AA;

Query Match 100.0%; Score 1252; DB 20; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYNVLHGAELPYVYTAHAHMSWCL 60
 DB 76 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYNVLHGAELPYVYTAHAHMSWCL 135
 QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMTNKGSAW 120
 DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMTNKGSAW 195
 QY 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 DB 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCWSKDPSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 228
 DB 256 PKPIESLMTRCWSKDPSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 303

RESULT 6
 AAY91000
 ID AAY91000 standard; Protein; 579 AA.

XX AC AAY91000;
 XX DT 04-SEP-2000 (first entry)
 XX DE Human TAK-1 protein sequence SEQ ID NO:2.
 XX DE Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;
 KW screening; signal transduction; inhibition; inflammatory cytokine;
 KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;
 KW antiinflammatory; suppression.
 XX OS Homo sapiens.
 XX PN WO200023610-A1.
 XX PD 27-APR-2000.
 XX PF 21-OCT-1999; 99WO-JP05817.
 XX PR 21-OCT-1998; 98JP-0299962.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;
 XX WPI; 2000-339707/29.
 XX DR N-PSDB; AAA39105.
 XX PT Method for screening inhibitors of TAK1 signal transduction for
 PT suppression of inflammatory cytokine production and use as
 PT antiinflammatory agents -
 XX
 XX Example 1; Page 80-84; 100pp; Japanese.

CC The present invention describes a method for screening compounds for
 CC inhibition of inflammatory cytokine signal transduction by contacting
 CC the sample with TAK1 and its receptor TAK1 and selecting for inhibition
 CC of TAK1/TAK1 binding. Also described is a method for screening compounds
 CC for inhibition of inflammatory cytokine signal transduction in which the

CC inhibition of TAK1 phosphorylation is selected for; and drug
 CC compositions for the treatment of inflammatory disorders containing as
 CC active component an inflammatory cytokine signal transduction inhibitor.
 CC TAK1 is an essential component of the signalling process which results
 CC in release of inflammatory cytokines such as interleukin-1 (IL-1),
 CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used
 CC for the selection of effective antiinflammatory agents. The present
 CC sequence represents human TAK-1, which is used in the exemplification of
 CC the present invention.
 XX

SQ Sequence 579 AA;

Query Match 100.0%; Score 1252; DB 21; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.1e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYNVLHGAELPYVYTAHAHMSWCL 60
 DB 76 VELRQLSRVNHPIVLYGACLPVCLVMEYAEAGSLYNVLHGAELPYVYTAHAHMSWCL 135
 QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMTNKGSAW 120
 DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMTNKGSAW 195
 QY 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 DB 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPPDEIGGPAFRIMWAVHNGTRPPLIKNL 255
 QY 181 PKPIESLMTRCWSKDPSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 228
 DB 256 PKPIESLMTRCWSKDPSPQSMEEIVKIMTHLMRYFPFGADEPLQYPCQ 303

RESULT 7
 ABB85033
 ID ABB85033 standard; Protein; 579 AA.

XX AC ABB85033;
 XX DT 16-MAY-2002 (first entry)
 XX DE Pain regulated protein sequence 28.
 XX KW Pain; analgesic; gene therapy; neurological disorder;
 KW neurodegenerative disease.
 XX OS Homo sapiens.
 XX PN WO200212338-A2.
 XX PD 14-FEB-2002.
 XX PF 03-AUG-2001; 2001WO-EP09011.
 XX PR 03-AUG-2000; 2000DE-1037759.
 XX PA (CHEF) GRUENENTHAL GMBH.
 XX PI Gillen C, Wetzel I, Whendt S, Weihe E, Schaefer MK;
 XX WPI; 2002-257469/30.
 XX DR N-PSDB; ABL88437.
 XX PT Identifying pain-regulating compounds, useful for treating chronic pain
 PT and for diagnosis, by measuring binding of compounds to specific
 PT peptides and proteins -
 XX
 XX Claim 1; Fig 44; 213pp; German.

CC The invention relates to identifying pain-regulating substances (A)
 CC comprises (i) incubating a test substance with a cell (or preparation
 CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
 CC either binding of the test substance to (B) or some functional parameter

that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analgesic activity, (A) along with nucleic acid (AB188411-AB198441) that encode proteins (B), AB98506-AB985037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B); cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polypeptide of the invention.

XX Sequence 579 AA;
SQ Query Match 100.0%; Score 1252; DB 23; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.1e-127; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0;
QY 1 VELQLSRVNHPIVVKLYGACINPVCLVMEYAEGGSLYNVLHGABPLPYTAAHMSWCL 60
DB 76 VELQLSRVNHPIVVKLYGACINPVCLVMEYAEGGSLYNVLHGABPLPYTAAHMSWCL 135
QY 61 QCSQGVAVLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIOTHTMTNKGSAW 120
DB 136 QCSQGVAVLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIOTHTMTNKGSAW 195
QY 121 MAPEVFEGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFEGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 PKPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFPGADEPLQYPCQ 228
DB 256 PKPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 8
AAY09547
ID AAY09547 standard; Protein; 590 AA.
XX
AC AAY09547;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human TAK1-6xHis protein.
XX
KW Human; TAK1; screening; inhibition; TGF-beta;
KW transforming growth factor beta.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO921010-A1.
XX
XX 29-APR-1999.
PD
XX
XX 22-OCT-1998; 98WO-JP04796.
PF
XX
XX 22-OCT-1997; 97JP-0290188.
PR
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX
XX Ohtomo T, Ono K, Tsuchiya M;
PI
XX
XX WPI; 1999-312645/26.
DR
XX
XX N-PSDB; AAX56285.
DR
XX
XX Screening for TGF- beta inhibitory substances, which are useful as
PT drugs for treatment of diseases relating to its disorder
XX
XX Example 1; Page 171-174; 195pp; Japanese.
PS

XX A method has been developed for screening for substances which inhibit
CC the binding of TAK1 polypeptide to TAK1 polypeptide. The method
CC comprises: (a) contacting the polypeptide in the presence of a sample;
CC and (b) detecting the amount of bound polypeptide, in which the sample

CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
CC indications e.g. as TGF-beta signal transmission inhibitors or
CC activators, or extracellular matrix protein production enhancement
CC inhibitors, or monocytic migration inhibitors or activators, or
CC activators, or monocyte migration inhibitors or activators, or
CC physiological activity induction inhibitors or activators, or
CC immunosuppression inhibitors or activators, or amyloid beta protein
CC precipitation inhibitors or activators, and such substances can also be
CC inhibitors of the TAK1 polypeptide function, particularly kinase
CC activity. The present sequence represents TAK1-6xHis from an example of
CC the present invention.
XX

SQ Sequence 590 AA;
Query Match 100.0%; Score 1252; DB 20; Length 590;
Best Local Similarity 100.0%; Pred. No. 3.2e-127; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 0;
QY 1 VELQLSRVNHPIVVKLYGACINPVCLVMEYAEGGSLYNVLHGABPLPYTAAHMSWCL 60
DB 76 VELQLSRVNHPIVVKLYGACINPVCLVMEYAEGGSLYNVLHGABPLPYTAAHMSWCL 135
QY 61 QCSQGVAVLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIOTHTMTNKGSAW 120
DB 136 QCSQGVAVLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIOTHTMTNKGSAW 195
QY 121 MAPEVFEGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFEGSNYSEKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 PKPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFPGADEPLQYPCQ 228
DB 256 PKPIESLMTRCWSKDPSPMSMEIIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 9
AAY28997
ID AAY28997 standard; Protein; 606 AA.
XX
AC AAY28997;
XX
DT 29-OCT-1999 (first entry)
XX
DE Human TGF-beta activated kinase (TAK) 1b amino acid sequence.
XX
KW Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
KW endotoxin shock; septicemia; human; HTAK1b.
XX
OS Homo sapiens.
XX
XX WO9940202-A1.
PN
XX
PD 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-JP00422.
PF
XX
XX 30-OCT-1998; 98JP-0309316.
PR
XX
XX 06-FEB-1998; 98JP-0026003.
PR
XX
XX (TANA) TANABE SEIYAKU CO.
PA
XX
XX Hasegawa K, Kageyama N, Sakurai H, Sugita T;
PI
XX
XX WPI; 1999-494298/41.
DR
XX
XX N-PSDB; AAX99697.
DR
XX
XX Nuclear factor kappa B activation inhibitors, useful as preventives
PT for, e.g. autoimmune diseases
CC
XX Examples; Page 39-43; 49pp; Japanese.
PS

XX The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the amino acid sequence of human TAK1b
 CC (hTAK1b) protein.

XX SQ Sequence 606 AA;
 Query Match 100.0%; Score 1252; DB 20; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VELRQLSRVNHPIVLYGACLNVPCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 60
 Db 76 VELRQLSRVNHPIVLYGACLNVPCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 135
 QY 61 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDFTACDIQTHMTNKGSAW 120
 Db 136 QCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDFTACDIQTHMTNKGSAW 195
 QY 121 MAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMVAVHNGTRPPLIKNL 180
 Db 196 MAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMVAVHNGTRPPLIKNL 255
 QY 181 PKPIESLMTRCWSKQSPQSMESIEIVKIMTHLMRYFFGADEPLQPCQ 228
 Db 256 PKPIESLMTRCWSKQSPQSMESIEIVKIMTHLMRYFFGADEPLQPCQ 303

RESULT 10

ABBS8061
 ID ABB58061 standard; Protein; 678 AA.
 XX AC ABB58061;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 975.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX FN WC200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX N-PSDB; ABL02164.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 975; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 678 AA;

Query Match 55.9%; Score 700; DB 22; Length 678;
 Best Local Similarity 57.5%; Pred. No. 5.4e-67;
 Matches 130; Conservative 35; Mismatches 57; Indels 4; Gaps 3;
 QY 2 ELRQLSRVNHPIVLYG--ACLNVPCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 59
 Db 60 EVKQLSRVNHPIVLYG--ACLNVPCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 118
 QY 60 LQCSQGVAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDFTACDIQTHMTNKGSAW 119
 Db 119 RQCAEGLAYLHSMQPKALIHRLDLPNLLVAGGTVLKICDFTACDIQTHMTNKGSAW 178
 QY 120 WMAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMVAVHNGTRPPLIKN 179
 Db 179 WMAPEVFGSNYSKCDVFSWGIIWEVITRRKPFDEIGGPAFRIMVAVHNGTRPPLIKN 237
 QY 180 LKPIESLMTRCWSKQSPQSMESIEIVKIMTHLMRYFFGADEPLQY 225
 Db 238 CPKRIEDLMTACTWKVPEDEFSMQYIVGVHMEIVKDYTGADKALEY 283

RESULT 11

ABBS0985
 ID ABB60985 standard; Protein; 252 AA.
 XX AC ABB60985;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 9747.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX FN WC200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX N-PSDB; ABL05088.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 9747; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and

cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 252 AA;

Query Match 33.1%; Score 414; DB 22; Length 252;
Best Local Similarity 41.8%; Pred. No. 1.9e-36;
Matches 82; Conservative 35; Mismatches 53; Indels 26; Gaps 4;

QY 2 ELRQISRVNHNINIVKLYGACLNIVC--LVMEVAGSGSYLVNLHGAEPDLPYTAHAMSVC 59
Db 54 ELYQUTKASHVNIIVLYGTSRHEGCALLMEFVGGSLSSFLH-AKSKPSYSHAHAFNWA 112

QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTMTNNKGSAA 119
Db 113 HQIAGIAYLHGMQPKAVIHRDIKPNILLCEKGLKICDFTVVDLSQSISCNAGTCR 172

QY 120 WNAPE-----VFEGSNYSEKCDVFSWGILMEVITRRKPPDEI 157
Db 173 YKAPEVRELEDFKSNRIINOPTGFKVLQGNKPKDCKDVSWAITFWELLSRKEPFEQY 232

QY 158 GGPAPRIMWAVHNGTR 173
Db 233 -NTLFELYMAINEGR 247

RESULT 12
AAG32053
ID AAG32053 standard; Protein; 367 AA.
AC AAG32053;
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38597.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38597.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 09-MAR-1999; 99US-0123180.
PR 23-MAR-1999; 99US-0123548.
PR 25-MAR-1999; 99US-0125788.
PR 29-MAR-1999; 99US-0126264.
PR 01-APR-1999; 99US-0126785.
PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 28-APR-1999; 99US-0130510.
PR 30-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 20-JUL-1999; 99US-0144352.
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PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.

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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147034.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151086.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 29.9%; Score 374; DB 21; Length 367;
Best local Similarity 39.4%; Pred. No. 7.4e-3;
Matches 86; Conservative 40; Mismatches 70; Indels 22; Gaps 9;

QY 2 ELRLSRVNHPIVVKLYGACLPV--CLVMEYAEGLSYNLV----HGAEPLPYTAAHA 55
Db 135 EVSMLANKHPNIVRFICACRKPWMCIVTEYAKGSSVRQFLTRQNEAVPLKL-----A 189
QY 56 MSWCLQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGTVLKICDFGTA-CDIQTH-MTN 113
Db 190 VKQALDVARGMAYVHG--RNFIHRLDKSDNLLISADKSI-KIADFGVARIEVQTEGMP 245
QY 114 NKSAAWMAPEVFEKGSYSEKCVFSGWGIILWEIVITRKPEDEIGG--PAPRIMWAYHNG 171
Db 246 ETGTYRWMAPEMTQHRAYNQKVDYSEFIVLWELITGLLPQNMTAVQAAFAV---VNRG 302
QY 172 TRPELIKNLPKIESLMTRCWSKDSORPSMEIEIVKIM 209
Db 303 VRTPVNDCLPVLSDIMTRCWDANFEVRPCFEVVEVKLL 340

RESULT 13
AAG32052
ID AAG32052 standard; Protein; 369 AA.
XX
AC AAG32052;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38596.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.

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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
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PR 22-OCT-1999; 99US-0161405.
PR 22-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 29.98; Score 374; DB 21; Length 369;
Best Local Similarity 39.48; Pred.No. 7.4e-32;
Matches 86; Conservative 40; Mismatches 70; Indels 22; Gaps 9;

QY 2 ELRQLSRVNHPIVVKLYGACINPV--CLVMEYAEGLSYNVL---HGAEPPLPYTTAAHA 55
Db 137 EVSNLANLKHPIVRFVIGACKPMVWCIVTEYAKGVSVRQFLTRQNEAVPLKL-----A 191

QY 56 MSWCLOCSQGVAYLHNSQPKALIHRLDKPPNLLLVAGTVLKIICDFGTA-CDIQTH-MTN 113
Db 192 VKQALDVARGMAYVHG---RNFIHRDLKSDNLLISADKSI-KIADFGVARIEVQTEGMTP 247

QY 114 NKGSAAWMAPEVFEKSGVSEKCVFSGIILWEIVTERKPEDEIGG--PAFRIMWVHNG 171
Db 248 ETGYRWMAPEMIQHRAYNOKVDVYSGVILWELITGLFPQNTAVQRAFAV---VNRG 304

QY 172 TRPPLIKNPKPIESLMTRCWSDKPSQPSMEIEIVKIM 209
Db 305 VRTVENDCLPVLSDINTRCDANPEVPCFVEVVKLL 342

RESULT 14
AAG32051
ID AAG32051 standard; Protein; 407 AA.
AC AAG32051;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38595.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134421.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135829.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 18-JUL-1999; 99US-0144331.
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PR 19-JUL-1999; 99US-0144333.

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PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.	QY	2	ELRQLSRVNHPIVLYGACLNVP--CLVMEYAEQGSLYNVL----	HGAELIPYYTAHAH	55
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PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.	QY	114	NKGSAAWMAPEVPEGSNYSEKDFVSWGIIWLVETTRRKPFEIGG--PAPRIMWAVHNG	171	
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Best Local Similarity 39.9%; Pred No. 9.5e-32;
Matches 87; Conservative 39; Mismatches 70; Indels 22; Gaps 9;

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Db 137 EVSMLAEFKHENIVRFICGACIKPMWCIVTEYAKGGSVRQFLTKRQNEAVPLKL-----A 191

Qy 56 MSWCLOCSQGVAYLHSMOPKALIHRLKPPNLLVAGGTVLKICDFGTA-CDIQTH-MTN 113
Db 192 VMQALDVARGMAYVHE---RNFIHRDLKSDNLLISADRSI-KIADFGVARIEVQTEGMP 247

Qy 114 NKGSAAWAPRVEFGSNYSKCDVFSWGIILWEVILTRKRPDEIGG--PAPRIMWAVHNG 171
Db 248 ETGYRWAPRMIQHRPTIQVDVYSFGIVLWELITGLLPQNMTAVQAFAV---VNRG 304

Qy 172 TRPPLIKNLKPISLMTRCWSKDPSPSMEIIVKIM 209
Db 305 VRPTVPADCLPVLGEIMTRCWDADPEVPCFAEIVNLL 342
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Search completed: December 4, 2003, 09:30:08
Job time : 78.7973 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:21:16 ; Search time 95.5135 Seconds
(without alignments)
615.997 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELQLSRVNHPIVKLYGA.....MTHLMRYFPGADEPLQYPCQ 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1252	100.0	566	4	Q9NTR2	Q9ntr2 homo sapien
5	1252	100.0	606	11	Q923A8	Q923a8 mus musculus
6	1221	97.5	616	13	Q736I3	Q736i3 xenopus lae
7	700	55.9	678	5	Q9V3Q6	Q9v3q6 drosophila
8	414	33.1	258	5	Q9VCV0	Q9vcv0 drosophila
9	379	30.3	422	10	Q8GV29	Q8gv29 oryza sativ
10	376	30.0	371	13	Q90ZV8	Q90zv8 brachydanio
11	375.5	30.0	2631	5	Q8MVR1	Q8mvr1 dictyosteli
12	374.5	29.9	2964	5	Q817W7	Q817w7 dictyosteli
13	374	29.9	411	10	Q9ZQ31	Q9zq31 arabidopsis
14	373	29.8	412	10	Q9M085	Q9m085 arabidopsis
15	373	29.8	417	10	Q8GV30	Q8gv30 oryza sativ
16	372	29.7	289	11	Q8BR73	Q8br73 mus musculus

17	372	29.7	454	11	Q9ESL3	Q9esl3 mus musculus
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19	371	29.6	455	4	Q9HCC4	Q9hcc4 homo sapien
20	371	29.6	800	4	Q9NYE9	Q9nye9 homo sapien
21	371	29.6	800	4	Q9NYL2	Q9nyl2 homo sapien
22	371	29.6	800	4	Q9HCC5	Q9hcc5 homo sapien
23	371	29.6	800	4	Q9HDD2	Q9hdd2 homo sapien
24	368	29.4	416	10	Q94C42	Q94c42 triticum ae
25	366	29.2	637	10	Q94J41	Q94j41 oryza sativ
26	363.5	29.0	1148	5	Q95VF6	Q95vf6 drosophila
27	363.5	29.0	1161	5	Q95UN8	Q95un8 drosophila
28	362	28.9	422	5	Q23846	Q23846 dictyosteli
29	362	28.9	1338	5	Q93927	Q93927 dictyosteli
30	360.5	28.8	608	11	Q8BIC8	Q8big8 mus musculus
31	360.5	28.8	1066	4	Q9H2N5	Q9h2n5 homo sapien
32	356.5	28.5	888	11	Q8CBX3	Q8cbx3 mus musculus
33	356	28.4	462	10	Q39886	Q39886 glycine max
34	355.5	28.4	370	10	Q9S7D5	Q9s7d5 arabidopsis
35	355	28.4	421	10	Q8GV28	Q8gv28 oryza sativ
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38	353.5	28.2	859	4	Q8WY25	Q8wy25 homo sapien
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44	349	27.9	1001	11	Q8VDG6	Q8vdg6 mus musculus
45	348	27.8	391	10	Q8LCP3	Q8lcp3 arabidopsis

ALIGNMENTS

RESULT 1

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DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE DJ154GJ4.1.3 (Mitogen-activated protein kinase kinase kinase 7 (TGF-beta activated kinase 1c (TAK1))) (Fragment).
GN MAP3K7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AL121964; CAB87604.1; --
DR HSSP; P12931; 1PMK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
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Query Match 100.0%; Score 1252; DB 4; Length 478;
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 Db 216 PKPIESLMTRCWSKDPSPQSRPSMEIEIVKIMTHLMRYFFGADEPLQYPCQ 263

RESULT 2

Q9NZ70 Q9NZ70 PRELIMINARY; PRT; 491 AA.
 AC Q9NZ70; Q9NZ70; 491 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE TGF beta-activated kinase splice variant d (DJ154G14.1.4) (Mitogen-activated protein kinase kinase 7 (TGF-beta activated kinase 1d (TAK1)))
 DE (TAK1))
 GN TAK1 OR MAP3K7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20568765; PubMed=11118615;
 RA Dempsey C.E., Sakurai H., Sugita T., Guesdon F.;
 RT "Alternative splicing and gene structure of the transforming growth factor beta-activated kinase 1."
 RT factor beta-activated kinase 1."
 RL Biochim. Biophys. Acta 1517:46-52(2000).
 RN [2]
 RP SEQUENCE OF 41-491 FROM N.A.
 RA Tracey A.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF218074; AAF27652.1; -;
 DR EMBL; AL121964; CAB87605.1; -;
 DR HSP; P08631; IAD5.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Ser thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 491 AA; 53739 MW; BYD8832E286A99CS CRC64;

Query Match 100.0%; Score 1252; DB 4; Length 491;
 Best Local Similarity 100.0%; Pred. No. 3.5e-121;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VELRQLSRVNHNPVCLVMEYAEAGSLVNLVHGAEPLPYTAAHMSWCL 60
 Db 76 VELRQLSRVNHNPVCLVMEYAEAGSLVNLVHGAEPLPYTAAHMSWCL 135
 Qy 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKI CDFTGACDIQTHMTNNKGSAAW 120
 Db 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKI CDFTGACDIQTHMTNNKGSAAW 195
 Qy 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 Db 196 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255

Qy 181 PKPIESLMTRCWSKDPSPQSRPSMEIEIVKIMTHLMRYFFGADEPLQYPCQ 228
 Db 256 PKPIESLMTRCWSKDPSPQSRPSMEIEIVKIMTHLMRYFFGADEPLQYPCQ 303
 RESULT 3
 Q9NTR1 Q9NTR1 PRELIMINARY; PRT; 539 AA.
 AC Q9NTR1; AC Q9NTR1; 539 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE DJ154G14.1.1 (Mitogen-activated protein kinase kinase 7 (TGF-beta activated kinase 1a (TAK1))) (Fragment).
 GN MAP3K7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AL121964; CAB87607.1; -;
 DR HSP; P12931; IFMK.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 539 AA; 60006 MW; E6183F553CC7F324 CRC64;

Query Match 100.0%; Score 1252; DB 4; Length 539;
 Best Local Similarity 100.0%; Pred. No. 4e-121;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VELRQLSRVNHNPVCLVMEYAEAGSLVNLVHGAEPLPYTAAHMSWCL 60
 Db 36 VELRQLSRVNHNPVCLVMEYAEAGSLVNLVHGAEPLPYTAAHMSWCL 95
 Qy 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKI CDFTGACDIQTHMTNNKGSAAW 120
 Db 96 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKI CDFTGACDIQTHMTNNKGSAAW 155
 Qy 121 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
 Db 156 MAPEVFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 215
 Qy 181 PKPIESLMTRCWSKDPSPQSRPSMEIEIVKIMTHLMRYFFGADEPLQYPCQ 228
 Db 216 PKPIESLMTRCWSKDPSPQSRPSMEIEIVKIMTHLMRYFFGADEPLQYPCQ 263

RESULT 4

Q9NTR2 Q9NTR2 PRELIMINARY; PRT; 566 AA.
 AC Q9NTR2; AC Q9NTR2; 566 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE DJ154G14.1.2 (Mitogen-activated protein kinase kinase 7 (TGF-beta activated kinase 1b (TAK1))) (Fragment).
 GN MAP3K7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AL121964; CAB87606.1; -.
DR HSSP; P12931; 1FMK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 566 AA; 62972 MW; 32CDAC1211B200CF CRC64;

Query Match 100.0%; Score 1252; DB 4; Length 566;
Best Local Similarity 100.0%; Pred. No. 4.2e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 60
DB 36 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 95
QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120
DB 96 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 155
QY 121 MAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 156 MAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 215
QY 181 KPPIESLMTRCWSKQSPQSPSEIEIVKIMTHLMRYPPGADEPLQYPCQ 228
DB 216 KPPIESLMTRCWSKQSPQSPSEIEIVKIMTHLMRYPPGADEPLQYPCQ 263

RESULT 5
Q923A8 PRELIMINARY; PRT; 606 AA.
AC Q923A8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:5989).
GN MAP3K7
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC006665; AAH06665.1; -.
DR MGD; MGI:1346877; Map3K7.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

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SQ SEQUENCE 606 AA; 67194 MW; AB8664F389272102 CRC64;

Query Match 100.0%; Score 1252; DB 11; Length 606;
Best Local Similarity 100.0%; Pred. No. 4.6e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 60
DB 76 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 195
QY 121 MAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
DB 196 MAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 KPPIESLMTRCWSKQSPQSPSEIEIVKIMTHLMRYPPGADEPLQYPCQ 228
DB 256 KPPIESLMTRCWSKQSPQSPSEIEIVKIMTHLMRYPPGADEPLQYPCQ 303

RESULT 6
Q73613 PRELIMINARY; PRT; 616 AA.
AC Q73613;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TAK1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=98130593; PubMed=9463380;
RA Shibuya H., Iwata H., Masuyama N., Gotoh Y., Yamaguchi K., Irie K.,
RA Matsumoto K., Nishida E., Ueno N.;
RT "Role of TAK1 and TAB1 in BMP signaling in early Xenopus
RT development.";
RL EMBO J. 17:1019-1028 (1998)
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U92030; AAC14008.1; -.
DR HSSP; P12931; 1FMK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 616 AA; 68464 MW; 493AD2A05ADC38B6 CRC64;

Query Match 97.5%; Score 1221; DB 13; Length 616;
Best Local Similarity 97.4%; Pred. No. 7.6e-118;
Matches 222; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 60
DB 65 VELROLSRVNHPIVKLYGACLPVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSACL 124
QY 61 QCSQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 120
DB 125 QCAQGVAYLHSMQPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAW 184
QY 121 MAPEVFECSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180

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Db 185 MAPEVEGNSYSEKCDVFSWCIILWEVITRRKPKDEITGGPAFRIMWVHNGTRPPLIKNL 244
Qy 181 KPPIESLMTKWSKDPQRSMSBIEIVKIMTHLMRYFFGADPLEYPCQ 228
    |||||
Db 245 KPPIESLMTKWSKDPQRSMSBIEIVKIMTHLMQYFFGADVSLQYPCQ 292
    |||||

RESULT 7
Q9V3Q6 PRELIMINARY; PRT; 678 AA.
AC Q9V3Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative TAKI protein (CG1388 protein) (LD42274P).
GN TAKI OR CG1388 OR CG18492.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turney R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RN SEQUENCE FROM N.A.
RP Takatsu Y., Nakamura M., Stapleton M., Danos M., Matsumoto M.,
RA O'Connor M.B., Shibuya H., Ueno N.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

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RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF003571; AAF50895.1; -.
DR EMBL; AF199466; AAF06815.1; -.
DR EMBL; AY051953; AAK93377.1; -.
DR HSP; P08631; IAD5.
DR FlyBase; FBgn0026323; Tak1.
DR InterPro; IPR001990; Granin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00001; Prot_kinase; 1.
DR PROSITE; PS00422; GRANINS 1; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 678 AA; 75674 MW; 87EBA80CDB8CDE45 CRC64;

Query March 55.9%; Score 700; DB 5; Length 678;
Best Local Similarity 57.5%; Pred. No. 9.5e-64;
Matches 130; Conservative 35; Mismatches 57; Indels 4; Gaps 3;

Qy 2 ELRSLRVNHPNIVKLYG--ACLPVCLVMEYAEAGSLYNVLHGAELPYYTAHAMSVC 59
    |||||
Db 60 EVKQLSRVKNPIIALHGSIYQATYLMFAEGGSLHNFHVG-KVKPAVSLAHMSWA 118
    |||||
Qy 60 LQCSQGVAYLHSMQPKALIHRLKPNLLVAGTVLTKICDFGACDIQTHMTNKGSA 119
    |||||
Db 119 RQCAEGLAYLHMTPKPLIHRDVKPLNLLTKGRNLKICDFGTVADKSTMTNNGSAA 178
    |||||
Qy 120 WMAPEVEGNSYSEKCDVFSWCIILWEVITRRKPKDEITGGPAFRIMWVHNGTRPPLIKN 179
    |||||
Db 179 WMAPEVEGNSYSEKCDVFSWCIILWEVITRRKPKDEITGGPAFRIMWVHNGTRPPLIKN 237
    |||||
Qy 180 LPKPIESLMTKWSKDPQRSMSBIEIVKIMTHLMRYFFGADPLEYQ 225
    |||||
Db 238 CPKXIEDLMTACWTKVPEDRPSMQYIVGVMEHIVKDYTGADKALEY 283
    |||||

RESULT 8
Q9V3Q6 PRELIMINARY; PRT; 258 AA.
AC Q9V3Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG4803-PA.
GN TAK12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Föster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassaman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banron J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.A., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003740; AAF56055.2; -;
DR FlyBase; FB0033015; Tak12.
SQ SEQUENCE 258 AA; 29480 MW; D117DA8922BFAE1E CRC64;
Query Match 33.1%; Score 414; DB 5; Length 258;
Best Local Similarity 41.8%; Pred. No. 1.2e-34;
Matches 82; Conservative 35; Mismatches 53; Indels 26; Gaps 4;
QY 2 ELRQLSRVHNHNIVKLYGACLNPCV--LVMEYAGSGSLYNVLHGAEPLPYVTAHAMSWC 59

Db 54 EYQLTAKSHVNIYELYTSRHEGACALLMEFVDCGSLSSFLH-AKSPSYSHAHAFNWA 112
QY 60 LQCSQGVAYLHSMQKALIHRLKPPNLLVAGGTVLKICDFTACDIQTHMTNNKGSAA 119
Db 113 HQIAQGIAYLHGMQKAVIHRDIKPLNTLLCEKGLKLCIDFGTVVDLSQSISCNAGTCR 172
QY 120 WMADE-----VFESNYSYSEKCDVFSWGILLVEVITRRRPFDEI 157
Db 173 YKAPEVRELFDFKSNRIINOFTGQKVLQGNKPKDEKCDVYSWAIPTFWILLSRKPEFQY 232
QY 158 GGPAPRIMWAVHNGTR 173
Db 233 -NTLPELYMAINEGKR 247
RESULT 9
Q8GV29 PRELIMINARY; PRT; 422 AA.
AC Q8GV29
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
GN DPX2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z.M., Zhang H.S., Huang J.;
RT "Molecular Cloning And Characterization Of A Novel Serine/Threonine
RT Protein Kinase Gene Family From Rice.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY156511; AAN84503.1; -;
KW Kinase.
SQ SEQUENCE 422 AA; 46587 MW; BCC22F1FC6PF62C CRC64;
Query Match 30.3%; Score 379; DB 10; Length 422;
Best Local Similarity 38.6%; Pred. No. 8.9e-31;
Matches 85; Conservative 43; Mismatches 70; Indels 22; Gaps 9;
QY 2 ELRQLSRVHNHNIVKLYGACLNPCV--CLVMEYAGSGSLYNVL----HGAELPYVTAHA 55
Db 190 EVMLATLIRHENIVKFIKACRKPVMVCIIVTEYAKGSGVRQILMKRQNSVPLKL-----A 244
QY 56 MSWCLQCSQGVAYLHSMQKALIHRLKPPNLLVAGGTVLKICDFTACDIQTH-MTN 113
Db 245 VKQALDVARGWAYVHAL---GFHRLKSDN-LIISGDKSIKIADFGVARIEVTEGTP 300
QY 114 NGSAAWMAPEVFSNYSYSEKCDVFSWGIIILWEVITRRKPEDIGG--PAPRIMWAVHNG 171
Db 301 ETGYRWMAPEMIQHPYDQKVDVYSGIVLWELITGLMTPANMTVAQAFAV---VNGK 357
QY 172 TRPELKNLPKPIESLMTKSCWKPSPQSPSEEEIVKIMTH 211
Db 358 VRPAIPQDCLPVLSEIMTRCWDPNPDVPRPPPTTEVVRMLEH 397
RESULT 10
Q90ZY8 PRELIMINARY; PRT; 371 AA.
AC Q90ZY8
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RP "A novel protein kinase, zNPK, from the zebrafish."
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL: AF265343; AA852416.1; -
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 371 AA; 42456 MW; 989188A8B20D296 CRC64;
Query Match 30.0%; Score 376; DB 13; Length 371;
Best Local Similarity 39.0%; Pred. No. 1.6e-30;
Matches 82; Conservative 37; Mismatches 81; Indels 10; Gaps 7;
QY 2 ELRQLSRVHPNIVKLYGACLNVPV-CLVMEYAGGSLYNVLHGAEPLPYTAAHMSWC 59
DB 84 EAILSVLSHKNITQFYGAILEAPNDGIVTEYASRGSLEYLSSADS-EEMDMQVMTWA 142
QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGTGLKICDFGTACDIQTHMTNKK--GS 117
DB 143 MEIAGMHYLHAEAPLVKIHRLDKSRNVVLTFA-DNVLKICDFG-ASKXVSHTHMSLVGT 200
QY 118 AAMWAPVFEVGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMW-AVHNGTRPPL 176
DB 201 FFWNAPEVQLSPVSETCDYSGVLMWMLTREVPEK--GFEGQLQVAVLWVEXHERPTI 258
QY 177 IKNLPKPIESLMTFCWSKQSPSMEIEV 206
DB 259 PSSCPASFAIDLMRCWNAEPKRPQFKQIL 288
RESULT 11
Q8MVRI PRELIMINARY; PRT; 2631 AA.
AC Q8MVRI;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cyclic GMP-binding protein C.
GN GBPC.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Bosgraaf L., Ruescher H., Smith J.L., Wessels D., Solls D.R.,
RA Van Haastert P.J.M.;
RT "A novel cGMP signalling pathway mediating myosin phosphorylation and
RT chemotaxis in Dictyostelium."
RL EMBL J. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22008080; PubMed=12011437;
RA Goldberg J.M., Bosgraaf L., Van Haastert P.J., Smith J.L.;
RT "Identification of four candidate cGMP targets in Dictyostelium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:6749-6754(2002).
DR EMBL; AF481923; AA034041.1; -
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000591; DEP.
DR InterPro; IPR004182; GRAM_dom.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000651; RasGEF.
DR InterPro; IPR001895; RasGRF_CDC25.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00027; cNMP_binding; 2.
DR Pfam; PF00610; DEP; 1.
DR Pfam; PF02893; GRAM; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEFN; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00049; DEP; 1.
DR SMART; SM00568; GRAM; 1.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 2.
DR PROSITE; PS0186; DEP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; GTP-binding; Transferase.
SQ SEQUENCE 2631 AA; 294124 MW; 5B87AABDOA637701 CRC64;
Query Match 30.0%; Score 375.5; DB 5; Length 2631;
Best Local Similarity 35.8%; Pred. No. 1.9e-29;
Matches 88; Conservative 44; Mismatches 75; Indels 39; Gaps 9;
QY 2 ELRQLSRVHPNIVKLYGACLNVPVCLVMEYAGGSLYNVLHGAEPLPYTAAHMSWCL- 60
DB 947 EYVYMSGLNHPNVMKISGFCITPLCMALYVRYGSLYSLLS-----NSSIEISWGLR 998
QY 61 -----QCSQGVAYLHSMQPKALIHRLDKPPNLL--VAGG--TVLKIICDFGTACDIQTHM 111
DB 999 LQIASEIAKQWHLHSHNP-PVTHRLDKSPNILLINGITEGNSVATIIDFGTS----- 1050
QY 112 TNKNGSAA-----WMAPEVFEVGSNYSEKCDVFSWGIILWEVITRRKPFDE--IGGP 160
DB 1051 TALYGGRAALIRCVDQPLWLGPEVLGATAYSEPSDVYSFGIILWLYTRAHPFDEFQFGQW 1110
QY 161 AFRIMWAVHNGTRPPLIKNLPKPIESLMTFCWSKQSPSMEIEVIMTHLMRYFPQAD 220
DB 1111 MSKLEDEIIRGLRETIPPTCPPEYVELIQSCWTHPEPSRFTTSIVEILGQIKKFF--AP 1168
QY 221 EPLQYP 226
DB 1169 LPFTHP 1174
RESULT 12
Q817W7 PRELIMINARY; PRT; 2964 AA.
AC Q817W7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pats1 (Fragment).
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Alysah J.C., Kuchnick L.L., Laroche D.A.;
RT "The identification of Pats1, a novel gene locus required for
RT cytokinesis in Dictyostelium discoideum."
RL Mol. Biol. Cell 0:0-0(2003).
DR EMBL; AY170918; AA012857.1; -
FT NON_TER 1
FT NON_TER 2964 2964
SQ SEQUENCE 2964 AA; 331830 MW; 0905BC2137318AB2 CRC64;
Query Match 29.9%; Score 374.5; DB 5; Length 2964;
Best Local Similarity 40.1%; Pred. No. 2.8e-29;

RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
[6]
RN SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Ishida J., Jones T., Kaniya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AL161578; CAB79835.1; -;
DR EMBL; AY085535; AAM62759.1; -;
DR EMBL; AY125513; AAM78105.1; -;
DR EMBL; BT000587; AAN18156.1; -;
DR HSP; P08631; IAD5.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR002290; Ser.thr.pkinase.
DR InterPro; IPR001245; Tyr.pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot.kinase; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR KATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 412 AA; 46083 MW; 644F35A90210D488 CRC64;

Query Match 29.8%; Score 373; DB 10; Length 412;
Best Local Similarity 39.9%; Pred. No. 3.6e-30;
Matches 87; Conservative 39; Mismatches 70; Indels 22; Gaps 9;

QY 2 ELRQLSRVNHNPNIKLYGACLNPV--CLVMEYAEAGGSLYNVL-----HGAELPLPYTAHA 55
DB 180 EVSMLAFKHNINRFTGACIKPWWCIVTYEYAKGGSVRQFLTKRQNFAPVLKL-----A 234

QY 56 MSWCLOCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTA-CDIOTH-MTN 113
DB 235 VMQALDVARGMAYVHVE---RNFHRLDKSDNLLISADRSI-KIADFGVARIEVTEGMP 290

QY 114 NKGSAAMWAPVEFGSNYSKCDVFSWGIILWEVITRKPFDEIGG--PAFRIMWYHNG 171
DB 291 ETGTYRWMAPEVIOHRPYTQKVDVYSFGIVLWELITGLLPFQNTAVQAFAV---VNRG 347

QY 172 TRPLIKNLKPKPTESLMTRCWSKDPSPORSMEIEIVKIM 209
DB 348 VRPTVPADCLPVGLGEIMTRCWDADPEVRPCFAEIVNLL 385

RESULT 15
Q8GV30 PRELIMINARY; PRT; 417 AA.
AC Q8GV30;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
GN DPK1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z.M., Zhang H.S., Huang J.;
RT "Molecular Cloning And Characterization Of A Novel Serine/Threonine
Protein Kinase Gene Family From Rice";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY156510; AAN84502.1; -;
KW Kinase.
SQ SEQUENCE 417 AA; 45927 MW; 1B66E3596653FAD7 CRC64;

Query Match 29.8%; Score 373; DB 10; Length 417;
Best Local Similarity 38.5%; Pred. No. 3.7e-30;
Matches 84; Conservative 41; Mismatches 71; Indels 22; Gaps 9;

QY 2 ELRQLSRVNHNPNIKLYGACLNPV--CLVMEYAEAGGSLYNVLHGAEE---PLPYTAHA 55
DB 185 EVSMLATLRHSNIVKFGACRKPWWCIVTYEYAKGGSVRNRLRRQNSVPLKL-----A 239

QY 56 MSWCLOCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTA-CDIOTH-MTN 113
DB 240 VKQALDVARGMAYVHGL---GFHRLDKSDN-LIISGDKSIKIADFGVARIEVTEGMP 295

QY 114 NKGSAAMWAPVEFGSNYSKCDVFSWGIILWEVITRKPFDEIGG--PAFRIMWYHNG 171
DB 296 ETGTYRWMAPEVIOHRPYTQKVDVYSFGIVLWELITGLLPFQNTAVQAFAV---VNRG 352

QY 172 TRPLIKNLKPKPTESLMTRCWSKDPSPORSMEIEIVKIM 209
DB 353 VRPAIPHDCLPALAEIMTRCWDANPDARPPFTEVVRML 390

Search completed: December 4, 2003, 09:33:02
Job time : 96.5135 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 09:34:57 ; Search time 4908.16 Seconds
(without alignments)
1900.384 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELRQLSRVNHNPVIVKLYGA.....MTHLMRYFPGADEPLQVPCQ 228

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Dalop 6.0 ,	Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USP2001/US09830144/runat_03122003_122509_23321/app_query.fasta_1.654
-DB=GenEmbl -QWMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144@cgn.1.1.3608 @runat_03122003_122509_23321 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.to.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.or.*

21: em.on.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.to.*

27: em.sts.*

28: em.un.*

29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pln.*
35: em.htg_rdi.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1252	100.0	1704	6	E38399	E38399 NF-kappa B
2	1252	100.0	1705	9	AB009358	AB009358 Homo sapi
3	1252	100.0	1745	9	AF218074	AF218074 Homo sapi
4	1252	100.0	1788	6	AR231198	AR231198 Sequence
5	1252	100.0	1788	6	AR307979	AR307979 Sequence
6	1252	100.0	2443	10	MUSTAK1	D74446 Mouse mRNA
7	1252	100.0	2656	6	AR231192	AR231192 Sequence
8	1252	100.0	2656	6	AR307973	AR307973 Sequence
9	1252	100.0	2757	9	BC017715	BC017715 Homo sapi
10	1252	100.0	2769	6	AX377912	AX377912 Sequence
11	1252	100.0	2769	9	AB009356	AB009356 Homo sapi
12	1252	100.0	2785	6	E38397	E38397 NF-kappa B
13	1252	100.0	2850	9	AB009357	AB009357 Homo sapi
14	1252	100.0	2866	6	E38398	E38398 NF-kappa B
15	1252	100.0	3107	10	BC006665	BC006665 Mus muscu
16	1221	97.5	2812	5	XU092030	U92030 Xenopus lae
17	1215	97.0	2745	5	BC049005	BC049005 Xenopus l
18	1133	30.5	135308	2	AC114407	AC114407 Mus muscu
19	700	55.9	3349	3	AF199466	AF199466 Drosophil
20	700	55.9	3386	3	AY051953	AY051953 Drosophil
21	599	47.8	32564	2	AC014558	AC014558 Drosophil
22	599	47.8	164942	3	AC011758	AC011758 Drosophil
23	599	47.8	302540	3	AE003571	AE003571 Drosophil
24	461.5	36.9	174275	5	BX119992	BX119992 Zebrafish
25	461.5	36.9	192888	2	BX005296	BX005296 Danio rer
26	392.5	31.3	3138	9	HSMSTM	Z48615 H.sapiens M
27	392.5	31.3	3454	6	AX337846	AX337846 Sequence
28	392.5	31.3	3454	9	HARNAMLK2	X90846 H.sapiens m
29	379	30.3	1269	6	AX653368	AX653368 Sequence
30	379	30.3	1269	8	AY156511	AY156511 Oryza sat
31	377	30.1	1130	6	AX653396	AX653396 Sequence
32	376	30.0	1445	5	AF265343	AF265343 Danio rer
33	375.5	30.0	8125	3	AF481923	AF481923 Dictyoste
34	374.5	29.9	8892	3	AY170918	AY170918 Dictyoste
35	374	29.9	1267	8	AY133876	AY133876 Arabidops
36	374	29.9	1798	8	AY046026	AY046026 Arabidops
37	373	29.8	1254	8	BT000587	BT000587 Arabidops
38	373	29.8	1631	8	AY085535	AY085535 Arabidops
39	373	29.8	1657	8	AY156510	AY156510 Oryza sat
40	373	29.8	1795	8	AY125513	AY125513 Arabidops
41	372.5	29.8	3931	9	AF251442	AF251442 Homo sapi
42	372	29.7	1429	10	AB049732	AB049732 Mus muscu
43	372	29.7	3079	10	BC023718	BC023718 Mus muscu
44	372	29.7	3146	10	AB049731	AB049731 Mus muscu
45	371.5	29.7	3092	6	AX675565	AX675565 Sequence

ALIGNMENTS

RESULT 1

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E38399      E38399      1704 bp      DNA      linear      PAT 31-JAN-2002
LOCUS      NP-kappa B activation inhibitory drug targeting TAK1 and method for
DEFINITION identifying the same.
ACCESSION      E38399
VERSION      E38399.1 GI:18626979
KEYWORDS      JP 2000197500-A/5.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 1704)
AUTHORS      Sugita,N., Sakurai,H., Kageyama,N. and Hasegawa,H.
TITLE      NP-kappa B activation inhibitory drug targeting TAK1 and method for
JOURNAL      identifying the same
PATENT      JP 2000197500-A 5 18-JUL-2000;
COMMENT      OS Unidentified
PN JP 2000197500-A/5
PD 18-JUL-2000
PR 04-FEB-1999 JP 1999026803
PI NAOHISA SUGITA,HIROAKI SAKURAI,NORIKO KAGEYAMA,PI HIROSHI
HASEGAWA
PC C12Q1/48,A61K31/00,A61K45/00,C12N5/10,C12N9/99,PC
C12Q1/02.
PC G01N33/15,G01N33/50,G01N33/566//C12N15/09,C12Q1/68,(C12N15/09,
C12R1:91)
PC C12N5/00,C12N15/00,(C12N15/00,C12R1:91)
CC Strandedness: Double;
CC Topology: Linear;
FH Key      Location/Qualifiers
FT source      1..1704
FT      /organism="Unidentified".
FEATURES      source
source      1..1704
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT      511 a 381 c 401 g 411 t
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Alignment Scores:
Pred. No.:      1.3e-117      Length:      1704
Score:      1252.00      Matches:      228
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0
US-09-830-144-2_COPY_76_303 (1-228) x E38399 (1-1704)
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Db      226      GTAGAGCTCGGCAGTATCCCGTGTGAACCATCTAATATGTAAAGCTTTATGAGCC 285
Qy      21      CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db      286      TGCCTTGAATCAGGTGCTGTGATGAATATCTGAAGGGGCTCTTATATAATGTG 345
Qy      41      LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db      346      CTGCATGGTCTGAACCATTTGCCATATTATCTCTGCCACGCAATGAGTGTGTGTTA 405
Qy      61      GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db      406      CAGTGTTCACCAAGAGGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 465
Qy      81      AspLeuLysProProAsnLeuLeuValAlaGlyThrValIleLysIleCysAsp 100
Db      466      GACCTGAACACCAACTTACTCTGCTGAGGGGGAGTCTTCAAAAATTGTGAT 525
Qy      101      PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120

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526      TTTGGTACACGCTGTGACATTCAGACACACATGACCAATAACAGGGGAGTGTGCTGG 585
121      MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
586      ATGGCACCTGAAGTTTGAAGGTAGTAATACAGTGAATAATGTGACGCTCTTCAGCTGG 645
141      GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
646      GGTATTATTCTTTGGGAAGTGATAACGCGCGGAACCCCTTGTGATGAGATTGGTGGCCCA 705
161      AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
706      GCITTCGAATCATGTGGGCTGTTCATATGGTACTCGACCAACACATGATAAAAAATTGA 765
181      ProLysProIleGlnSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
766      CCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTGGTCTAAAGATCCTCCACGCGCCT 825
201      SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
826      TCAATGGAGGAATTGGAATAAATAGCTCACTTGATGCGGTACTTTCCAGGAGCAGAT 885
221      GluProLeuGlnTyrProCysGln 228
886      GAGCCATTACAGTATCCTTGTCTAG 909
RESULT 2
AB009358
LOCUS      Homo sapiens mRNA for TGF-beta activated kinase 1c, complete cds.
DEFINITION      AB009358
ACCESSION      AB009358
VERSION      AB009358.2 GI:8978251
KEYWORDS      tAK1c; TGF-beta activated kinase 1c.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Sakurai,H., Shigemori,N., Hasegawa,K. and Sugita,T.
TGF-beta-activated kinase 1 stimulates NF-kappa B activation by an
NF-kappa B-inducing kinase-independent mechanism
Biochem. Biophys. Res. Commun. 243 (2), 545-549 (1998)
2 (sites)
Dempsey,C.E., Sakurai,H., Sugita,T. and Guesdon,F.
Alternative splicing and gene structure of the transforming growth
factor beta-activated kinase 1
Biochim. Biophys. Acta 1517 (1), 46-52 (2000)
20568765
11118615
3 (bases 1 to 1705)
Sakurai,H., Shigemori,N., Hasegawa,K., Sugita,T. and Guesdon,F.
Direct Submission
Submitted (01-DEC-1997) Francois Guesdon, University of Sheffield,
Royal Hallamshire Hospital, Division of Molecular and Genetic
Medicine, Functional Genomics Group; Glossop road, Sheffield S10
2UF, United Kingdom (E-mail:f.a.guesdon@sheffield.ac.uk,
Fax:44-114-271-3846)
On Jul 8, 2000 this sequence version replaced gi:2924627.
COMMENT      Location/Qualifiers
FEATURES      source
1..1705
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pT7TAK1c"
/cell_line="HeLa"
1..1557
/note="TAK1c"
/codon_start=1
/product="TGF-beta activated kinase 1c"
/protein_id="BAA25027.2"
/db_xref="GI:8978252"
CDS

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NLLVAGGTVLKICDFGTACDIQTHMTNNKGSAAWMAPEVEGSGNSYSEKCDVFSWGII
LWEVITRKPPDEIGGPAFRIMWAVHNGTRPLKNLPKPIESLMTKRCWSKDPORS
MEEVTKMTLHMRYPGADPELOPCQYSDRGNSATSTGFMIDIASNTSNKSDTN
MEQVPATNDTIKRLSKLKNQAQKQESGRLSLGASRGSSVESLPPTSEKRSADM
SEIPEARLAAATTAAYSKPKRGHKTASFGNILDVPEIVISGNGQPRRSITODLTVTGTEP
QGVSSRSSPSVRMTTSGPTSEKPSRHPWTPDDSTDTNGSDNSIPMAYLTLRHQLQ
ARTSCRTGPG"
BASE COUNT      511 a      381 c      402 g      411 t
ORIGIN
Alignment Scores:
Pred. No.:      1.3e-117      Length:      1705
Score:          1252.00      Matches:      228
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9      Gaps:      0
US-09-830-144-2_COPY_76_303 (1-228) x AB009358 (1-1705)
Qy      1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
Db      226 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTCTAATATTGTAAGCTTTATGAGACC 285
Qy      21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db      286 TCGTTGAATCCAGTGTCTTGTGTGATGAATATGCTGAAGGGGGCTCTTTATATAATGTG 345
Qy      41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db      346 CTGCAATGTGCTGAACCATTCATATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 405
Qy      61 GlnCysSerGlnGlyValAlaTatYrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db      406 CAGTGTTCCTCAGAGAGTGGCTTATCTTCACAGCATGCACCAACCAAGCGCTAATTCACAGG 465
Qy      81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db      466 GACCTGAAACCAACCAACTTACTGTCTGTGTCAGGGGGGACAGTTCTAAAAATTTGTGAT 525
Qy      101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
Db      526 TTTGTATACAGCTGTGACATTCAGACACACATGACCAATACCAAGGGAGTGCTGCTTGG 585
Qy      121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
Db      586 ATGGCACCTGAAGTTTGTGAAGTAGTAAATACAGTGAATAATGTGACGTCTTCAGCTGG 645
Qy      141 GlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db      646 GGTATATTCTTTGGGAAGTGATAACCGCTGGAAACCTTTGATGAGATTGGTGGCCCA 705
Qy      161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleHisAsnLeu 180
Db      706 GCTTTCGGAATCATGTGGGCTGTTTCAATATGTACTCCAGCACCACTGATAAAAAATTTA 765
Qy      181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
Db      766 CCTAAGCCCATTTAGAGCCTGATGACTCTGTGTGTTGGTCTTAAGATCCTTCCAGCGCCCT 825
Qy      201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db      826 TCAATGGAGGAAATGTGAATAATATGACTCACTTGATCGGTACTTTTCCAGGACGAGAT 885
Qy      221 GluProLeuGlnTyrProCysGln 228
Db      886 GAGCCATTACAGTATCCTTGTGCAG 909
RESULT 3
AF218074
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LOCUS      AF218074      1745 bp      mRNA      linear      PRI 18-DEC-2000
DEFINITION Homo sapiens TGF beta-activated kinase splice variant d (TAK1)
mRNA, complete cds.
ACCESSION  AF218074
VERSION    AF218074.1 GI:6746614
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1745)
AUTHORS   Dempsey,C.E., Sakurai,H., Sugita,T. and Guesdon,F.
TITLE     Alternative splicing and gene structure of the transforming growth
factor beta-activated kinase 1
JOURNAL   Biochim. Biophys. Acta 1517 (1), 46-52 (2000)
MEDLINE   20568765
PUBMED    11118615
REFERENCE  2 (bases 1 to 1745)
AUTHORS   Dempsey,C.E. and Guesdon,F.
TITLE     Direct Submision
JOURNAL   Submitted (21-DEC-1999) Division of Molecular and Genetic Medicine,
University of Sheffield, School of Medicine, Glossop Road,
Sheffield S10 2UF, United Kingdom
FEATURES   Location/Qualifiers
source     1..1745
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gene       1..1745
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           /note="TAK1d"
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           /protein_id="AAF27652.1"
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           LWEVITRKPPDEIGGPAFRIMWAVHNGTRPLKNLPKPIESLMTKRCWSKDPORS
           MEVTKMTLHMRYPGADPELOPCQYSDRGNSATSTGFMIDIASNTSNKSDTN
           MEQVPATNDTIKRLSKLKNQAQKQESGRLSLGASRGSSVESLPPTSEKRSADM
           SEIPEARLAAATTAAYSKPKRGHKTASFGNILDVPEIVISGNGQPRRSITODLTVTGTEP
           QGVSSRSSPSVRMTTSGPTSEKPSRHPWTPDDSTDTNGSDNSIPMAYLTLRHQLQ"
BASE COUNT      526 a      375 c      412 g      432 t
ORIGIN
Alignment Scores:
Pred. No.:      1.33e-117      Length:      1745
Score:          1252.00      Matches:      228
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9      Gaps:      0
US-09-830-144-2_COPY_76_303 (1-228) x AF218074 (1-1745)
Qy      1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
Db      232 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTCTAATATTGTAAGCTTTATGAGACC 291
Qy      21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db      292 TCGTTGAATCCAGTGTCTTGTGTGATGAATATGCTGAAGGGGGCTCTTTATATAATGTG 351
Qy      41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db      352 CTGCAATGTGCTGAACCATTCGCTATATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 411
Qy      61 GlnCysSerGlnGlyValAlaTatYrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db      611 GAGCCATTACAGTATCCTTGTGCAG 909
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Db 412 CAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 471
 Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 472 GACCTGAACACCAACTTACTCTGTTGCGAGGGGAGAGTTCTAAAAAATTTGTGAT 531
 Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTIP 120
 Db 532 TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATACAAAGGGAGGCTGCTTGG 591
 Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTIP 140
 Db 592 ATGSCACCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATCTGACGCTTCAGCTGG 651
 Qy 141 GlyIleLeuLeuTIPGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 652 GGTATTATTCTTTGGGAAGTGATACCGTCGGAAACCTTTGATGAGATTGGTGGCCCA 711
 Qy 161 AlaPheArgIleMetTIPAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 712 GCYTTCGATCATGCGGCTGTTCATATGTTACTCGACACACACATGATAAAAAATTTA 771
 Qy 181 ProLysProIleGluSerLeuMetThrArgCysTIPSerLysAspProSerGlnArgPro 200
 Db 772 CCTAAGCCCATTTGAGACCTGATGACTCGTTGTTGGTCTAAAGATCCTTCCAGCGCCT 831
 Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 832 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGGGTACTTTCCAGGAGCAGAT 891
 Qy 221 GluProLeuGlnTyrProCysGln 228
 Db 892 GAGCCATTACAGTATCCTTTGTTCAG 915

RESULT 4

AR231198
 LOCUS AR231198 1788 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 14 from patent US 6451617.
 ACCESSION AR231198
 VERSION AR231198.1 GI:27272086
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1788)
 AUTHORS Ono, K., Ohtomo, T. and Tsuchiya, M.
 TITLE Method of screening TGF- β . inhibitory substances
 JOURNAL Patent: US 6451617-A 14 17-SEP-2002;
 FEATURES Location/Qualifiers
 source 1..1788
 /organism="unknown"
 BASE COUNT 551 a 394 c 413 g 430 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,37e-117 Length: 1788
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AR231198 (1-1788)

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 Db 232 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCCTAATATTGTAAGCTTTATGGAGCC 291
 Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
 Db 292 TGCCTGAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 351
 Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTIPCysLeu 60

Db 352 CTGATGGTCTGAACCACTTGCCCATATTATCTGCTGCCCAAGCAAGTGTGGTGTTA 411
 Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db 412 CAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 471
 Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 472 GACCTGAACACCAACTTACTCTGTTGCGAGGGGAGAGTTCTAAAAAATTTGTGAT 531
 Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTIP 120
 Db 532 TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATACAAAGGGAGGCTGCTTGG 591
 Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTIP 140
 Db 592 ATGSCACCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATCTGACGCTTCAGCTGG 651
 Qy 141 GlyIleLeuLeuTIPGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 652 GGTATTATTCTTTGGGAAGTGATACCGTCGGAAACCTTTGATGAGATTGGTGGCCCA 711
 Qy 161 AlaPheArgIleMetTIPAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 712 GCYTTCGATCATGCGGCTGTTCATATGTTACTCGACACACACATGATAAAAAATTTA 771
 Qy 181 ProLysProIleGluSerLeuMetThrArgCysTIPSerLysAspProSerGlnArgPro 200
 Db 772 CCTAAGCCCATTTGAGACCTGATGACTCGTTGTTGGTCTAAAGATCCTTCCAGCGCCT 831
 Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 832 TCAATGAGGAAATTTGAAATAATGACTCACTTGATGGGTACTTTCCAGGAGCAGAT 891
 Qy 221 GluProLeuGlnTyrProCysGln 228
 Db 892 GAGCCATTACAGTATCCTTTGTTCAG 915

RESULT 5

AR307979
 LOCUS AR307979 1788 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 14 from patent US 6551840.
 ACCESSION AR307979
 VERSION AR307979.1 GI:31698736
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1788)
 AUTHORS Ono, K., Ohtomo, T. and Tsuchiya, M.
 TITLE Method of screening TGF- β .-inhibiting substances
 JOURNAL Patent: US 6551840-A 14 22-APR-2003;
 FEATURES Location/Qualifiers
 source 1..1788
 /organism="unknown"
 BASE COUNT 551 a 394 c 413 g 430 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,37e-117 Length: 1788
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AR307979 (1-1788)

Qy 1 ValGluLeuArgGlnLeuSerArgValAlaAsnHisProAsnIleValLysLeuTyrGlyAla 20
 Db 232 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCCTAATATTGTAAGCTTTATGGAGCC 291

Db 982 TCAATGAGGAAATTGTGAAATAATGACTCACTTGATGGTACTTCCCGAGGCGGAT 1041
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 1042 GAGCCATTACAGTATCCTTGTGAG 1065
RESULT 7
AR2311192 AR2311192 2656 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 3 from patent US 6451617.
ACCESSION AR2311192
VERSION AR2311192.1 GI:27272080
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2656)
AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
TITLE Method of screening TGF-beta. inhibitory substances
JOURNAL Patent: US 6451617-A 3 17-SEP-2002;
FEATURES
source Location/Qualifiers
1..2656
/organism="unknown"
BASE COUNT 778 a 557 c 620 g 701 t
ORIGIN
Alignment Scores:
Pred. No.: 2,13e-117 Length: 2656
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-830-144-2_COPY_76_303 (1-228) x AR2311192 (1-2656)
Qy 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
Db 408 GTAGAGCTTCGGCAGTATCCCGTGTGACCATCTTAATATTGTAAGCTTTATGGAGCC 467
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 468 TGCCTTGATCCAGGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATG 527
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 528 CTGCATGGTGTGAACCATTCGCCATATTAATGCTGCGCCACGCAATGAGTTGGTGT 587
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db 588 CAGTGTTCACCAAGAGTGGCTTATCTTTCACAGCATGCAACCCCAAGAGCTTAATTCACAGG 647
Qy 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 648 GACCTGAAACCAACCAACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuLysGlySerAlaAlaTyr 120
Db 708 TTTGGTACAGCTGTGACATTCACACACATGACCAATACACAGGGAGTGGCTGTGG 767
Qy 121 MetAlaProGluValPheGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 768 ATGGCAGCTGTGAGTTTGAAGTAGTAAATACAGTGAAATGTGAGTCTTCAGCTGG 827
Qy 141 GlyIleLeuTyrGluValIleThrArgGlySerPropheAspGluIleGlyGlyPro 160
Db 828 GGTATTATCTTTGGGAAGTGAATAACGGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 887
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 888 GCTTTCCGAATCATGTGGGCTGTTTATATGATGCTGACCACTGATATAAATTTA 947

Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 948 CCTAAGCCCATTCAGAGCCTGATGACTGCTTGTGGTCTAAGATCCTCCAGGCCCT 1007
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 1008 TCAATGAGGAAATTTGTGAAATAATGACTCACTTGATGGTACTTTCCAGGAGCAGAT 1067
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 1068 GAGCCATTACAGTATCCTTGTGAG 1091
RESULT 8
AR307973 AR307973 2656 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 3 from patent US 6551840.
ACCESSION AR307973
VERSION AR307973.1 GI:31698730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2656)
AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
TITLE Method of screening TGF-beta.-inhibiting substances
JOURNAL Patent: US 6551840-A 3 22-APR-2003;
FEATURES
source Location/Qualifiers
1..2656
/organism="unknown"
BASE COUNT 778 a 557 c 620 g 701 t
ORIGIN
Alignment Scores:
Pred. No.: 2,13e-117 Length: 2656
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-830-144-2_COPY_76_303 (1-228) x AR307973 (1-2656)
Qy 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
Db 408 GTAGAGCTTCGGCAGTATCCCGTGTGACCATCTTAATATTGTAAGCTTTATGGAGCC 467
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 468 TGCCTTGATCCAGGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATG 527
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 528 CTGCATGGTGTGAACCATTCGCCATATTAATGCTGCGCCACGCAATGAGTTGGTGT 587
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db 588 CAGTGTTCACCAAGAGTGGCTTATCTTTCACAGCATGCAACCCCAAGAGCTTAATTCACAGG 647
Qy 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 648 GACCTGAAACCAACCAACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuLysGlySerAlaAlaTyr 120
Db 708 TTTGGTACAGCTGTGACATTCACACACATGACCAATACACAGGGAGTGGCTGTGG 767
Qy 121 MetAlaProGluValPheGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 768 ATGGCAGCTGTGAGTTTGAAGTAGTAAATACAGTGAAATGTGAGTCTTCAGCTGG 827
Qy 141 GlyIleLeuTyrGluValIleThrArgGlySerPropheAspGluIleGlyGlyPro 160
Db 768 ATGGCAGCTGTGAGTTTGAAGTAGTAAATACAGTGAAATGTGAGTCTTCAGCTGG 827
Qy 141 GlyIleLeuTyrGluValIleThrArgGlySerPropheAspGluIleGlyGlyPro 160
Db 828 GGTATTATCTTTGGGAAGTGAATAACGGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 887
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 828 GGTATTATCTTTGGGAAGTGAATAACGGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 887

161 AlaPheArgIleMetTrrAlaValHisAsnGlyThrArgProProLeuLeuIleAsnLeu 180
 888 GCTTTCGAATCATGTGGCGCTGTTCAATAGTACTACACACCACTGATAAAAAATTTA 947
 181 ProLysProIleGluSerLeuMetThrArgCysTrrSerLysAspProSerGlnArgPro 200
 948 CCTAAGCCCATTTGAGAGCTGATGACTGTTGTTGTTCTAAGATCCCTTCCAGCGCCCT 1007
 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 1008 TCAATGAGGAAATGTGAAATAATGACTCACTTGATCGGTACTTTCCAGGAGCAGAT 1067
 221 GluProLeuGlnTyrProCysGln 228
 1068 GAGCCATTACAGTATCTCTTGTCAG 1091

BC017715 2757 bp mRNA linear PRI 06-DEC-2001
 DEFINITION Homo sapiens, mitogen-activated protein kinase kinase 7,
 clone MGC:21263 IMAGE:3906837, mRNA, complete cds.
 BC017715
 ACCESSION BC017715.1 GI:17389342
 VERSION MGC.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2757)
 Direct Submission
 Strausberg,R.
 Submitted (03-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Prepared by: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 22 Row: 1 Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507360.
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 /db_xref="taxon:9606"
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CDS

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 LWEVITRKPEDEIGGFAPRIMWVHNGTREPPLKLNPKPIESLMTRCWSKDPORPS
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 SEIARIAAATTGNGQPRRSIQDLTVTTEPGQVSSRSRSPVSMITTSGPTSEKPTR
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BASE COUNT 819 a 566 c 647 g 725 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2,22e-117 Length: 2757
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BC017715 (1-2757)

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 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 483 TGCTTGATCCAGTGTGCTTTGATGGAATATGCTGAAGGGGGCTCTTTATATATG 542
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 543 CTGATGCTGTGTAACCATTCGCATATTATCTGCTGCCCGACGATAGTGTGTTA 602
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db 603 CAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 662
 QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyThrValLeuLysIleCysAsp 100
 Db 663 GACCTGAAACCAACCAACTTACTGCTGTTGTCAGGGGGGACAGTTCTAAAAATTTGTGAT 722
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
 Db 723 TTTGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGGAGTCTCTCTGG 782
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
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 QY 161 AlaPheArgIleMetTrrAlaValHisAsnGlyThrArgProProLeuLeuIleAsnLeu 180
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 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrrSerLysAspProSerGlnArgPro 200
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 QY 221 GluProLeuGlnTyrProCysGln 228
 Db 1083 GAGCCATTACAGTATCTCTTGTCAG 1106

RESULT 10
 AX377912
 LOCUS AX377912 2769 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 107 from Patent WO0212338.
 ACCESSION AX377912
 VERSION AX377912.1 GI:19573976
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Gillen, C., Wetzels, I., Wnendt, S., Weihe, E. and Schaefer, M.K.
 AUTHORS Screening method
 TITLE Patent: WO 0212338-A 107 14-FEB-2002;
 JOURNAL Gruenenthal GmbH (DE)
 FEATURES
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 Location/Qualifiers
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 Alignment Scores:
 Pred. No.: 2,236-117 Length: 2769
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 448 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAGGGGCTCTTATATAATGTG 507
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
 Db 508 CTGCATGCTGCTGAACCATTTGCCATATTACTGCTGCCACGCAATGAGTTGTTTGA 567
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db 568 CAGTGTTCACAGAGGAGTGTCTTCTTCACAGATGCAACCAAGCGCTAATTCACAGG 627
 QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 628 GACCTGAACACCAACCACTTACTGCTGTTGCAGGGGGACAGTTCTAATAATTTGTGAT 687
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
 Db 688 TTTTGGTACAGCTGTGACATTCACACACATACCAATACCAAGGGAGTGTCTGTGG 747
 QY 121 MetAlaProGluValPheGluGlySerAspTyrSerGlnLysCysAspValPheSerTrp 140
 Db 748 ATGGCACTGAGCTTTTGAAGGTAGTAAATACAGTGAATAATGTGACGCTTCAGCTGG 807
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 Db 808 GGTATTATTCTTTGGGAAGTGATAACCGCTCGGAACCCCTTTGATGAGTTGTGGCCCA 867
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 868 GCTTTCCGAATCATGTGGCTGTTCATAATGTGACTCGACCACTGATGATAAAAAATTTA 927
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
 Db 928 CTTAAGCCCATTTGAGACCTGATGACTGCTGTGTGTGTCTTAAGATCTTCCAGGCCCT 987
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 QY 221 GluProLeuGlnTyrProCysGln 228
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 RESULT 11
 LOCUS AB009356 2769 bp mRNA linear PRI 04-MAR-1998
 DEFINITION Homo sapiens mRNA for TGF-beta activated kinase 1a, complete cds.
 ACCESSION AB009356
 VERSION AB009356.1 GI:2924623
 KEYWORDS TAK1a; TGF-beta activated kinase 1a.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Sakurai, H., Shigemori, N., Hasegawa, K. and Sugita, T.
 TITLE TGF-beta-activated kinase 1 stimulates NF-kappa B activation by an NF-kappa B-inducing kinase-independent mechanism
 JOURNAL Biochem. Biophys. Res. Commun. 243 (2), 545-549 (1998)
 MEDLINE 9480845
 REFERENCE 2 (bases 1 to 2769)
 AUTHORS Sakurai, H.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1997) Hiroaki Sakurai, Lead Generation research laboratory, Tanabe Seiyaku Co. Ltd.; 16-89, Kashima-3-chome, Yodogawa-ku, Osaka, Osaka 532, Japan (E-mail:hsakurai@tanabe.co.jp, Tel:++81 6 300 2571, Fax:++81 6 300 2593)
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 BASE COUNT 811 a 565 c 640 g 753 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,236-117 Length: 2769
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-830-144-2_COPY_76_303 (1-228) x AB009356 (1-2769)
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 Db 388 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 447

3 Feb

QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db 448 TGCCTTGATCCAGTGTCTCTTGATGGAATATGCTGAGGGGGCTCTTTATATATATG 507
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db 508 CTGCATGCTGTGAACCAATTGCATATTATATCTGCTGCCACCAATGAGTGTGTTT 567
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db 568 CAGTGTTCCTCCAGGAGTGGCTTATCTTACAGCATGCAACCAACCAAGCGCTAATTCACAGG 627
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
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Db 688 TTTGGTACAGCCTGTGACATTGACACACACATGACCAATAACAAGGGGAGTGTCTTTGG 747
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Db 808 GGTATTATCTTTGGAGAGTGTATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 867
QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 868 GCTTTCCGAATCATGTGGCTGTTTCATAATGCTACTGCACCACTGATATAAAAAATTTA 927
QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
Db 928 CCTAAGCCCATGTGAGCCTGATGACTCGTTGTTGCTTAAGATCCCTTCCAGCGCCCT 987
QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
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RESULT 12
E38397
LOCUS 2785 bp DNA linear PAT 31-JAN-2002
DEFINITION NF-kappa B activation inhibitory drug targeting TAK1 and method for
identifying the same.
ACCESSION E38397
VERSION E38397.1 GI:18626977
KEYWORDS JP 2000197500-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 2785)
AUTHORS Sugita,N., Sakurai,H., Kageyama,N. and Hasegawa,H.
TITLE NF-kappa B activation inhibitory drug targeting TAK1 and method for
identifying the same
JOURNAL Patent: JP 2000197500-A 3 18-JUL-2000;
TANABE SEIYAKU CO LTD
COMMENT OS Unidentified
PN JP 2000197500-A/3
PD 18-JUL-2000
PF 04-FEB-1999 JP 1999026803
PR
PI NAOHISA SUGITA,HIROAKI SAKURAI,NORIKO KAGEYAMA, PI HIROSHI
HASEGAWA
PC C12Q1/48,A61K31/00,A61K45/00,A61K45/00,C12N5/10,C12N9/99, PC
C12Q1/92,
PC G01N33/15,G01N33/50,G01N33/566//C12N15/09,C12Q1/68,(C12N15/09,
PC C12R1:91),
PC C12N5/00,C12N15/00,(C12N15/00,C12R1:91)

CC Strandedness: Double;
CC Topology: Linear;
FH key Location/Qualifiers
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BASE COUNT 827 a 565 c 640 g 753 t
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Score: 100.00% Conservativity: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
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QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
Db 388 GTAGAGCTTCGCGAGTATCCGCTGGAACCATCTATATATTGAAGCTTTATGGAGCC 447
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db 448 TGCCTTGATCCAGTGTCTCTTGATGGAATATGCTGAGGGGGCTCTTTATATATG 507
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db 508 CTGCATGCTGTGAACCACTTATGCTGCTGCCACCAATGCTGCTGCTTTTATATATG 567
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db 568 CAGTGTTCCTCCAGGAGTGGCTTATCTTACAGCATGCAACCAACCAAGCGCTAATTCACAGG 627
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 628 GACCTGAAACCAACCACTTACTGCTGCTGAGGGGGACAGTTCTAAAAATTTTGAT 687
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
Db 688 TTTGGTACAGCCTGTGACATTGACACACACATGACCAATAACAAGGGGAGTGTCTTTGG 747
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
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QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 868 GCTTTCCGAATCATGTGGCTGTTTCATAATGCTACTGCACCACTGATATAAAAAATTTA 927
QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
Db 928 CCTAAGCCCATGTGAGCCTGATGACTCGTTGTTGCTTAAGATCCCTTCCAGCGCCCT 987
QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 988 TCATGGAGGAATTTGTGAATAATGACTACTTGAATGCGGTACTTTCCAGGAGCAGAT 1047
RESULT 13
AB009357

LOCUS AB009357 2850 bp mRNA linear PRI 04-MAR-1998
 DEFINITION Homo sapiens mRNA for TGF-beta activated kinase 1b, complete cds.
 ACCESSION AB009357
 VERSION AB009357.1 GI:2924625
 KEYWORDS TAK1b; TGF-beta activated kinase 1b.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Sakurai,H., Shigemori,N., Hasegawa,K. and Sugita,T.
 TITLE TGF-beta-activated kinase 1 stimulates NF-kappa B activation by an NF-kappa B-inducing kinase-independent mechanism
 JOURNAL Biochem. Biophys. Res. Commun. 243 (2), 545-549 (1998)
 MEDLINE 98153801
 PUBMED 9480845
 REFERENCE 2 (bases 1 to 2850)
 AUTHORS Sakurai,H.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1997) Hiroaki Sakurai, Lead Generation research laboratory, Tanabe Seiyaku Co. Ltd.; 16-89, Kashima-3-chome, Yodogawa-ku, Osaka, Osaka 532, Japan (E-mail:hsakurai@tanabe.co.jp, Tel:++81 6 300 2571, Fax:++81 6 300 2593)
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US-09-830-144-2_COPY_76_303 (1-228) x AB009357 (1-2850)

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 ACCESSION E38398
 VERSION E38398.1 GI:18626978
 KEYWORDS JP 2000197500-A/4.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 2866)
 AUTHORS Sugita,N., Sakurai,H., Kageyama,N. and Hasegawa,H.
 TITLE NF-kappa B activation inhibitory drug targeting TAK1 and method for identifying the same.
 JOURNAL Patent: JP 2000197500-A 4 18-JUL-2000;
 COMMENT TANABE SEIYAKU CO LTD
 OS Unidentified
 PN JP 2000197500-A/4
 PD 18-JUL-2000
 PF 04-FEB-1999 JP 1999026803
 PR
 PI NAOHISA SUGITA,HIROAKI SAKURAI,NORIKO KAGEYAMA, PI HIROSHI HASEGAWA
 PC C12Q1/48,A61K31/00,A61K31/00,A61K45/00,C12N5/10,C12N9/99, PC C12Q1/02,
 PC G01N33/15,G01N33/50,G01N33/566//C12N15/09,C12Q1/68,(C12N15/09, PC C12R1:91),
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Query Match:      100.00%
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Db 388 GTAGAGCTTCGGCAGTATCCGCTGATGGAACCATCTCTAATATTTGTAAGCTTTATCGAGCC 447
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Db 688 TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATACAGGGGAGTGTCTGCTTGG 747
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Qy 221 GluProLeuGlnTyrProCysGln 228
Db 1048 GAGCCATTACAGTATCTTGTGCAG 1071
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BC006665
LOCUS
DEFINITION
  Mus musculus mitogen activated protein kinase kinase 7, mRNA
  (cDNA clone MGC:5989 IMAGE:3499247), complete cds.
ACCESSION
  BC006665
VERSION
  BC006665.1 GI:13879375
KEYWORDS
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SOURCE
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ORGANISM
  Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 3107)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

TITLE

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22389257
12477932

REFERENCE
MEDLINE
PUBMED

2 (bases 1 to 3107)
Direct Submission
Strausberg, R.
Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

TITLE

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov

REMARK

Contact: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navevati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 9 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity to protein.

FEATURES
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gene

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Db	433	TGCCTGAATCCAGTATGCTTGTGATGGAATATGCAGAGGGGGCTCATTTGATAAATGTG	492
Qy	41	LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu	60
Db	493	CTGCATGGTGTGAACCATTCGCTTACTACACTGCTCATGCCATGAGCTGTGTGTTTA	552
Qy	61	GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg	80
Db	553	CAGTGTCCCAAGAGTGGCTTACTGCACAGCATGCAGCCCAAGGCGCTGATTCACAGG	612
Qy	81	AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp	100
Db	613	GACCTCAAGCCTCCAAACTTGTGCTGCTGAGGAGGACAGTTCATAAAATCTGGCAT	672
Qy	101	PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr	120
Db	673	TTTCGTACAGCTTGTGACATCCAAACACACATGACCAATAATAAGGGAGTGTGCTTGG	732
Qy	121	MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr	140
Db	733	ATGGCCCTGAAGCTTTGAAGGTAGCAATTACAGTGAAAGTGTGATGCTTCAGCTGG	792
Qy	141	GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro	160
Db	793	GGTATTATCTCTGGGAAGTGATAACACGCCGGAACCCCTTCGATGAGATCGGTGGCCCA	852
Qy	161	AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu	180
Db	853	GCTTTCAAGATCATGTGGGCTGTTCAATAATGGCACTCGACCACCATCATCAAAATTTA	912
Qy	181	ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro	200
Db	913	CCTAAGCCCATTGAGAGCTTGATGACACGCTGTGTGGTCTAAGGACCCATCTCAGCGCCT	972
Qy	201	SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp	220
Db	973	TCAATGGAGGAAATTTGTGAAATAATAATGACTCACTTGATGCGGTACTTCCCGAGCGGAT	1032

Qy 221 GluProLeuGlnTyrProCysGln 228
 Db 1033 GAGCCATTACAGTATCTTGTCTAG 1056

Search completed: December 4, 2003, 11:39:56
 Job time : 4917.16 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 09:34:12 ; Search time 397.459 Seconds
(without alignments)
1548.515 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252
Sequence: 1 VELRLSRVNHPIVILYGA.....MTHLMRYFPGADEPLQYPCQ 228

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq.19Jun03 -QPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq.19Jun03.*

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25: /SID81/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	1704	20	AAAX99698 Human TGF-beta act
2	1252	100.0	1788	20	AAAX56285 Human TAK1-6xHis e
3	1252	100.0	1959	18	AAAT85095 Mouse transforming
4	1252	100.0	2443	18	AAAT85094 Human TAK1 encodin
5	1252	100.0	2656	20	AAAX56279 Human TAK-1 nucleo
6	1252	100.0	2656	21	AAAX39105 Pain regulated cDN
7	1252	100.0	2769	24	ABL88437 Human TGF-beta act
8	1252	100.0	2785	20	AAAX99696 Human TGF-beta act
9	1252	100.0	2866	20	AAAX99697 Drosophila melanog
10	700	55.9	3367	23	ABL02489 Drosophila melanog
11	599	47.8	10997	23	ABL02488 Drosophila melanog
12	414	33.1	759	23	ABL08337 Pancreas cancer re
13	392.5	31.3	3454	24	ABL70018 Arabidopsis thalia
14	374	29.9	1224	21	AAAC43254 Arabidopsis thalia
15	373	29.8	1631	21	AAAC39537 Human NOV7, a mixe
16	371.5	29.7	3092	24	ABN85385 Human encoding huma
17	371	29.6	1063	22	AAH34976 cDNA encoding huma
18	371	29.6	1365	21	AAZ99727 DNA encoding a hum
19	371	29.6	1706	21	AAAY5674 Human protein enco
20	371	29.6	2120	21	AAZ99726 Cardiovascular sys
21	371	29.6	2191	22	AAH92263 Human survival reg
22	371	29.6	2194	21	AAZ99734 Cardiovascular sys
23	371	29.6	2220	21	AAZ99735 Novel protein kina
24	371	29.6	2254	21	AAZ99736 Motif zipper conta
25	371	29.6	2403	22	ABQ60980 Human TGF-beta rec
26	371	29.6	2592	24	AAH75336 Human cervical can
27	371	29.6	2622	22	AAH73366 Cardiovascular sys
28	371	29.6	3967	22	AAZ99737 Cardiovascular sys
29	370	29.6	2069	21	AAZ99736 Drosophila melanog
30	370	29.6	2272	21	ABL04365 Human kinase (PKIN
31	363.5	29.0	3072	23	ABL04365 Human PKIN-12 cDNA
32	361.5	28.9	3141	22	AAAD18824 Novel human gene.
33	361.5	28.9	3538	24	ABQ86165 Novel human protei
34	355.5	28.4	3066	24	ABQ86165 Nucleotide sequenc
35	355	28.4	2157	22	AAH46913 Human kinase and p
36	355	28.4	3111	25	ABZ23269 Polynucleotide seq
37	355	28.4	3111	25	ABZ23269 Polynucleotide seq
38	355	28.4	3111	25	ABZ23269 Human cDNA differe
39	355	28.4	3518	24	ABZ23195 Polynucleotide seq
40	353.5	28.2	2732	25	ABZ23195 Human cDNA differe
41	353.5	28.2	2830	25	ABZ23195 Polynucleotide seq
42	353.5	28.2	3365	24	ABK84203 Polynucleotide seq
43	353.5	28.2	3365	25	ABZ23194 Human leucine zipp
44	353.5	28.2	3389	16	AAAT01031 Human leucine-zipp
45	353.5	28.2	3389	18	AAAT89349

ALIGNMENTS

RESULT 1
AAAX99698
ID AAAX99698 standard; cDNA to mRNA; 1704 BP.
XX
AC AAAX99698;
XX
DT 18-OCT-1999 (first entry)
XX
DE Human TGF-beta activated kinase (TAK) 1c encoding nucleotide sequence.
XX
KW Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
KW intracellular disease; atrophic dermatitis; psoriasis; viral infection;
KW endotoxin shock; septicemia; human; hTAK1c; ss.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
 FT 1..1704
 FT /*tag= a
 FT /product= "hTAK1c"
 XX WO9940202-A1.
 XX 12-AUG-1999.
 XX 02-FEB-1999; 99WO-JP00422.
 XX 30-OCT-1998; 98JP-0309316.
 PR 06-FEB-1998; 98JP-0026003.
 XX (TANA) TANABE SEIYAKU CO.
 XX Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 FI WPI; 1999-494298/41.
 DR P-PSDB; AAY28998.
 XX Nuclear factor kappa B activation inhibitors, useful as preventives
 FT for, e.g. autoimmune diseases
 XX Examples; Page 43-46; 49pp; Japanese.
 XX The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the nucleotide sequence of human TAK1c
 CC (hTAK1c) protein.
 XX
 SQ Sequence 1704 BP; 511 A; 381 C; 401 G; 411 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.75e-133 Length: 1704
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-830-144-2_COPY_76_303 (1-228) x AAX99698 (1-1704)
 QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
 Db 226 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCCCTTAATATGTAAGCTTTATGAGCC 285
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 286 TGCCTGAATCCAGTGTCTGTGTGATGAATATGCTGAAGGGGGCTTTATATAATGTG 345
 QY 41 LeuHisGlyValAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 346 CTGCATGGTGCTGAACCATTCATATATACCTGCTGCCACCAATGAGTTGGTGTGTTA 405
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuLeuHisArg 80
 Db 406 CAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCACCAACCGCTAATTCACAGG 465
 QY 81 AsnLeuLysProProAsnLeuLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 466 GACCTGAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTCTTAAAAATTGTGAT 525
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
 Db 526 TTGGTACAGCTGTGACATTCAGACACATGACCAATACACAGGGGAGTGTGCTGG 585
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140

Db 586 ATGCACCTGAAGTTTTGAAGGTAGTAATTACAGTAAAAAATGTGACGCTTCAGCTGG 645
 QY 141 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 646 GGTATTATTCTTTGGGAAGTGATAACGCTCGGAACCCCTTTGATGAGATTGGTGGCCA 705
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 706 GCTTTCCGAATCATGTGGCTGTTCAATAATGTACTCGACCCACCATGATAAAAAATT 765
 QY 181 ProllysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
 Db 766 CCTAAGCCCATTCAGAGCCCTGATGCTGTGTGGTCTAAAGATCCTTCCACGGCCCT 825
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 826 TCAATGGAGGAATTTGAAAAATAATGACTCATTGTATGCGGTACTTTCAGGAGCAGAT 885
 QY 221 GluProLeuGlnTyrProCysGln 228
 Db 886 GAGCCATTACAGTATCCTTGTCTAG 909
 RESULT 2
 AAX56285
 ID AAX56285 standard; DNA; 1788 BP.
 AC AAX56285;
 XX 21-JUL-1999 (first entry)
 XX Human TAK1-6xHis encoding DNA.
 DE Human TAK1-6xHis encoding DNA.
 XX Human; TAK1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 CDS 7..1779
 FT /*tag= a
 XX WO9921010-A1.
 XX 29-APR-1999.
 XX 22-OCT-1998; 98WO-JP04796.
 XX 22-OCT-1997; 97JP-0290188.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Ohtomo T, Ono K, Tsuchiya M;
 WPI; 1999-312645/26.
 P-PSDB; AAY09547.
 XX Screening for TGF- beta inhibitory substances, which are useful as
 XX drugs for treatment of diseases relating to its disorder
 XX Example 1; Page 167-171; 195pp; Japanese.
 CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAK1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAK1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or

CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes TAK1-6XHis from an example of
 CC the present invention.

XX Sequence 1788 BP; 551 A; 394 C; 413 G; 430 T; 0 other;

Alignment Scores:

Pred. No.: 4.01e-133 Length: 1788
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AAX56285 (1-1788)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
 Db GTAGAGCTTCGGCAGTATCCCGGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 291
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db TGGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 351
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
 Db CTGCATGGTGTGAACCATCTCCCATATTATATCTGCTGCCACGCAATGAGTTGGTTTA 411
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db CAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTACACAGG 471
 QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db GACCTGAACACCAACACTTACTGCTGTTGTCAGGGGGGACAGTCTTAATAATTTGTGAT 531
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
 Db TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTCTTGG 591
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
 Db ATGGCACCCTGAAGTTTTCGAAGGTAGTAATTAACAGTGAATAATGTGACGCTCTCAGCTGG 651
 QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db GGTATTATCTTTGGGAAGTGTATACCGCTCGGAACCCCTTGTGATGAGATTGGTGGCCCA 711
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db GCTTTCGGAATCATGTGGCTGTTTCATTAATGGTACTGACCAACCATCTATAAAAAATTA 771
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
 Db CCTAAGCCCATGTGAGAGCCTCATGCTGTTGTGGTCTTAAGATCCTTCCACGGCCCT 831
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db TCAATGGAGGAATTTGGAATAATATGACTCATCTGTATGCGGTACTTTCCAGGAGCAGAT 891
 QY 221 GluProLeuGlnTyrProCysGln 228
 Db GAGCCATTACAGTATCTCTTGTGAC 915

RESULT 3

AAAT85095
 ID AAAT85095 standard; cDNA; 1959 BP.
 XX
 AC AAAT85095;
 XX

DT 19-NOV-1997 (first entry)
 XX Human transforming growth factor-beta activated kinase TAK-1 cDNA.
 XX TGF-beta; signal transduction; TGF-beta activated kinase;
 KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;
 KW protein kinase; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 183..1922
 FT /*tag= a
 FT /product= TAK-1

XX JP09163990-A.

XX 24-JUN-1997.

XX 27-SEP-1996; 96JP-0256747.

XX 24-JUL-1996; 96US-0685625.

XX 29-SEP-1995; 95JP-0253549.

XX (CHUS) CHUGAI PHARM CO LTD.

XX (UENO) UENO N.

XX WPI; 1997-380171/35.

XX P-PSDB; AAW27093.

XX DNA encoding transforming growth factor-beta-activated kinase, TAK-1
 PT - useful for studying the TGF-beta signal transduction system

XX Claim 9; Page 13-15; 20pp; Japanese.

XX The present sequence encodes human transforming growth factor-beta
 CC (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the
 CC TAK-1 protein which is involved in the TGF-beta family signal
 CC transduction system. TAK-1, also known as activator of MAPK Kinase
 CC (AMK-1), is an enzyme which is activated by TGF-beta and bone
 CC morphogenetic protein (BMP) and activates MAPK kinase by
 CC phosphorylation.

XX Sequence 1959 BP; 571 A; 447 C; 481 G; 460 T; 0 other;

Alignment Scores:

Pred. No.: 4.57e-133 Length: 1959
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AAAT85095 (1-1959)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
 Db GTAGAGCTTCGGCAGTATCCCGGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 467
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db TGGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
 Db CTGCATGGTGTGAACCATCTCCCATATTATATCTGCTGCCACGCAATGAGTTGGTTTA 587
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db CAGTGTTCCTCCAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTACACAGG 647
 QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100

Db 648 GACCTGAACACCAACAACTTACTGCTGTTGCAGGGGGGACAGTCTTCAAAAAATTGTGAT 707
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
 Db 708 TTTGGGTACAGCCTGTGACATTCAGACACACATGACCAATAACAAGGGAGTGTCTGTGG 767
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
 Db 768 ATGGCACTGAGTGTGTTGAAGGTAGTAATTACAGTGAATAATGTGACGTCTTCAGCTGG 827
 QY 141 GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 828 GGTATTATCTTTGGGAAGTGATACACGCTGCGAAACCCCTTTCATGAGATTGTGGCCCA 887
 QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 888 GCTTTCGGAATCATGTGGGCTGTTTCATAATGGTACTGACCCACCTGATATAAAAAATTTA 947
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
 Db 948 CCTAAGCCCATTCAGACCTGATGACTCGTGTGTTGGTCTAAGATCCTTCCAGGCGCCT 1007
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 1008 TCAATGGAGGAAATTTGAAAAATAATGACTCACTTGATGGGTACTTTCCAGGAGCAGAT 1067
 QY 221 GluProLeuGlnTyrProCysGln 228
 Db 1068 GAGCCATTACAGTATCCTTGTGAC 1091

RESULT 4

AAT85094
 ID AAT85094 standard; cDNA; 2443 BP.

AC AAT85094;

19-NOV-1997 (first entry)

Mouse transforming growth factor-beta activated kinase TAK-1 cDNA.

TGF-beta; signal transduction; TGF-beta activated kinase;

MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;

protein kinase; ss.

Mus musculus.

Key Location/Qualifiers
 CDS 157..1896
 FT /*tag= a
 FT /product= TAK-1

JP09163990-A.

24-JUN-1997.

27-SEP-1996; 96JP-0256747.

24-JUL-1996; 96US-0685625.

29-SEP-1995; 95JP-0253549.

(CHUS) CHUGAI PHARM CO LTD.

(UENO/) UENO N.

WPI; 1997-380171/35.

P-PSDB; AAW27092.

DNA encoding transforming growth factor-beta-activated kinase, TAK-1

- useful for studying the TGF-beta signal transduction system

Claim 2; Page 10-12; 20pp; Japanese.

The present sequence encodes mouse transforming growth factor-beta

(TGF-beta) activated kinase, TAK-1. The DNA is used to produce the

CC TAK-1 protein which is involved in the TGF-beta family signal
 CC transmission system. TAK-1, also known as activator of MAPK Kinase
 CC (AMK-1), is an enzyme which is activated by TGF-beta and bone
 CC morphogenetic protein (BMP) and activates MAPK kinase by
 CC phosphorylation.

XX
 SQ Sequence 2443 BP; 669 A; 567 C; 647 G; 559 T; 1 other;

Alignment Scores:

Pred. No.: 6,26e-133 Length: 2443
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AAT85094 (1-2443)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
 Db 382 GTGGAGCTCCGGCAGTGTGCGGTGTGAACCATCTTAACATTGTCAAGTTGTACGGAGCC 441
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 442 TGCCTGAATCCAGTATGTCTTGTGATGGAATATGCAGAGGGGGCTCATTTGATAAATGTG 501
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 502 CTGCATGTGTGCTGAACCATTTGCCTTACTACACTGCTCTCATGCCATGAGCTGTGTGTTA 561
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db 562 CAGTGTTCACAGAGGTGGCTTACCTGCACAGATGCAGCCCAAGCGCTGATTCACAGG 621
 QY 81 AspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 622 GACCTCAAGCTCCAAACTTGTCTGTTGTCAGAGGAGGACAGTTCTAAAAATCTCGCAT 681
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
 Db 682 TTTGGTACAGCTTGTGACATCCAAACACACATGACCAATTAATAAGGGAGTGTCTGTGG 741
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
 Db 742 ATGGCGCTGAAGTGTGTTGAAGGTAGCAATTACAGTGAAGGTGTGATGCTTCAGCTGG 801
 QY 141 GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 802 GGTATTATCCTCTGGGAAGTGATAACACGCGCGAAACCCCTTCGATGAGATCGGTGGCCCA 861
 QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 862 GCTTTCAGAAATCATGTGGGCTGTTCATAATGGCATCGCACCATCATGATCAAAATTTA 921
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
 Db 922 CCTAAGCCCATTCAGAGCTTCATGACACGCTGTGGTCTAAGGACCATCTCAGCGCCCT 981
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 982 TCAATGGAGGAAATTTGAAAAATAATGACTCACTTGATGGGTACTTCCAGGAGCGGAT 1041
 QY 221 GluProLeuGlnTyrProCysGln 228
 Db 1042 GAGCCATTACAGTATCCTTGTGAC 1065

RESULT 5

AA556279

ID AA556279 standard; DNA; 2656 BP.

XX AA556279;

AC AA556279;

DT 21-JUL-1999 (first entry)

XX DE Human TAK1 encoding DNA.
 XX KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 XX KW transforming growth factor beta; ss.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX FT CDS 183..1922
 XX FT /*tag= a
 XX PN WO9921010-A1.
 XX PD 29-APR-1999.
 XX PF 22-OCT-1998; 98WO-JP04796.
 XX PR 22-OCT-1997; 97JP-0290188.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ohtomo T, Ono K, Tsuchiya M;
 XX DR WPI; 1999-312645/26.
 XX DR P-PSDB; AAY09542.
 XX PT Screening for TGF- beta inhibitory substances, which are useful as
 XX PT drugs for treatment of diseases relating to its disorder
 XX PS Example 1; Page 150-154; 195pp; Japanese.
 XX CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transmission inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes human TAK1.
 XX SQ Sequence 2656 BP; 778 A; 557 C; 620 G; 701 T; 0 other;

Alignment Scores:
 Pred. No.: 7.05e-133 Length: 2656
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AAX56279 (1-2656)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 20
 Db 408 GTAGAGCTTCGGCAGTATCCGCTGTGATGGATATCTAATATTTGTAAGCTTTATGAGCC 467
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 468 TGCTTGATCCAGTGTCTTGTGATGGATATCTGTAAGGGGGCTCTTATATATGTG 527
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 528 CTGCATGTGTGTAACCATTCGCATATATATATATATATATATATATATATATATATAT 587
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80

Db 598 CAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCCGCTAATTCACAGG 647
 QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 Db 648 GACCTGAAACCAACCAACTTACTGTGTGTTGCAGGGGGACAGTTCTAAAAAATTTGTGAT 707
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaIleTrp 120
 Db 708 TTTGGTACAGCCTGTGCATTCAGACACACATGACCAATAACAGGGGAGTGCTGCTTGG 767
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
 Db 768 ATGCACCTGAAGTTTGAAGGTAGTAATTCACAGTGAATAATGACAGCTCTTCAGCTGG 827
 QY 141 GlyIleLeuLeuTrpGluValIleThrArgArgLysPropheAspGluIleGlyGlyPro 160
 Db 828 GGTATTATCTTTGGGAAGTGATAACGGTCCGAAACCCCTTTGATGAGATTGGTGGCCCA 887
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 888 GCTTTCCGAATCATGTGGGCTGTTCAATAATGGTACTCGACCACCACTGATAAAAATTTTA 947
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
 Db 948 CCTAAGCCCATTTGAGAGCTGATGACTGCTGTGGTCTAAGATCCTTCCAGGCGCCT 1007
 QY 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 1008 TCAATGGAGGAAATTTGTGAAAAATAATGACTCACTTGATGCGGTACTTTCCAGGACGAGT 1067

QY 221 GluProLeuGlnTyrProCysGln 228
 Db 1068 GAGCCATTACAGTATCCTTGTGAG 1091

RESULT 6
 AAA39105
 ID AAA39105 standard; DNA; 2656 BP.
 AC AAA39105;
 DT 04-SEP-2000 (first entry)
 DE Human TAK-1 nucleotide sequence SEQ ID NO:1.
 XX KW Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;
 KW screening; signal transduction; inhibition; inflammatory cytokine;
 KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;
 KW antiinflammatory; suppression; ds.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX FT CDS 183..1922
 XX FT /*tag= a
 XX FT /product= "TAK-1"
 XX PN WO200023610-A1.
 XX PD 27-APR-2000.
 XX PF 21-OCT-1999; 99WO-JP05817.
 XX PR 21-OCT-1998; 98JP-0299962.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;
 XX DR WPI; 2000-339707/29.
 XX DR P-PSDB; AAY91000.
 XX PT Method for screening inhibitors of TAK1 signal transduction for

PT suppression of inflammatory cytokine production and use as
 PT anti-inflammatory agents -

PS Example 1; Page 73-80; 100pp; Japanese.

XX The present invention describes a method for screening compounds for
 CC inhibition of inflammatory cytokine signal transduction by contacting
 CC the sample with TAK1 and its receptor TAB1 and selecting for inhibition
 CC of TAK1/TAB1 binding. Also described is a method for screening compounds
 CC for inhibition of inflammatory cytokine signal transduction in which the
 CC inhibition of TAK1 phosphorylation is selected for; and drug
 CC compositions for the treatment of inflammatory disorders containing as
 CC active component an inflammatory cytokine signal transduction inhibitor.
 CC TAK1 is an essential component of the signalling process which results
 CC in release of inflammatory cytokines such as interleukin-1 (IL-1),
 CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used
 CC for the selection of effective anti-inflammatory agents. The present
 CC sequence encodes human TAK-1, which is used in the exemplification of the
 CC present invention.

SQ Sequence 2656 BP; 778 A; 557 C; 620 G; 701 T; 0 other;

Alignment Scores:

Pred. No.: 7.05e-133 Length: 2656
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AAA39105 (1-2656)

Qy 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 20
 Db 408 GTAGAGCTTCGGCAGTTATCCGCTGACACATCCTAATATGTAAGCTTTATGGAGCC 467
 Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 Db 468 TGCTTGATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTTTTATATATG 527
 Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
 Db 528 CTGCATGGTGTGAACCATTCGCCATATATATCTGCTCCACGCAATGAGTTGTGTTA 587
 Qy 61 GluCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 80
 Db 588 CAGGTCTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 647
 Qy 81 AspleuIysProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp 100
 Db 648 GACCTGAACACCAACTTACTGTCTGTGTCAGGGGGGACAGTTCTTAAAAATTTGAT 707
 Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuIysGlySerAlaAlaTrp 120
 Db 708 TTTGGTACAGCGCTGTGCAATTCACACACATGACCAATACCAAGGGGAGTGTCTGTG 767
 Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTrp 140
 Db 768 ATGGACCTGAAGTTTTTGAAGGTAGTAAATACAGTGAATAATGTGACGTTCTCAGCTGG 827
 Qy 141 GlyIleIleLeuTrpGluValIleThrArgArgIysProPheAspGluIleGlyGlyPro 160
 Db 828 GGTATTATTCTTTGGGAAGTGATACCGCTCGGAACCTTTGATGAGATTGTGGCCCA 887
 Qy 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 888 GCTTTCGGAATCATGTGGCTGTTCATAATGTACTCGACCACTGATAAAAAATTAT 947
 Qy 181 ProIysProIleGluSerLeuMetThrArgCysTrpSerIysAspProSerGlnAtrpPro 200
 Db 948 CCAAGCCCAATGAGACCGCTGATGCTGTGTGGTAAAGATCCTTCCAGCGCCCT 1007
 Qy 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220

Db 1008 TCAATGAGGAATTTGAAATAATGACTCACTTGATCGGTACTTCCAGGAGCAGAT 1067

Qy 221 GluProLeuGlnTyrProCysGln 228

Db 1068 GAGCCATTACAGTATCCTTGTTCAG 1091

RESULT 7

ABL88437

ID ABL88437 standard; cDNA; 2769 BP.

XX ABL88437;

XX AC ABL88437;

XX DT 16-MAY-2002 (first entry)

XX DE Pain regulated cDNA sequence 80.

XX KW Pain; analgesic; gene therapy; neurological disorder;

XX KW neurodegenerative disease; gene; ss.

XX OS Homo sapiens.

XX PN WO200212338-A2.

XX PD 14-FEB-2002.

XX PF 03-AUG-2001; 2001WO-EP09011.

XX PR 03-AUG-2000; 2000DE-1037759.

XX PA (CHEF) GRUENENTHAL GMBH.

XX PI Gillen C, Wetzel S, I, Wrendt S, Weihe E, Schaefer MK;

XX DR WPI; 2002-257469/30.

XX PS P-PSDB; ABB85033.

PT Identifying pain-regulating compounds, useful for treating chronic pain
 PT and for diagnosis, by measuring binding of compounds to specific
 PT peptides and proteins -
 PS Claim 1; Fig 44; 213pp; German.
 CC The invention relates to identifying pain-regulating substances (A)
 CC comprises (i) incubating a test substance with a cell (or preparation
 CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
 CC either binding of the test substance to (B) or some functional parameter
 CC that is altered by this binding. The method is useful for identifying
 CC pain-regulating substances (A) with analgesic activity. (A) along with
 CC nucleic acid (ABL88411-ABL88441) that encode proteins (B),
 CC ABB85006-ABB85037) that interact with (A); (B); vectors containing the
 CC nucleic acid; antibodies against (B); cells that express (B) and agents
 CC that bind to (B), are all useful for treating pain, particularly chronic
 CC pain, including use in gene therapy. The same materials can also be used
 CC for diagnosis, e.g. of neurological and neurodegenerative diseases. The
 CC present sequence is that of a polynucleotide of the invention.

SQ Sequence 2769 BP; 811 A; 565 C; 640 G; 753 T; 0 other;

Alignment Scores:

Pred. No.: 7.48e-133 Length: 2769
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x ABL88437 (1-2769)

Qy 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 20
 Db 388 GTAGAGCTTCGGCAGTTATCCGCTGTAACCATCTTAATATGTAAGCTTTATGGAGCC 447

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QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
DB 448 TGCCTGAATCCAGTGGCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATG 507
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
DB 508 CTGCATGGTGTGAACCATGGCATATATCTGCTGCCACGCAATGATGGTGTGTTA 567
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArg 80
DB 568 CAGTGTTCGCAAGGAGTGGCTATCTCTACAGCATCAACCCCAAGCGCTAATTCACAG 627
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
DB 628 GACCTGAACCCCAACCTTACTGGTTCGAGGGGGGACAGTCTCTAAAAATTTGTGAT 687
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
DB 688 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTCTGG 747
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
DB 748 ATGGCACCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATGTGACGCTTCAGCTGG 807
QY 141 GlyIleLeuTyrGluValIleThrArgGlyProPheAspGluIleGlyGlyPro 160
DB 808 GGTATTATCTTTGGGAAGTGATAACGCGTCGGAACCCCTTTGATGAGTTGGTGGCCCA 867
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuLysAsnLeu 180
DB 868 GCTTTCCGAATCATGTGGGCTGTTCATAATGTACTGACCAACCTGATGAATAATTTA 927
QY 181 ProLysProLysGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
DB 928 CCTAAGCCCATTCAGAGCCCTGATGACTCGTGTGTGGTCTAAGATCCTCCAGCGCCCT 987
QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
DB 988 TCAATGAGGAAATTTGAAAAATAATGACTCACTTGTATGCGGTACTTTCCAGAGCAGAT 1047
QY 221 GluProLeuGlnTyrProCysGln 228
DB 1048 GAGCCATTACAGTATCCTTGTCTAG 1071

RESULT 8
AAAX99696
ID AAAX99696 standard; cDNA to mRNA; 2785 BP.
AC
XX
XX AAAX99696;
XX
DT 18-OCT-1999 (first entry)
XX
DE Human TGF-beta activated kinase (TAK) 1a encoding nucleotide sequence.
XX
KW Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
KW endotoxin shock; septicemia; human; hTAK1a; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 163..1902
FT /*tag= a
FT /*product= "hTAK1a"
XX
EN WO9940202-A1.
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-JP00422.
XX
XX 30-OCT-1998; 98JP-0309316.

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PR 06-FEB-1998; 98JP-0026003.
XX
PA (TANA ) TANABE SEIYAKU CO.
XX
PI Hasegawa K, Kageyama N, Sakurai H, Sugita T;
XX
XX WPI; 1999-494298/41.
XX
DR P-PSDB; AAY28996.
XX
XX Nuclear factor kappa B activation inhibitors, useful as preventives
PT for, e.g. autoimmune diseases
XX
PS Examples; Page 35-39; 49pp; Japanese.
XX
CC The invention provides a method for identifying or screening a nuclear
CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
CC test substance on modulating the function(s) of TGF-beta activated kinase
CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
CC intractable diseases with inflammation (such as atrophic dermatitis and
CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
CC present sequence represents the nucleotide sequence of human TAK1a
CC (hTAK1a) protein.
XX
SQ Sequence 2785 BP; 827 A; 565 C; 640 G; 753 T; 0 other;
XX
XX
Alignment Scores:
Pred. No.: 7,54e-133 Length: 2785
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-09-830-144-2_COPY_76_303 (1-228) x AAX99696 (1-2785)
QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
DB 388 GTAGAGCTTCGGCAGTATCCCGTGTGACCATCTTAATATTGTAAAGCTTTATGGAGCC 447
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
DB 448 TGCTTGAATCCAGTGTGTCTGTGATGGAATATGCTGAAGGGGGCTCTTTATATAATG 507
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
DB 508 CTGCATGGTGTGAACCATGGCATATATCTGCTGCCACGCAATGATGGTGTGTTA 567
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArg 80
DB 568 CAGTGTTCGCAAGGAGTGGCTTATCTTCAGCATGCAACCCCAAGCGCTAATTCACAG 627
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
DB 628 GACCTGAACCCCAACCTTACTGGTTCGAGGGGGGACAGTCTCTAAAAATTTGTGAT 687
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
DB 688 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTCTGG 747
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
DB 748 ATGGCACCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATGTGACGCTTCAGCTGG 807
QY 141 GlyIleLeuTyrGluValIleThrArgGlyProPheAspGluIleGlyGlyPro 160
DB 808 GGTATTATCTTTGGGAAGTGATAACGCGTCGGAACCCCTTTGATGAGTTGGTGGCCCA 867
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuLysAsnLeu 180
DB 868 GCTTTCCGAATCATGTGGGCTGTTCATAATGTACTGACCAACCTGATGAATAATTTA 927
QY 181 ProLysProLysGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200

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US-09-830-144-2_COPY_76_303 (1-228) x ABL02488 (1-10997)

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QY      2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIlysLeuTyrGly----- 19
Db      2652 GAGGTGAAGAGTTGTCGGCGTGAAGACCCCAACATATCGCTCTGCACGGGATATCC 2711
QY      20 AlaCysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db      2712 TCGTACCAGCAGCCACCTACCTGATATGAGTTCGCCGAAGTGTGATCGTGCACAC 2771
QY      40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db      2772 TTCTTTCACGGC---AAGGTGAAGCCCGCATATTTCTGCCCCACCCATGAGCTGGCG 2828
QY      60 LeuGlnCysSerGln----- 64
Db      2829 CGCCATGTGCAGAGTAGTGTCTGTCGAGGGCGGGCGGTTATAACGTAGGGTCAA 2888
QY      64 ----- 64
Db      2889 CCCCCTAGCGCTTTCATCCATTCGTTGAAATTATCTGTGAAATAATGACTCAATGG 2948
QY      64 ----- 64
Db      2949 ATTGTGTAATTCACATTCGTTGCATGATTACTTAAACAATTTCAATAGCTATTCGCAT 3008
QY      64 ----- 64
Db      3009 AACCAGAAATAAATAATAGTAATTTGTTAAAGTTAGCCCTAATTACATTTCATTTG 3068
QY      65 ----- GlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisAr 80
Db      3069 TTTTCTCTCTAGGCTGTCATATTTGTCATCCATGACGCCCAAAACCACTAATCATCG 3128
QY      80 GAspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAs 100
Db      3129 CCAGCTGAAGCCGCTGAACCTCTCTTGACCAACAGGACCAATCTCAAGATATGCA 3188
QY      100 pPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTr 120
Db      3189 CTTGCGCAGGTGGCGGCAAGTCGACCATGATGACCAATCGCGGCGAGTGGCGCTG 3248
QY      120 pMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTr 140
Db      3249 GATGGCGCCGAGGCTTCGAGGCTCCAAAGTATACGGAGAAGTGTGACATTTTAGCTG 3308
QY      140 pGlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyLysPr 160
Db      3309 GGCCATGTCTATGGAGGTTCTGTCCAGGAAGCAGCCCTTTAAAGGCATCGACAAT-- 3366
QY      160 AlaPheArgIleMetTyrAlaValHisAsnGlyThr----- 172
Db      3367 -GCCTACACCATCCAGTGAAGATCTACAAGGTGC-GTCCCTCAATTCACCTTTTCC 3424
QY      173 ----- ArgProProLeuIleLysAsnLe 180
Db      3425 ATCGAGCTTATCGAGATCTGCTCTCGAGGTGAACGCCCGCGCTGCTGACCACTTG 3484
QY      180 uProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPr 200
Db      3485 CCCCAGCGCATCGAGGACCTGATACCCGCTGTGAAACCGGTGCGCCGAGATCGGCC 3544
QY      200 sSerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGluValAs 220
Db      3545 GTCCGATGAGTACATAGTGGCGTTATGCACGAGATCGTCAAGGACTATACGGGGCGGA 3604
QY      220 pGluProLeuGlnTyr 225
Db      3605 CAAGGCCCTGGAATAC 3620
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RESULT 12

ABL08337

. ID ABL08337 standard; cDNA; 759 BP.

```
XX      ABL08337;
AC      26-MAR-2002 (first entry)
DT      Drosophila melanogaster expressed polynucleotide SEQ ID NO 19493.
XX      Drosophila melanogaster expressed polynucleotide SEQ ID NO 19493.
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ss.
XX      Drosophila melanogaster.
OS      WO200171042-A2.
XX      27-SEP-2001.
XX      23-MAR-2001; 2001WO-US09231.
XX      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
XX      (PEKE ) PE CORP NY.
XX      Venter JC, Adams M, Li PWD, Myers EW;
XX      WPI: 2001-656860/75.
XX      P-PSDB; ABB64234.
XX      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX      Claim 1; SEQ ID NO 19493; 21pp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins
CC      (ABB5737-ABB72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX      SQ      Sequence 759 BP; 226 A; 162 C; 198 G; 173 T; 0 other;

Alignment Scores:
Pred. No.:      1,17e-37      Length:      759
Score:          414.00      Matches:      82
Percent Similarity: 59.69%      Conservative: 35
Best Local Similarity: 41.84%      Mismatches: 53
Query Match:      33.07%      Indels:      26
DB:              23      Gaps:      4

US-09-830-144-2_COPY_76_303 (1-228) x ABL08337 (1-759)
QY      2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIlysLeuTyrGlyAlaCys 21
Db      160 GAGATCTACCAAGTACAAAGCCAGCCATGTCACATAGTTGAGCTCTACGGCACATCG 219
QY      22 LeuAsnProValCys-----LeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db      220 AGGCACGAGGATCGCCCTCTGTGATGAATTCGTAGACGGTGAATCTCTGTCCAGT 279
QY      40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db      280 TTCTGTCAC---GCGAAAGCAAGCAAGTATTTCGATGTCGCCACCCCTTCACTGGCG 336
QY      60 LeuGlnCysSerGlnGlyValAlaTyrIleHisSerMetGlnProLysAlaLeuIleHis 79
Db      337 CATCAGATCGCTCAGGGCATAGCCTATCTGTCATGTCATGCGATGCGAGCCGAAAGCAGTAATTCAT 396
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Qy 80 ArgAspLeuLysProAsnLeuLeuValAlaGlyThrValLeuLysIleCys 99
Db 397 CGGATATAAGCACTCAATACACTGTCGAGAGGAGCTCAAACTGAAGATTGC 456
Qy 100 AspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLysGlySerAlaAla 119
Db 457 GATTTCGGAAGTGTGTGGACCTATCCCAATCGATATCGTCAATGCGGCACCTGCAGA 516
Qy 120 TrpMetAlaProGlu----- 124
Db 517 TACAAAGCGCCGAGGTAAGGAGTGTGTGATTTCAAATCCAAATCAATGAATAATCAAC 576
Qy 125 -----ValPheGluGlySerAsnTyrSerGluLysCysAspVal 137
Db 577 CAACCAACCGCGCTTTCAAAAGTTTCTACAAGAAATAAACCCGATGAAGAAAGTGGCATGTG 636
Qy 138 PheSerTrpGlyIleLeuLysValIleThrArgLysProPheAspGluIle 157
Db 637 TATAGTTGGCTATTACTTTTGGAAATATGTGCGCAAGAGCCATTGTGACCAATAT 696
Qy 158 GlyGlyProAlaPheArgIleMetTrpAlaValHisAsnGlyThrArg 173
Db 697 ---AATACGCTTTTGAACCTGATACATGCTATTAAATGAAGCAAGAGA 741

RESULT 13
ABL70018
ID ABL70018 standard; DNA; 3454 BP.
XX AC ABL70018;
XX DT
XX DE 15-MAY-2002 (first entry)
XX DE Pancreas cancer related gene sequence SEQ ID NO:8355.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX EN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234509P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-234924P.
XX PR 25-SEP-2000; 2000US-235077P.
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XX PR 25-SEP-2000; 2000US-235134P.
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XX PR 26-SEP-2000; 2000US-235637P.
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XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
XX PR 28-SEP-2000; 2000US-236033P.
XX PR 28-SEP-2000; 2000US-236034P.

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PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 28-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237117P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
(AVAL-) AVALON PHARM.
Yong PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;
WPI; 2002-188264/24.
Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set -
Claim 1; SEQ ID 8355; 44pp; English.
The present invention describes a method (M1) for screening for an
anti-neoplastic agent. The method involves exposing cells to a chemical
agent to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening
an anti-neoplastic agent, and can be used for producing a product which
is the data collected with respect to the anti-neoplastic agent as a
result of M1, and the data is sufficient to convey the chemical
structure and/or properties of the agent. M1 can be used in the
treatment of cancer such as colon, breast, stomach, lung, thyroid,
oesophageal, ovarian, kidney, prostate or pancreatic cancer,
adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
carcinoma, papillary carcinoma and Wilm's tumour.
SQ Sequence 3454 BP; 594 A; 1217 C; 1136 G; 507 T; 0 other;
Alignment Scores:
Pred. No.: 2.93e-34 Length: 3454
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.55% Indels: 17
DB: 24 Gaps: 6
US-09-830-144-2_COPY_76_303 (1-228) x ABL70018 (1-3454)
Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 721 GAAGCCCGGCTCTTTGGAGCGCTCGAGCACCCCAACATAATTCCTTAGGGGGCCCTGC 780
Qy 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 781 CTCAACCCCCACACCTCTGCTAGTAGAGTAGATGATGCGGGGTGGTGCCTGAGCAGG 840
Qy 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCys 59
Db 841 GTGCTGGCAGGTGCGCGGGTGCCACCTCACGTG-----CTGGTCAACTGGGT 888

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QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProHysAlaLeuLeuHis 79
Db 889 GTGAGGTGGCGGGGCGATGAACCTACTACAAATGATGCCCTGTGCCATCATCCAC 948
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
Db 949 CGGACCTCAAGTCAATCAATCTCTGATCTGGAGGCCATCGAAGACCAACCTCGCA 1008
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
Db 1009 GACACGGTGTCAAGATCAAGGATTCGGCTTCGCCGAGTGGCAACAGCCACCAAG 1068
QY 112 ThrAsnAsnLysGlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyr 131
Db 1069 ATGACGCTGGGGGACCTACGCTGTGATGGCGCGGAGTTATCCCTCTCTCCCTTTC 1128
QY 132 SerGluLysCysAspValPheSerTrpGlyIleLeuLeuTrpGluValIleThrArgArg 151
Db 1129 TCCAAAGACGTGATGTCTGGAGCTTCGGGTGTCTGTGGAGCTGCTGACGGGGGAG 1188
QY 152 LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
Db 1189 GTCCCTACCTGAGATC-----GAGCCCTTGGCGTGGCGTATGGCGTGGCTATGAAT 1242
QY 171 GlyThrArgProProLeuLysAsnLeuProLysProLysProLysLeuMetThrArg 190
Db 1243 AAGCTGACGTGCCCATTCCTCCACGTGCCCGAGCCCTTGGCGGCTCTCTGGAGAA 1302
QY 191 CysTrpSerLysAspProSerGlnArgProSerMetGluLulleValLys 207
Db 1303 TGCTGGAGCCACAGACCCCGGCCAGATTTGGTAGCATCTTGAAG 1353
RESULT 14
AAC43254
ID AAC43254 standard; DNR; 1224 BP.
AC AAC43254;
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XX DT
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 38594.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX PD
XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
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PR 19-JUL-1999; 99US-0144335.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.


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PR 27-JUL-1999; 99US-0145919;
PR 28-JUL-1999; 99US-0145951;
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PR 26-OCT-1999; 99US-0161361;
PR 28-OCT-1999; 99US-0161920;
PR 28-OCT-1999; 99US-0161992;
PR 28-OCT-1999; 99US-0161993;
PR 29-OCT-1999; 99US-0162142;

Alignment Scores:
Pred. No.: 8.8e-33
Score: 374.00
Percent Similarity: 57.80%
Best Local Similarity: 39.45%
Query Match: 29.87%
DB: 21
Gaps: 9

US-09-830-144-2_COPY_76_303 (1-228) x AAC43254 (1-1224)

Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 523 GAGGTGCTATGCTTGTCTAATTTGAAGCACCACCAACATTGTGAGGTTTCATTGGTGCATGT 582
Qy 22 LeuAsnProVal-----CysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 583 CGCAGCCAAATGGTGTGTGTATAGTACTGATACGCCAAAGAGAGGTTCACTGAGGCAG 642
Qy 40 ValLeu-----HisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAla 55
Db 643 TTTTGTAGGACAGACAGACCGGCGTCTCCTTTGAAGTTA-----GCT 687
Qy 56 MetSerTrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLys 75
Db 688 GTTAAACAGGCTTTGGATGTTGTAGGGTATGGCTTATGTCATGGA-----CGC 738
Qy 76 AlaLeuIleHisArgAspLeuLysProAsnLeuLeuValAlaGlyGlyThrVal 95
Db 739 AACTTCATACAGAGATCTCAAGTCAGATAACCTTCTCATCTCAGCAGATAGTCCATC 798
Qy 96 LeuLysIleCysAspPheGlyThrAla---CysAspIleGlnThrHis---MetThrAsn 113
Db 799 ---AAGATTGCAGATTTTGGTTGTCAGAAATTCGAAGTTCAACCGAAGGAATGCACCA 855
Qy 114 AsnLysGlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGlu 133
Db 856 GAAACTGGAACCTTACAGATGGATGGCTCCAGAGATGATACAGCATAGAGCCGTACAATCAA 915
Qy 134 LysCysAspValPheSerTrpGlyIleIleTrpGluValIleThrArgArgLysPro 153
Db 916 AAAGTGGATGTATAGTTTCGGGATTTGCTCGGGGAGTTTAATCAGAGGACTCTTACCG 975
Qy 154 PheAspGluIleGlyGly-----ProAlaPheArgIleMetTrpAlaValHisAsnGly 171
Db 976 TTCAGAACATGACAGCTGTACAGGCAGCGTTTCGGGTT-----GTAAACAGAGGA 1026
Qy 172 ThrArgProProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCys 191
Db 1027 GTGGTCCAAACAGTCCCAACAGATGTCTCCGGTGTGAGTGACATTAATGACTCGATGT 1086
Qy 192 TrpSerLysAspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db 1087 TGGATGCTAATCCAGAAAGTCCGTCATGTTTGTGGAGGTTGTGAAGCTGCT 1140

RESULT 15
AAC39537
ID AAC39537 standard; DNA; 1631 BP.
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XX	AAC39537;	18-JUN-1999;	99US-0139462
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AC		PR	99US-0139750
DT	17-OCT-2000 (first entry)	PR	99US-0139763
XX		PR	99US-0139817
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 24996.	PR	99US-0139899
DE		PR	99US-0140353
XX		PR	99US-0140354
KW	Hybridisation assay; genetic mapping; gene expression control;	PR	99US-0140695
KW	protein identification; signal transduction pathway;	PR	99US-0140823
KW	metabolic pathway; promoter; termination sequence; ss.	PR	99US-0140991
XX		PR	99US-0141287
OS	Arabidopsis thaliana.	PR	99US-0141842
XX		PR	99US-0142154
XX	EP1033405-A2.	PR	99US-0142055
PN		PR	99US-0142393
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PR	14-JUN-1999;	PR	99US-0148171
PR	16-JUN-1999;	PR	99US-0148319
PR	16-JUN-1999;	PR	99US-0148341
PR	18-JUN-1999;	PR	99US-0148565
PR	17-JUN-1999;	PR	99US-0148684
PR	18-JUN-1999;	PR	99US-0149368
PR	18-JUN-1999;	PR	99US-0149175
PR	18-JUN-1999;	PR	99US-0149456
PR	18-JUN-1999;	PR	99US-0149457
PR	18-JUN-1999;	PR	99US-0139458
PR	18-JUN-1999;	PR	99US-0139459
PR	18-JUN-1999;	PR	99US-0139460
PR	18-JUN-1999;	PR	99US-0139461
PR	18-JUN-1999;	PR	99US-0149930
PR	18-JUN-1999;	PR	99US-0149930

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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0153070.
PR 10-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 15-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154779.
PR 20-SEP-1999; 99US-0155139.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 04-OCT-1999; 99US-0157753.
PR 05-OCT-1999; 99US-0157865.
PR 06-OCT-1999; 99US-0158029.
PR 07-OCT-1999; 99US-0158232.
PR 08-OCT-1999; 99US-0158369.
PR 12-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 1,72e-32 Length: 1631
Score: 373.00 Matches: 87
Percent Similarity: 57.80% Conservative: 39
Best Local Similarity: 39.91% Mismatches: 70
Query Match: 29.79% Indels: 22
DB: 21 Gaps: 9

US-09-830-144-2_COPY_76_303 (1-228) x AAC39537 (1-1631)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 773 GAAGTTTCATGCTTGTCATTTTGAAGCATCTACATCGTTAGGTTTATGGTCGGTGC 832
QY 22 LeuAsnProVal-----CysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 833 ATTAACCGATGGTGTGGTGCCTGACTGAATATGCANAAAGGAGGCTCTGTCCAGACAG 892
QY 40 ValLeu-----HisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAla 55

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Search completed: December 4, 2003, 09:53:35
Job time : 407.459 secs

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Db 893 TTTCTGACTAAGACAGACAAACCGAGCTGTGCTTTGAAGTTA-----GCT 937
QY 56 MetSerTrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLys 75
Db 938 GTTATGTCAGGCGTGTGGATGTTGCCAGGGGTATGGCTTAGCTCCATGAG-----CGC 988
QY 76 AlaLeuIleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrVal 95
Db 989 AACTTTATACACCGGATCTAAAGTCAGATAACCTCCTCATATCAGCTGATCGTCCATC 1048
QY 96 LeuLysIleCysAspPheGlyThrAla---CysAspIleGlnThrHis---MetThrAsn 113
Db 1049 ---AAGATTGCTGATTTTGGTGTTCAGAAATGAAGTTCAACCCAGGGATGACACCA 1105
QY 114 AsnLysGlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGlu 133
Db 1106 GAGACTGGAACTTACAGATGGATGGCACACAGAGATGCCACAGACACCCCTACACTCAA 1165
QY 134 LysCysAspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysPro 153
Db 1166 AAAGTGGACGTGTATAGTTTGGAAATCGTGTGTGGAGTTGATTACAGGTCTGTACCG 1225
QY 154 PheAspGluIleGlyGly-----ProAlaPheArgIleMetTrpAlaValHisAsnGly 171
Db 1226 TTCAGAACATGACCGCGGTTTCAGGCTGCATTTCAGATG-----GTGAACACAGAGA 1276
QY 172 ThrArgProProLeuIleLysAsnLeuProLysProLysProLysGluSerLeuMetThrArgCys 191
Db 1277 GTCCGTCCAAACAGTCCACAGCAGATTGTCTTCTGTGCTTGGAGAGATCATGACAGTTGC 1336
QY 192 TrpSerLysAspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db 1337 TGGGATGCGGACCCCTGAAAGTCGTCCTTGTGTTTGGAGAGATTGTCAATCTTCTG 1390

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 07:04:49 ; Search time 17.1149 Seconds
(without alignments)
3783.871 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 361
Sequence: 1 caaagccgacctaaccct.....agagcgtggtgacagcaccg 204

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09830144/runat_03122003_122343_21194/app_query.fasta_1.1230
-DB=A Geneseq 19Jun03 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=-1 -WATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEA_SIZE=500 -MINLEN=0 -NCPU=6 -ICPU=3
-USER=US09830144 @CGN 1.1.0 @runat_03122003_122343_21194 -MAPLEN=2000000000
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	359	99.4	504	18	AAW26706	Human TAB1 (TAK1 b
2	359	99.4	504	18	AAW26707	Human TAB1 (TAK1 b
3	359	99.4	504	20	AAU09541	Human TAB1 protein
4	359	99.4	504	21	AAU91001	Human TAB-1 protei
5	359	99.4	504	21	AAU59450	Human TAB1 protein
6	359	99.4	513	20	AAU09550	Human TAB1 protein
7	359	99.4	516	24	ABU11578	Human MDDT polyep
8	359	99.4	517	20	AAU09546	Human TAB1-FLAG pr
9	352	97.5	84	21	AAU56692	Human prostate can
10	91.5	24.3	125	21	AAU26755	Zea mays protein f
11	88	23.4	1938	24	ABP76682	Streptomyces virid
12	83	22.1	353	24	ABU19816	Androgen-independe
13	82	22.7	1888	22	ABG23214	Novel human diago
14	79.5	21.1	1938	24	ABU98398	Streptomyces virid
15	79.5	22.0	1938	24	ABP76681	Streptomyces virid
16	77.5	20.6	399	24	ABP70654	Recombinant rat fi
17	77	21.3	16	20	AAU09549	Human TAB1 peptide
18	77	20.5	310	22	AAU51391	Propionibacterium
19	76.5	21.2	109	22	AAU39932	Propionibacterium
20	76.5	20.3	146	21	AAU26855	Zea mays protein f
21	76.5	20.3	224	22	ABG16138	Novel human diago
22	76	20.2	266	22	ABG18528	Novel human diago
23	75.5	20.1	689	19	AAU72025	HSV-2 strain SB5 C
24	75	20.8	2038	20	AAU14595	Human T-type volta
25	75	20.8	2044	20	AAU14594	Human T-type volta
26	74.5	19.8	686	22	ABU11397	Human secreted pro
27	74	19.7	127	21	AAU05630	Arabidopsis thalia
28	74	20.5	134	22	AAU63313	Propionibacterium
29	74	19.7	168	21	AAU05629	Arabidopsis thalia
30	74	20.5	205	22	AAU32502	Novel human secret
31	74	19.7	252	21	AAU05628	Arabidopsis thalia
32	74	19.7	1093	14	AAU41001	Human myotonic dys
33	73.5	20.4	130	22	AAU64265	Propionibacterium
34	73.5	20.4	276	22	AAU51816	Propionibacterium
35	73.5	19.5	575	22	ABG21970	Novel human diago
36	73.5	19.5	1938	24	ABP76678	Streptomyces virid
37	73.5	19.5	1938	24	ABP76679	Streptomyces virid
38	73	19.4	1938	24	ABP76681	Streptomyces virid
39	72.5	19.3	201	19	AAU20852	Human neurofilamen
40	72.5	19.3	262	23	ABP69409	Human polypeptide
41	72.5	19.3	386	18	AAU18664	Fragmented human N
42	72.5	20.1	1938	24	ABP76678	Streptomyces virid
43	72	19.1	95	22	AAU45336	Propionibacterium
44	72	19.9	138	22	AAU93357	Human protein sequ
45	72	19.1	495	24	ABP75497	Human secretory po

ALIGNMENTS

RESULT 1
AAW26706
ID AAW26706 standard; Protein; 504 AA.
XX
AC AAW26706;
XX
DT 25-MAR-2003 (updated)
DT 14-APR-1998 (first entry)
XX
Human TAB1 (TAK1 binding protein).
XX
TAB1; TAK1 binding protein; transforming growth factor-beta;
signal transduction; human.
XX
Homo sapiens.
XX
Key Location/Qualifiers
FH Misc-difference 52

/note= "variant has Arg as residue 52"

FT XX EP03571-A2.
 PN XX 29-OCT-1997.
 XX XX 24-APR-1997; 97EP-0302808.
 XX XX 20-NOV-1996; 96US-0752891.
 PR XX 24-APR-1996; 96JP-0126282.
 PR XX 28-OCT-1996; 96JP-0300856.
 XX XX (CHUS) CHUGAI SEIYAKU KK.
 XX XX Matsumoto K, Nishida E;
 PI WPI; 1997-515318/48.
 XX DR N-PSDB; AAT91175.
 XX XX DNA encoding TAK1 binding protein TAB1 - member of transforming
 PT growth factor beta receptor signal production pathway, which
 PT activates TAK-1 kinase activity upon binding
 XX XX
 PS Example 5; Page 17-19; 30pp; English.
 XX This protein comprises human TAB1, a novel member of the
 CC transforming growth factor-beta receptor signal transduction
 CC pathway, which activates TAK-1 kinase activity upon binding. Its
 CC amino acid sequence was deduced from a cDNA clone (see AAT91175)
 CC obtained from a kidney library; a variant TAB1 (see AAW26706) has
 CC Arg rather than Ser at amino acid position 52. Also claimed are:
 CC isolated DNA encoding a protein modified by a substitution,
 CC deletion and/or addition of 1 or more amino acids of the 504-residue
 CC TAB1 sequence; (2) DNA which can hybridise with the 1560 bp TAB1
 CC nucleic acid sequence; (3) isolated DNA encoding a protein
 CC comprising amino acids 21-579 or 437-504 of the 504 TAB1 sequence;
 CC (4) DNA encoding a fusion protein comprising an above protein or
 CC polypeptide; (5) expression vector comprising an above DNA; and
 CC (6) host cell, preferably a mammalian or yeast cell, transformed by
 CC the expression vector. Cells expressing TAB1 and TAK1 can be used
 CC to screen for TGF-beta signalling pathway inhibitors by contacting
 CC the cells with a test compound, and measuring the TAK1 kinase
 CC activity.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX Sequence 504 AA;
 SQ

Alignment Scores:
 Pred. No.: 9.39e-34 Length: 504
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.45% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x AAW26706 (1-504)

QY 1 CAAGCCGACCTTAACTTCAGTCACACACGACGAGCAGTCACG 60
 |||||
 Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456
 |||||
 QY 61 TCTGACGAGGCTTCTCCGCTCCGCCGCCACCTCCGCCCTGGGAGGAGGT 120
 |||||
 Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
 |||||
 QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACGCGCTCTGGAGCGTGGACATGGC 180
 |||||
 Db 477 ArgValGluProTyValAspPheAlaGluPheIyrArgLeuIrpSerValAspHisGly 496
 |||||
 QY 181 GAGCAGAGCGTGTGTACAGCACCG 204
 |||||
 Db 497 GluGlnSerValValThrAlaPro 504

RESULT 2
 AAW26707
 ID AAW26707 standard; Protein; 504 AA.
 XX XX AAW26707;
 XX XX 25-MAR-2003 (updated)
 DT 14-APR-1998 (first entry)
 XX XX Human TAB1 (TAK1 binding protein).
 XX XX TAB1; TAK1 binding protein; transforming growth factor-beta;
 KW signal transduction; human.
 XX XX Homo sapiens.
 OS XX
 FH Key Location/Qualifiers
 FT Misc-difference 52
 FT /note= "variant has Ser as residue 52"
 XX XX
 PN EP03571-A2.
 XX XX 29-OCT-1997.
 PD XX 24-APR-1997; 97EP-0302808.
 PF XX 20-NOV-1996; 96US-0752891.
 XX 24-APR-1996; 96JP-0126282.
 PR 28-OCT-1996; 96JP-0300856.
 XX XX (CHUS) CHUGAI SEIYAKU KK.
 PA Matsumoto K, Nishida E;
 XX WPI; 1997-515318/48.
 XX DR N-PSDB; AAT91178.
 XX XX DNA encoding TAK1 binding protein TAB1 - member of transforming
 PT growth factor beta receptor signal production pathway, which
 PT activates TAK-1 kinase activity upon binding
 XX XX
 PS Example 5; Page 19-21; 30pp; English.
 XX This protein comprises human TAB1, a novel member of the
 CC transforming growth factor-beta receptor signal transduction
 CC pathway, which activates TAK-1 kinase activity upon binding. Its
 CC amino acid sequence was deduced from a cDNA clone (see AAT91176)
 CC obtained from a kidney library; a variant TAB1 (see AAW26706) has
 CC Ser rather than Arg at amino acid position 52. Also claimed are:
 CC isolated DNA encoding a protein modified by a substitution,
 CC deletion and/or addition of 1 or more amino acids of the 504-residue
 CC TAB1 sequence; (2) DNA which can hybridise with the 1560 bp TAB1
 CC nucleic acid sequence; (3) isolated DNA encoding a protein
 CC comprising amino acids 21-579 or 437-504 of the 504 TAB1 sequence;
 CC (4) DNA encoding a fusion protein comprising an above protein or
 CC polypeptide; (5) expression vector comprising an above protein or
 CC (6) host cell, preferably a mammalian or yeast cell, transformed by
 CC the expression vector. Cells expressing TAB1 and TAK1 can be used
 CC to screen for TGF-beta signalling pathway inhibitors by contacting
 CC the cells with a test compound, and measuring the TAK1 kinase
 CC activity.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX Sequence 504 AA;
 SQ

Alignment Scores:
 Pred. No.: 9.39e-34 Length: 504
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.45% Indels: 0
 DB: 18 Gaps: 0

Pred. No.:	9.39e-34	Length:	504
------------	----------	---------	-----

The present invention describes a method for screening compounds for inhibition of inflammatory cytokine signal transduction by contacting the sample with TAK1 and its receptor TAB1 and selecting for inhibition of TAK1/TAB1 binding. Also described is a method for screening compounds for inhibition of inflammatory cytokine signal transduction in which the inhibition of TAK1 phosphorylation is selected for, and drug compositions for the treatment of inflammatory disorders containing as active component an inflammatory cytokine signal transduction inhibitor. TAK1 is an essential component of the signalling process which results in release of inflammatory cytokines such as interleukin-1 (IL-1), IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used

CC for the selection of effective antiinflammatory agents. The present
 CC sequence represents human TAB-1, which is used in the exemplification of
 CC the present invention.

XX SQ Sequence 504 AA;

Alignment Scores: 9.39e-34 Length: 504
 Pred. No.: 359.00 Matches: 68
 Score: 100.00% Conservatives: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 99.45% Gaps: 0
 DB: 21

US-09-830-144-3_COPY_1338_1541 (1-204) x AAY91001 (1-504)

QY 1 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCTCCAGC 60
 Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSer 456
 QY 61 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTGGCGAGGAGCGGT 120
 Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
 QY 121 CGTGTTCGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
 Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 496
 QY 181 GAGCAGAGCGTGTGCACGACCG 204
 Db 497 GluGlnSerValValThrAlaPro 504

RESULT 5

AAY59450
 ID AAY59450 standard; Protein; 504 AA.

XX AC AAY59450;

XX DT 24-MAR-2000 (first entry)

XX DE Human TAB1 protein sequence.

XX KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta.

XX OS Homo sapiens.

XX PN JF11326328-A.

XX PD 26-NOV-1999.

XX PF 13-MAY-1998; 98JP-0130378.

XX PR 13-MAY-1998; 98JP-0130378.

XX PA (MATS/) MATSUMOTO K.

XX DR WPI; 2000-078337/07.

XX DR N-PSDB; AAZ48861.

XX PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein -

XX PS Claim 2; Page 25-26; 43pp; Japanese.

XX CC This sequence represents the human TAB1 protein.

XX CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be

CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.

XX SQ Sequence 504 AA;

Alignment Scores: 9.39e-34 Length: 504
 Pred. No.: 359.00 Matches: 68
 Score: 100.00% Conservatives: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 99.45% Gaps: 0
 DB: 21

US-09-830-144-3_COPY_1338_1541 (1-204) x AAY59450 (1-504)

QY 1 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCTCCAGC 60
 Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSer 456
 QY 61 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTGGCGAGGAGCGGT 120
 Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
 QY 121 CGTGTTCGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
 Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 496
 QY 181 GAGCAGAGCGTGTGCACGACCG 204
 Db 497 GluGlnSerValValThrAlaPro 504

RESULT 6

AAY09550
 ID AAY09550 standard; Protein; 513 AA.

XX AC AAY09550;

XX DT 21-JUL-1999 (first entry)

XX DE Human TAB1 protein SEQ ID NO:43.

XX KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta.

XX OS Homo sapiens.

XX PN WO9921010-A1.

XX PD 29-APR-1999.

XX PF 22-OCT-1998; 98WO-JP04796.

XX PR 22-OCT-1997; 97JP-0290188.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Ontomo T, Ono K, Tsuchiya M;

XX DR WPI; 1999-312645/26.

XX DR N-PSDB; AAX56310.

XX PT Screening for TGF- beta inhibitory substances, which are useful as
 PT drugs for treatment of diseases relating to its disorder
 XX Example 13; Page 186-188; 195pp; Japanese.

XX CC A method has been developed for screening for substances which inhibit

the binding of TAK1 polypeptide to TAB1 polypeptide. The method comprises: (a) contacting the polypeptide in the presence of a sample; and (b) detecting the amount of bound polypeptide, in which the sample can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming growth factor (TGF)-beta inhibitory substances can be used in drugs for indications e.g. as TGF-beta signal transmission inhibitors or activators, or extracellular matrix protein production enhancement inhibitors, or activators, or cell proliferation prevention inhibitors or activators, or monocyte migration inhibitors or activators, or physiological activity induction inhibitors or activators, or immunosuppression inhibitors or activators, or amyloid beta protein precipitation inhibitors or activators, and such substances can also be inhibitors of the TAK1 polypeptide function, particularly kinase activity. The present sequence represents human TAB1.

XX SQ Sequence 513 AA;

Alignment Scores:
Pred. No.: 9.41e-34 Length: 513
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 20 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x AAY09550 (1-513)

QY 1 CAAGCCGAGCTTAACCTGAGTTCACCAACGACGACGAGCAGCTCCAGC 60
Db 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSer 465
QY 61 TCTGACGAGGCGCTTCCGCTCCGCGCCGCCACTCGCTCCGCTCCGCGAGACGGT 120
Db 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485
QY 121 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCCTCTGGAGCGTGCACATGGC 180
Db 486 ArgValGluProTyrValAspPheAlaGluPheIyrArgLeuTrpSerValAspHisGly 505
QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
Db 506 GluGlnSerValValThrAlaPro 513

RESULT 7

ABU11578
ID ABU11578 standard; Protein; 516 AA.

XX AC ABU11578;
XX 12-FEB-2003 (first entry)
XX DE Human MDDT polypeptide SEQ ID 525.

XX MDDT; human; disease detection and treatment molecule polypeptide;
XX anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
XX haemostatic; nephrotropic; antianaemic; antiproliferative; hepatotropic;
XX gene therapy; protein replacement therapy; cell proliferative disorder;
XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
XX anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
XX Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
XX psoriasis; hepatitis.

XX Homo sapiens.

XX WO200279449-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002WO-US09944.

XX 28-MAR-2001; 2001US-279619P.

XX 29-MAR-2001; 2001US-280067P.

XX 29-MAR-2001; 2001US-280068P.

PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX (INCY-) INCYTE GENOMICS INC.
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX Dufford GE, Hillman JL, Yu JY, Tusson O, Yap PE, Amshay SR;
XX Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI; 2003-059431/05.
DR N-ESDB; ABX34568.

XX New purified disease detection and treatment molecule proteins and
XX polynucleotides, useful for diagnosing, treating or preventing cancers
XX (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
XX or hepatitis
XX Claim 27; SEQ ID NO 525; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule
XX polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
XX osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
XX antianaemic, antiproliferative and hepatotropic activity. The polynucleotides
XX and the polypeptides of the invention can be used for gene therapy,
XX protein replacement therapy and are useful for treating a variety of
XX diseases or conditions. These polypeptides or polynucleotides are
XX particularly useful for diagnosing, treating or preventing cell
XX proliferative disorders (e.g. cancers including adenocarcinoma,
XX leukaemia, lymphoma, melanoma or sarcoma), anaemia, Crohn's
XX disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
XX syndromes, inflammation, osteoporosis, thrombocytopenia, psoriasis or
XX hepatitis. ABU11578-ABU11845 represent the MDDT polynucleotides encoded
XX by ABU11578-ABU11845, described in the disclosure of the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 516 AA;

Alignment Scores:

Pred. No.: 9.42e-34 Length: 516
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 20 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x ABU11578 (1-516)

QY 1 CAAGCCGAGCTTAACCTGAGTTCACCAACGACGACGAGCAGCTCCAGC 60
Db 449 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSer 468
QY 61 TCTGACGAGGCGCTTCCGCTCCGCGCCGCCACTCGCTCCGCTCCGCGAGACGGT 120
Db 469 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 488
QY 121 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCCTCTGGAGCGTGCACATGGC 180
Db 489 ArgValGluProTyrValAspPheAlaGluPheIyrArgLeuTrpSerValAspHisGly 508
QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
Db 509 GluGlnSerValValThrAlaPro 516

RESULT 8
AAY09546

ID	AAV09546 standard; Protein; 517 AA.
XX	
AC	AAV09546;
XX	
DT	21-JUL-1999 (first entry)
XX	
DE	Human TAB1-FLAG protein.
XX	
KW	Human; TAB1; TAK1; screening; inhibition; TGF-beta; transforming growth factor beta.
XX	
OS	Homo sapiens.
XX	Synthetic.
PN	WO9921010-A1.
XX	
PD	29-APR-1999.
XX	
PF	22-OCT-1998; 98WO-JP04796.
XX	
PR	22-OCT-1997; 97JP-0290188.
XX	(CHUS) CHUGAI SEIYAKU KK.
PA	
PI	Ohtomo T, Ono K, Tsuchiya M;
XX	
DR	WPI; 1999-312645/26.
XX	N-PDSB; AAX56282.
XX	
PT	Screening for TGF- beta inhibitory substances, which are useful as drugs for treatment of diseases relating to its disorder
XX	
PS	Example 1; Page 163-166; 195pp; Japanese.
XX	
CC	A method has been developed for screening for substances which inhibit the binding of TAK1 polypeptide to TAB1 polypeptide. The method comprises: (a) contacting the polypeptide in the presence of a sample; and (b) detecting the amount of bound polypeptide, in which the sample can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming growth factor (TGF)-beta inhibitory substances can be used in drugs for indications e.g. as TGF-beta signal transduction inhibitors or activators, or extracellular matrix protein production enhancement inhibitors or activators, or cell proliferation prevention inhibitors or activators, or monocyte migration inhibitors or activators, or physiological activity induction inhibitors or activators, or immunosuppression inhibitors or activators, or amyloid beta protein precipitation inhibitors or activators, and such substances can also be inhibitors of the TAK1 polypeptide function, particularly kinase activity. The present sequence represents TAB1-FLAG from an example of the present invention.
XX	
SQ	Sequence 517 AA;
Alignment Scores:	
Pred. No.:	9.42e-34 Length: 517
Score:	359.00 Matches: 68
Percent Similarity:	Conservative: 0
Best Local Similarity:	Mismatches: 0
Query Match:	Indels: 0
DB:	Gaps: 0
US-09-830-144-3_COPY_1338_1541 (1-204) x AAY09546 (1-517)	
QY	1 CAAGCCGACTTAACCTTCAGTCCACCACAGCAGCAGCAGCAGCAGTCCAGC 60
Dd	437 GlnSerProThrLeuThrIeuGlnSerThrAnThrHisThrGlnSerSerSerSer 456
QY	61 TCTGACGGAGGCCTCTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCAGACGT 120
Dd	457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluaspGly 476
QY	121 CGTGTTGAGCCCTATGTGGACTTTTGCTAGTTTTACCGCTCTTGAGCGCTGACCATGCG 180

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QY 1 CAAAGCCGACCTTAACCTCGAGTCCACCAACAGCACAGCAGCAGCAGCTCCAGC 60
    |||||
Db 17 GlnSerProThrLeuThrLeuGlnSerThrAenThrHisThrGlnSerSerSer 36
    |||||
QY 61 TCTGACGAGGCTCTTCGCTCCCGGCCGCCCACTCGCTCCCGCTGGCGAGACGGT 120
    |||||
Db 37 Ser**GlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 56
    |||||
QY 121 CGTGTGACCCCTATGTGACCTTCTGAGTTTACCGCTCTCGAGCGTGACCATGGC 180
    |||||
Db 57 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 76
    |||||
QY 181 GAGCAGACGCGTGTGCACAGCACCG 204
    |||||
Db 77 GluGlnSerValValThrAlaPro 84
    |||||

RESULT 10
AAG26755
ID AAG26755 standard; Protein; 125 AA.
XX
AC AAG26755;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 31330.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
FD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-011825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135622.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 07-AUG-1999; 99US-0147303.
PR 08-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 14-AUG-1999; 99US-0148565.
PR 15-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 19-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 21-AUG-1999; 99US-0149929.
PR 22-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 24-AUG-1999; 99US-0150566.
PR 25-AUG-1999; 99US-0150884.
PR 26-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151066.
PR 28-AUG-1999; 99US-0151080.
PR 29-AUG-1999; 99US-0151303.
PR 30-AUG-1999; 99US-0151438.
PR 31-AUG-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 02-SEP-1999; 99US-0153070.
PR 03-SEP-1999; 99US-0153758.
PR 04-SEP-1999; 99US-0154018.
PR 05-SEP-1999; 99US-0154039.
PR 06-SEP-1999; 99US-0154779.
PR 07-SEP-1999; 99US-0155139.
PR 08-SEP-1999; 99US-0155486.
PR 09-SEP-1999; 99US-0155659.
PR 10-SEP-1999; 99US-0156458.
PR 11-SEP-1999; 99US-0156596.
PR 12-SEP-1999; 99US-0157117.
PR 13-SEP-1999; 99US-0157753.
PR 14-SEP-1999; 99US-0157865.
PR 15-SEP-1999; 99US-0158029.
PR 16-SEP-1999; 99US-0158232.
PR 17-SEP-1999; 99US-0158369.
PR 18-SEP-1999; 99US-0159293.
PR 19-SEP-1999; 99US-0159294.
PR 20-SEP-1999; 99US-0159295.
PR 21-SEP-1999; 99US-0159329.
PR 22-SEP-1999; 99US-0159330.
PR 23-SEP-1999; 99US-0159331.
PR 24-SEP-1999; 99US-0159637.
PR 25-SEP-1999; 99US-0159638.
PR 26-SEP-1999; 99US-0159584.
PR 27-SEP-1999; 99US-0160741.
PR 28-SEP-1999; 99US-0160767.
PR 29-SEP-1999; 99US-0160768.
PR 30-SEP-1999; 99US-0160770.
PR 01-OCT-1999; 99US-0160814.
PR 02-OCT-1999; 99US-0160815.
PR 03-OCT-1999; 99US-0160980.
PR 04-OCT-1999; 99US-0160981.
PR 05-OCT-1999; 99US-0161404.
PR 06-OCT-1999; 99US-0161405.
PR 07-OCT-1999; 99US-0161406.
PR 08-OCT-1999; 99US-0161359.
PR 09-OCT-1999; 99US-0161360.
PR 10-OCT-1999; 99US-0161361.
PR 11-OCT-1999; 99US-0161920.
PR 12-OCT-1999; 99US-0161922.
PR 13-OCT-1999; 99US-0161993.
PR 14-OCT-1999; 99US-0162142.
PR 15-OCT-1999; 99US-0162142.
PR 16-OCT-1999; 99US-0162142.
PR 17-OCT-1999; 99US-0162142.
PR 18-OCT-1999; 99US-0162142.
PR 19-OCT-1999; 99US-0162142.
PR 20-OCT-1999; 99US-0162142.
PR 21-OCT-1999; 99US-0162142.
PR 22-OCT-1999; 99US-0162142.
PR 23-OCT-1999; 99US-0162142.
PR 24-OCT-1999; 99US-0162142.
PR 25-OCT-1999; 99US-0162142.
PR 26-OCT-1999; 99US-0162142.
PR 27-OCT-1999; 99US-0162142.
PR 28-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 0.0293
Score: 91.50
Percent Similarity: 53.12%
Best Local Similarity: 45.31%
Query Match: 24.34%
DB: 21
Length: 125
Matches: 29
Conservative: 5
Mismatch: 24
Indels: 6
Gaps: 3

US-09-830-144-3_COPY_1338_1541 (1-204) x AAG26755 (1-125)
QY 194 ACCAGCTCTGCTCGCATGTCACAGCTCCAGAGCGGTAAACTCAGCAAGTCACACA 135
Db 50 SerThrCysSerProSerSerThr---ProArgArgProSerProSerSerProThr 68
QY 134 TAGGGCTCAACAGACCGCTCTCGCAGCGGAGAGCGAGTGGGCGGCGGAGCGGAAG 75
Db 69 AlaSerSerThrAlaAlaSerCysPro-AlaSerAlaSerAlaArgAlaTrp----- 85
QY 74 AGGCTCCGT---CAGAGCTGGAGCTGCTCTGCGTGTGCGTGTGGTGGAGTGCAGG 18
Db 86 -GlyLeuArgCysSerAlaTrpProThrCysSerSerThrThrAlaTrpSerThrAlaAl 105
QY 17 GTTAAGGTGCG 8
Db 105 aPheArgSer 108

RESULT 11
ID ABP76682
ID ABP76682 standard; Protein; 19938 AA.
AC ABP76682;
XX
DT 26-FEB-2003 (first entry)
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 6.
KW Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
XX medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
OS Streptomyces viridochromogenes.
XX
XX WC200268436-A1.
XX
XX 06-SEP-2002.
XX
XX 24-AUG-2001; 2001WO-EP09815.
XX
XX 25-FEB-2001; 2001DE-1009166.
XX
XX (COMB-) COMBINATURE BIOPHARM AG.
XX
XX Weitnauer G, Muehlenweg A, Trefzer A, Bechtold A;
XX
XX WPI; 2003-018650/01.
XX
XX N-PSDB; ABZ37516.
XX
XX
XX New avilamycin derivatives, useful for treatment of infections, and
XX nucleic acid encoding avilamycin synthesis enzymes -
XX
XX Example 1; Page 68-301; 319pp; German.
XX
XX The invention relates to avilamycin derivatives (I) with antibacterial,
XX virucide, protozoacide and fungicide activity. (I) are useful for
XX treatment of infections (bacterial, viral, protozoal or fungal), in human
XX or veterinary medicine, particularly where caused by Staphylococcus
XX aureus. (I) are more hydrophilic than known avilamycins. The present
XX sequence is that of an avilamycin synthesis enzyme from the Streptomyces
XX viridochromogenes Avilamycin A biosynthetic gene cluster
XX (ABZ37515-ABZ37516).
XX
XX Sequence 19938 AA;
SQ
```


PS Claim 20; SEQ ID No 53573; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention. CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1888 AA;

Alignment Scores:

Pred. No.:	0.596	Length:	1888
Score:	82.00	Matches:	27
Percent Similarity:	40.70%	Conservative:	8
Best Local Similarity:	31.40%	Mismatches:	27
Query Match:	22.71%	Indels:	24
DB:	22	Gaps:	4

US-09-830-144-3_COPY_1338_1541 (1-204) x ABG23214 (1-1888)

QY 8 CGACCTTAACCTCGAGTCCA-----CCACACGCACACGACGACGAGCT 55

Db 1794 ArgProProPheThrGlnThrSerLeuHisProValArgProArgGluGlnGlnAla 1813

QY 56 CCAGCTCTGACGAGGCGCTCTCCGCTCCCGCCCGCCCACTCGCTCCCGCTGCGGAGG 115

Db 1814 ProProCysThrSerAlaAlaSerAlaProGlnThrGlnThrArgAlaProThrProArg 1833

QY 116 AC-----GTCTGTTGAGCCCTATGTG----- 139

Db 1834 SerProThrArgCysCysArgProLysThrArgThrCysProSerProProTpsSerPro 1853

QY 140 -----ACTTTGCTGAGTTTACGCTCTGAGCGTGAGC----- 175

Db 1854 SerThrArgThrThrAlaThrCysSerProSerGlyArgGlyThrThrArgProCysArg 1873

QY 176 ATGCGCAGCAGCGGTGG 193

Db 1874 LeuSerSerAlaTip 1879

RESULT 14

ABB98398

ID ABB98398 standard; Protein; 19938 AA.

XX AC ABB98398;

XX 05-MAR-2003 (first entry)

DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.

XX Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;

KW medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.

XX Streptomyces viridochromogenes.

OS WO200268436-A1.

XX WO200268436-A1.

XX 06-SEP-2002.

PD 06-SEP-2002.

XX 24-AUG-2001; 2001WO-EP09815.

XX 25-FEB-2001; 2001DE-1009166.

XX (COMB-) COMBINATURE BIOPHARM AG.

XX Weitnauer G, Muehlenweg A, Trefzer A, Bechtold A;

XX WPI; 2003-018650/01.

XX N-PSDB; AB237515.

XX New avilamycin derivatives, useful for treatment of infections, and

XX nucleic acid encoding avilamycin synthesis enzymes

XX Example 1; Page 68-301; 319pp; German.

XX The invention relates to avilamycin derivatives (I) with antibacterial,

XX virucide, protozoacide and fungicide activity. (I) are useful for

XX treatment of infections (bacterial, viral, protozoal or fungal), in human

XX or veterinary medicine, particularly where caused by Staphylococcus

XX aureus. (I) are more hydrophilic than known avilamycins. The present

XX sequence is that of an avilamycin synthesis enzyme from the Streptomyces

XX viridochromogenes Avilamycin A biosynthetic gene cluster

XX (AB237515-AB237516).

XX SQ Sequence 19938 AA;

Alignment Scores:

Pred. No.:	1.65	Length:	19938
Score:	79.50	Matches:	21
Percent Similarity:	47.62%	Conservative:	9
Best Local Similarity:	33.33%	Mismatches:	20
Query Match:	21.14%	Indels:	13
DB:	24	Gaps:	3

US-09-830-144-3_COPY_1338_1541 (1-204) x ABB98398 (1-19938)

QY 190 CGCTCTGCTCGCATGTCTCCACGCTCCAGAGCGGTAAACTCAGAAAGTCCACATAGG 131

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QY 130 GCTCAACACAGCACCTCTCTCGCCAGCG-----GGAGCGAGTGGCGCGCGGAGC 80

Db 18650 ProArgArgArgProArgSerAlaProGlyArgArgAlaGlyArgGlnValGlyArg 18669

QY 79 GGAAGAGGC-----CTCCGTCAGAGCTGGAGCTGCTGC 47

Db 18670 GlyArgAlaAsnAlaArgGlnSerArgLeuGlyArgValArgAlaGlyProLeuCys 18689

QY 46 TCTCGGTGT 38

Db 18690 AsnSerCys 18692

RESULT 15

ABP76681

ID ABP76681 standard; Protein; 19938 AA.

XX AC ABP76681;

XX 26-FEB-2003 (first entry)

DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 5.

XX Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;

KW medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.

XX Streptomyces viridochromogenes.

OS WO200268436-A1.

XX WO200268436-A1.

XX 06-SEP-2002.

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XX 24-AUG-2001; 2001WO-EP09815.
XX
XX 25-FEB-2001; 2001DE-1009166.
XX
XX (COMB-) COMBINATURE BIOPHARM AG.
XX
XX Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
XX
XX MPI; 2003-018650/01.
XX
XX N-PSDB; ABZ37516.
XX
XX New avilamycin derivatives, useful for treatment of infections, and
XX nucleic acid encoding avilamycin synthesis enzymes
XX
XX Example 1; Page 68-301; 319pp; German.
XX
XX The invention relates to avilamycin derivatives (I) with antibacterial,
XX virucide, protozoacide and fungicide activity. (I) are useful for
XX treatment of infections (bacterial, viral, protozoal or fungal), in human
XX or veterinary medicine, particularly where caused by Staphylococcus
XX aureus. (I) are more hydrophilic than known avilamycins. The present
XX sequence is that of an avilamycin synthesis enzyme from the Streptomyces
XX viridochromogenes Avilamycin A biosynthetic gene cluster
XX (ABZ37515-ABZ37516).
XX
XX SQ Sequence 19938 AA;

Alignment Scores:
Pred. No.:      1.65      Length:      19938
Score:          79.50      Matches:      29
Percent Similarity: 37.50%      Conservative: 1
Best Local Similarity: 36.25%      Mismatches: 24
Query Match:      22.02%      Indels:      26
DB:               24          Gaps:       5

US-09-830-144-3_COPY_1338_1541 (1-204) x ABP76681 (1-19938)

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Db      2075 ArgPro---ProCysGlyThrProTrpSerProProArgArgAlaArgArgTrpPro 2093
QY      56  CCAGCTCTGACGGAGGCTCTCCGCTCCCGGC-----CGGCCCACTCGCTCCCGC 106
Db      2094 ProProAlaArgAlaGlyGlySerAlaProGlyCysGlyThrProArgArgGlySer-Pr 2113
QY      107 CTGG-----CGAGGACGGTCGTGTTGAGCCCTATGTGGACTTTG 145
Db      2113 oTrpAlaTyArgSerGlyThrAlaArgGlyArgSerAla-----2126
QY      146 CTGAGTTTACCGCTCTGGAGCGTGACCATGGCGAGCAGCGTGTGACAGCAC 203
Db      2127 -----ProProThrArgArgArgProTrpSerGlyGlySerGlyAspSerSer 2142

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Search completed: December 4, 2003, 09:02:56
 Job time : 29.1149 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: December 4, 2003, 09:00:20 ; Search time 6.2027 Seconds
(without alignments)
2783.114 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 361

Sequence: 1 caaagccgacctaaccct.....agaggtgtgacagaccg 204

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Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delpop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310859 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database : Issued Patents AA.*

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3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	99.4	504	2	US-08-752-891-2
2	359	99.4	504	2	US-08-752-891-6
3	359	99.4	504	2	US-09-144-178-2
4	359	99.4	504	2	US-09-144-178-6
5	359	99.4	504	3	US-09-406-854-2
6	359	99.4	504	3	US-09-406-854-6
7	359	99.4	504	4	US-09-529-279-2
8	359	99.4	504	4	US-10-158-895-2
9	359	99.4	513	4	US-09-529-279-43
10	359	99.4	513	4	US-10-158-895-43
11	359	99.4	517	4	US-09-529-279-11
12	359	99.4	517	4	US-10-158-895-11

13	100.5	27.8	136	4	US-09-252-991A-22734	Sequence 22734, A
14	92.5	24.6	189	4	US-09-252-991A-17056	Sequence 17056, A
15	89.5	23.8	303	4	US-09-252-991A-17999	Sequence 17999, A
16	86.5	23.0	496	4	US-09-252-991A-22592	Sequence 22592, A
17	84.5	22.5	363	4	US-09-252-991A-20195	Sequence 20195, A
18	84	22.3	333	4	US-09-252-991A-24478	Sequence 24478, A
19	84	22.3	721	4	US-09-252-991A-28293	Sequence 28293, A
20	83.5	22.2	338	4	US-09-252-991A-18820	Sequence 18820, A
21	83.5	22.2	480	4	US-09-252-991A-20125	Sequence 20125, A
22	83	22.1	264	4	US-09-252-991A-24262	Sequence 24262, A
23	82	21.8	269	4	US-09-252-991A-26605	Sequence 26605, A
24	81.5	21.7	200	4	US-09-252-991A-19793	Sequence 19793, A
25	81.5	21.7	355	4	US-09-252-991A-23226	Sequence 23226, A
26	81	21.5	201	4	US-09-252-991A-25745	Sequence 25745, A
27	81	21.5	1228	4	US-09-252-991A-17764	Sequence 17764, A
28	80.5	21.4	239	4	US-09-252-991A-25387	Sequence 25387, A
29	80.5	21.4	589	4	US-09-252-991A-32631	Sequence 32631, A
30	80	21.3	338	4	US-09-252-991A-19609	Sequence 19609, A
31	79.5	22.0	136	4	US-09-252-991A-23572	Sequence 23572, A
32	79	21.0	243	4	US-09-252-991A-26015	Sequence 26015, A
33	79	21.0	350	4	US-09-252-991A-19537	Sequence 19537, A
34	78.5	20.9	268	4	US-09-252-991A-27950	Sequence 27950, A
35	78.5	20.9	297	4	US-09-252-991A-18932	Sequence 18932, A
36	78	20.7	416	4	US-09-252-991A-32875	Sequence 32875, A
37	78	20.7	710	4	US-09-252-991A-24946	Sequence 24946, A
38	77.5	20.6	246	4	US-09-252-991A-23345	Sequence 23345, A
39	77.5	20.6	345	4	US-09-252-991A-32325	Sequence 32325, A
40	77	21.3	16	4	US-09-529-279-41	Sequence 41, Appl
41	77	21.3	16	4	US-10-158-895-41	Sequence 41, Appl
42	77	20.5	279	4	US-09-252-991A-26860	Sequence 26860, A
43	77	20.5	586	4	US-09-252-991A-28601	Sequence 28601, A
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45	76.5	21.2	224	4	US-09-252-991A-19251	Sequence 19251, A

ALIGNMENTS

RESULT 1 US-08-752-891-2

; Sequence 2, Application US/0875891

; Patent No. 5837819

; GENERAL INFORMATION: 11/7/98

; APPLICANT: MATSUMOTO, Kunihiro

; APPLICANT: NISHIDA, Eisuke

; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESS: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/752,891

; FILING DATE: 20-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 8-300856

; FILING DATE: 28-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 8-126282

; FILING DATE: 24-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 17981/111

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-891-2

Alignment Scores:	
Pred. No.:	2,61e-34
Score:	359.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.45%
DB:	2
Length:	504
Matches:	68
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

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437	GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer	456
61	TCGTACGAGGAGGCTCTCCGCTCCGGCCGCCACATCGCTCCGCTGCGAGGACGCT	120
457	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly	476
121	CGTGTTGAGCCCATGTGACATTTTGCTCAGTATTTTACCGCCTCTGGACGCTGGACCATGGC	180
477	ArgValGluProTyrValAspPheAlaGluPheItyrArgLeuTrpSerValAspHisGly	496
181	GAGCAGAGCGTGGTCACGACCG	204
497	GluGlnSerValValThrAlaPro	504

RESULT 2

US-08-752-891-6
; Sequence 6, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17961/111
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 9041136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-891-6

Alignment Scores:		
Pred. No.:	2.61e-34	Length:
Score:	359.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	99.45%	Indels:
DB:	2	Gaps:
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		68

US-09-830-144-3 COPY 1338 1541 (1-204) x US-08-752-891-6 (1-504)

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Db		
61	TCGTACGAGAGACCTCTCCGCTCCGCGCGCCACATCGCTCCGCTGCGAGGACGT	120
QY		
457	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	476
Db		
121	CGTGTTGAGCCCTATGTGGACTTTGCTGAGTTTTACCGCCTCTCGAGCGTGGACCATGGC	180
QY		
477	ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly	496
Db		
181	GAGCAGAGCGTGGTGACAGCACC	204
QY		
497	GluGlnSerValValThrAlaPro	504
Db		

RESULT 3

US-09-144-178-2
Sequence 2, Application US/09144178
Patent No. 5989862
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

102 e.

1022


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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x US-09-529-279-2 (1-504)
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QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTCGCTCCGCTCCGCGAGGACGGT 120
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
QY 121 CGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 180
Db 477 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 496
QY 181 GAGCAGAGCGTGTGACAGCACC 204
Db 497 GluGlnSerValThrAlaPro 504

RESULT 8
US-10-158-895-2
; Sequence 2, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-2

Alignment Scores:
Pred. No.: 2,61e-34 Length: 504
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x US-10-158-895-2 (1-504)
QY 1 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456
QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTCGCTCCGCTCCGCGAGGACGGT 120
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
QY 121 CGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 180
Db 477 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 496
QY 181 GAGCAGAGCGTGTGACAGCACC 204
Db 497 GluGlnSerValThrAlaPro 504
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RESULT 9
US-09-529-279-43
; Sequence 43, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-43

Alignment Scores:
Pred. No.: 2,62e-34 Length: 513
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

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Db 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 465
QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTCGCTCCGCTCCGCGAGGACGGT 120
Db 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485
QY 121 CGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 180
Db 486 ArgValGluProTrpValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 505
QY 181 GAGCAGAGCGTGTGACAGCACC 204
Db 506 GluGlnSerValThrAlaPro 513

RESULT 10
US-10-158-895-43
; Sequence 43, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Alignment Scores:
Pred. No.: 2,62e-34 Length: 513
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x US-10-158-895-43 (1-513)
QY 1 CAAGCCGACCTTAACCTGAGTCCACACACGACGAGGAGCTCCAGC 60
Db 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 465
QY 61 TCTGACGGAGGCTCTCCGCTCCCGCCCGCCCACTCCCTCCCGCTCCGCGGAGGACGGT 120
Db 466 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 485
QY 121 CGTGTTGAGCCCTATGTGAGCTTTGCTGAGTTTACCCGCTCTGGAGCGTGACCATGGC 180
Db 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuThrSerValAspHisGly 505
QY 181 GAGCAGAGCGTGTGACAGCACCG 204
Db 506 GluGlnSerValThrAlaPro 513

RESULT 11
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-11

Alignment Scores:
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Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

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QY 61 TCTGACGGAGGCTCTCCGCTCCCGCCCGCCCACTCCCTCCCGCTCCGCGGAGGACGGT 120
Db 457 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 476
QY 121 CGTGTTGAGCCCTATGTGAGCTTTGCTGAGTTTACCCGCTCTGGAGCGTGACCATGGC 180
Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuThrSerValAspHisGly 496

RESULT 12
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-11

Alignment Scores:
Pred. No.: 2,63e-34 Length: 517
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45% Indels: 0
DB: 4 Gaps: 0

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Db 457 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 476
QY 121 CGTGTTGAGCCCTATGTGAGCTTTGCTGAGTTTACCCGCTCTGGAGCGTGACCATGGC 180
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RESULT 13
US-09-252-991A-22734
; Sequence 22734, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 09:07:25 ; Search time 36.2973 Seconds
(without alignments)
2090.550 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 361

Sequence: 1 caaagccgacctaaccot.....agagcgtggacagcaccg 204

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 1368560

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description

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2	359	99.4	504	14	US-10-123-427-2	Sequence 2, Appli
3	359	99.4	504	14	US-10-123-427-6	Sequence 6, Appli
4	359	99.4	504	14	US-10-158-895-2	Sequence 2, Appli
5	359	99.4	513	12	US-10-384-743-43	Sequence 43, Appli
6	359	99.4	513	14	US-10-158-895-43	Sequence 43, Appli
7	359	99.4	517	12	US-10-384-743-11	Sequence 11, Appli
8	359	99.4	517	14	US-10-158-895-11	Sequence 11, Appli
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13	77	21.3	16	14	US-10-158-895-41	Sequence 41, Appli
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15	74	19.9	252	16	US-10-278-536-180	Sequence 180, App
16	72	19.9	574	12	US-10-168-097A-76	Sequence 76, Appli
17	72	19.9	574	12	US-10-239-431A-38	Sequence 38, Appli
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35	70.5	19.5	55	9	US-09-864-761-38194	Sequence 38194, A
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ALIGNMENTS

RESULT 1
US-10-384-743-2
; Sequence 2, Application US/10384743
; Publication No. US2003016228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/Jp98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 4
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 ; Sequence 2, Application US/10158895
 ; Publication No. US20020155624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/158,895
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 504
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-158-895-2

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 Best Local Similarity: 100.00%
 Query Match: 99.45%
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 Gaps: 0

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 QY 61 TCTGACGGAGGCCTCTCCGCTCCGGCCCGCCACCTCGCTCCCGCTGGCGAGGACGGT 120
 Db 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 485
 QY 121 CGTGTGTAGCCCTATGTGGACTTTGTGCTGAGTTTTACCGCCTCTCGAGCGTGGACCATGGC 180
 Db 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTpsrValAspHisGly 505

Alignment Scores:
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Alignment Scores:
 Pred. No.: 1.47e-30
 Score: 359.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
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 Gaps: 0

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; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO


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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-158-895-41

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Alignment Scores:		
Pred. No.:	4.94	Length:
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Best Local Similarity:	100.00%	Mismatches:
Query Match:	21.33%	Indels:
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		15

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|||

RESULT 14

US-10-260-937-16
: Sequence 16, Application US/10260937
: Publication No. US20030220306A1
: GENERAL INFORMATION: Daniel
: APPLICANT: Simmons, Daniel
: APPLICANT: Chandrasekharan, N. Vishvanath
: TITLE OF INVENTION: NOVEL CYCLOXYGENASE VARIANTS AND
: TITLE OF INVENTION: METHODS OF USE

Alignment Scores:	
Pred. NO.:	13.5
Score:	74.50
Percent Similarity:	43.55%
Best Local Similarity:	40.32%
Query Match:	19.81%
DR:	12
Length:	613
Matches:	25
Conservative:	2
Mismatches:	21
Indels:	14
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QY 14 AAGG 11
Dp 438 uAra 439

RESULT 15

Qy 46 TCTGCGTGTGCGTGTGGTGGACTGCAGGGTTAAGGTGCGGC 5
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RESULT 12

US-10-384-743-41
; Sequence 41, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278

Alignment Scores:	4.84	Length:	15
Pred. No.:	77.00	Matches:	15
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	21.33%	Gaps:	0
DB:	12		

US-09-830-144-3 COPY 1338 1541 (1-204) X US-10-384-743-41 (1-16)

QY 1 CAAAGCCCGACCTTAACCTGTCAGTCCACCAACAGCGACAGCAG 45
|||
pb 2 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGln 16

RESULT 13

US-10-158-895-41
; Sequence 41, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: CNO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING
; TGF-BETA INHIBITORY SUBSTANCES

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 07:06:54 ; Search time 4.82432 Seconds
(without alignments)
3977.116 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 361

Sequence: 1 caagcccgacctaaccct.....agagcggtgacagcaccg 204

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09830144/runat_03122003_122344_21226/app_query.fasta_1.1230
-DB=SwissProt 41 -QFWT=fastan -SUFFIX=rsrp -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144 @CGN 1 1 16 @runat_03122003_122344_21226 -NCFU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	99.4	504	1 TAB1 HUMAN	Q15750 homo sapien
2	73	20.2	518	1 VL2 HPV47	P22425 human papil
3	72	19.9	1199	1 P121 RAT	P52591 rattus norv
4	71	19.7	132	1 VE4 HPV2A	P25483 human papil
5	71	19.7	519	1 VL2 HPV14	P36749 human papil
6	71	19.7	521	1 VL2 HPV49	P36762 human papil
7	71	19.7	578	1 DSD8 PANCI	Q9x2b2 pantoea cic
8	70.5	19.5	518	1 VL2 HPV12	P36748 human papil
9	70	19.4	198	1 GSCI MOUSE	P56916 mus musculu
10	70	19.4	518	1 VL2 HPV20	P50794 human papil
11	70	19.4	520	1 VL2 HPV19	P36752 human papil
12	69	19.1	895	1 GNDS RAT	Q03386 rattus norv
13	68.5	18.2	239	1 RGSJ MOUSE	Q9q2b1 mus musculu
14	68.5	18.2	537	1 RGSJ RAT	P26896 rattus norv
15	68.5	18.2	824	1 TGM1 RAT	P23606 rattus norv
16	68	18.1	361	1 IE63 PRVKA	Q85232 pseudorabie
17	66	17.6	99	1 NIC1 HUMAN	Q9ug19 homo sapien
18	66	18.3	427	1 TEA4 MOUSE	Q62296 mus musculu

19	66	18.3	431	1 NOCT HUMAN	Q9uk39 homo sapien
20	66	18.3	518	1 VL2 HPV05	P06918 human papil
21	66	18.3	518	1 VL2 HPV08	P06419 human papil
22	66	18.3	518	1 VL2 HPV36	P50827 human papil
23	66	17.6	817	1 TGM1 HUMAN	P22735 homo sapien
24	66	18.3	1371	1 UBPJ HUMAN	O94966 homo sapien
25	65.5	18.1	523	1 VL2 HPV24	P50798 human papil
26	65	17.3	465	1 E2F3 HUMAN	O00716 homo sapien
27	65	18.0	518	1 VL2 HPV5B	P26540 human papil
28	65	17.3	774	1 HCN3 HUMAN	Q9p123 homo sapien
29	65	17.3	1034	1 POL HV2CA	P24107 human immu
30	64.5	17.2	177	1 R10L ARATH	Q9s09 arabidopsis
31	64.5	17.2	352	1 PRL1 CAEEL	Q22053 caenorhabdi
32	64.5	17.2	864	1 KUTK HUMAN	P29376 homo sapien
33	64.5	17.2	1111	1 GLI1 MOUSE	P47806 mus musculu
34	64	17.0	216	1 RGSJ MOUSE	O9cx84 mus musculu
35	64	17.0	216	1 RGSJ RAT	O70521 rattus norv
36	64	17.0	277	1 HXDB NOTVI	P31263 notophthalm
37	64	17.0	450	1 A2AA RAT	P22909 rattus norv
38	64	17.0	578	1 CES6 HUMAN	Q9bxq6 homo sapien
39	64	17.7	621	1 VP40 HSVBC	P54817 bovine herp
40	63.5	16.9	237	1 PSA5 ORYSA	Q91su1 oryza sativ
41	63.5	17.6	243	1 IM17 ARATH	Q9sp35 arabidopsis
42	63.5	16.9	388	1 A2AB ORYAP	O19032 orycteropus
43	63.5	17.6	824	1 AD08 HUMAN	P78325 homo sapien
44	63	17.5	253	1 LI39 CAEEL	P34684 caenorhabdi
45	63	16.8	450	1 A2AA MOUSE	Q01338 mus musculu

ALIGNMENTS

RESULT 1

ID	TAB1 HUMAN	STANDARD	PRT	504 AA.
AC	Q15750;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Mitogen-activated protein kinase kinase 7 interacting protein 1			
DE	(TAK1-binding protein 1).			
GN	MAP3K7IP1 OR TAB1.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=96216294; PubMed=8639164;			
RA	Shibuya H., Yamaguchi K., Shirakabe K., Tonegawa A., Gotoh Y.,			
RA	Ueno N., Irie K., Nishida E., Matsumoto K.;			
RT	"TAB1: an activator of the TAK1 MAPKK in TGF-beta signal			
RT	transduction.";			
RL	Science 272:1179-1182 (1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Baggaley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhumi P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	McClay J., McLaren S., McMurray A., Milne S.A., Mortimore B.J.,			
RA	Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			

102b

5

RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,	121	CGTGTGAGCCCTATGTGGACTTTCTGAGTTTACCGCTCTGAGCGGTGACCATGGC	180
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,	122		181
RA	Soderlund C., Spraggon L., Steward C.A., Sulton J.E., Swann R.M.,	477	ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly	496
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,	181	GAGCAGAGCGTGGTGCACGACGACCG	204
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,	497	GluGlnSerValValThrAlaPro	504
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S.A., Rogers J., Shimizu N.,			
RA	Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudo J.,	RESULT 2		
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,	VL2_HPV47		
RA	Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,	ID	VL2_HPV47	STANDARD; PRT; 518 AA.
RA	Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,	AC	P22425;	
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen H., Pan H.,	DT	01-AUG-1991 (Rel. 19, Created)	
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,	DT	01-AUG-1991 (Rel. 19, Last sequence update)	
RA	Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,	DT	01-OCT-1996 (Rel. 34, Last annotation update)	
RA	Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,	DE	Minor capsid protein L2.	
RA	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,	GN	L2.	
RA	Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,	OS	Human papillomavirus type 47.	
RA	Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,	OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	
RA	Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,	OC	Papillomavirus.	
RA	Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,	OX	NCBI_TaxID=10594;	
RA	Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,	RN	[1]	
RA	McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,	RP	SEQUENCE FROM N.A.	
RA	Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,	RX	MEDLINE=90281611; PubMed=2162112;	
RA	Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,	RT	Kiyono T., Adachi A., Ishibashi M.;	
RA	Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,	RT	"Genome organization and taxonomic position of human papillomavirus	
RA	Tilahun Y., Wright H.;	RL	type 47 inferred from its DNA sequence.";	
RT	"The DNA sequence of human chromosome 22.";			
RL	Nature 402:489-495 (1999).			
CC	-!- FUNCTION: MAY BE AN IMPORTANT SIGNALING INTERMEDIATE BETWEEN TGFB			
CC	RECEPTORS AND MAP3K7/TAK1.			
CC	-!- SUBUNIT: Interacts with MAP3K7 and with BIRC7.			
CC	-!- TISSUE SPECIFICITY: Ubiquitous.			
CC	-!- SIMILARITY: Contains 1 PP2C-like domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	EMBL; U49928; AAC12660.1; --			
DR	EMBL; Z83845; CAB55304.1; --			
DR	Genew; HGNC:18157; MAP3K7IP1.			
DR	MIM; 602615; --			
DR	GO; GO:0008047; F:enzyme activator activity; TAS.			
DR	GO; GO:000515; F:protein binding activity; TAS.			
DR	GO; GO:0000185; P:activation of MAPKK; TAS.			
DR	InterPro; IPR001932; PP2C-like.			
DR	Pfam; PF00481; PP2C; 1.			
DR	SMART; SM00332; PP2CC; 1.			
FT	DOMAIN 64 368			
FT	DOMAIN 452 457			
FT	POLY-SER.			
SQ	SEQUENCE 504 AA; 54644 MW; A45743288718983A CRC64;			
Alignment Scores:				
Pred. No.:	7.82e-31	Length:	504	
Score:	359.00	Matches:	68	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	99.45%	Indels:	0	
DB:	1	Gaps:	0	
US-09-830-144-3_COPY_1338_1541 (1-204) x TAB1_HUMAN (1-504)				
QY	1 CAAGCCGAGCTTAACCTGAGTCCACACGACGACGACGACGAGCAGCTCCAGC	60		
Db	437 GlnSerProThrLeuThrLeuGlnSerThrAnthrHisThrGlnSerSerSerSer	456		
QY	61 TCTGACGAGGCGCTCTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGGAGACGGT	120		
Db	457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	476		
QY	11 CCTTAACCTGACGCTCCA-----CCACACGACGACGACGACGAGCAGCTCCA	58		
Db	141 ProLeuProGluGlyProThrIleAspSerProValValThrThrThrGlySerSer	160		
QY	59 GCTCTGACGAGCGCTCTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGGAGCAGC	118		
Db	161 AlaValLeuGluValAlaProGluProValProThrArgValArgIleAlaArgThr	180		
QY	119 GTCGTGTGAGCCCTATGTGACTTTCGTG-----AGTTTACCGCTCTGAGCGGTG	172		
Db	181 GlnTyrHisAsnProSerPheGlnIleuThrGlnSerThrProAlaGlnGlyGluSer	200		
QY	173 ACCATGGCG 181			
Db	201 SerLeuAla 203			
RESULT 3				
P121_RAT				
ID	P121_RAT	STANDARD; PRT; 1199 AA.		


```

OX NCBI_TaxID=10605;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC -----
DR EMBL; X74467; CA52504.1; -.
DR PIR; S36471; S36471.
DR InterPro; IPR000784; Late L2.
DR Pfam; PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 519 AA; 56873 MW; 52E21620474CD1E8 CRC64;

Alignment Scores:
Pred. No.: 6.83 Length: 519
Score: 71.00 Matches: 16
Percent Similarity: 50.00% Conservative: 11
Best Local Similarity: 29.63% Mismatches: 23
Query Match: 19.67% Indels: 4
DB: 1 Gaps: 1

US-09-830-144-3_COPY_1338_1541 (1-204) x VL2_HPV14 (1-519)
QY 2 AAGCCCGCACTTAACCTGCAGTCCACCAACA-----CGCACAGCAGACA 49
Db 138 GluValHisProGlyProSerArgProThrAspThrProValThrSerThrGly 157
QY 50 GCAGCTCCAGCTCAGCAGGAGCTTCGCTCCGCGCGCGCGCAGCTGCTCCGCTG 109
Db 158 GlySerSerAlaIleLeuGluValAlaProGluProThrProSerArgValArgVal 177
QY 110 GCAGCAGCTGCTGTTGAGCCCTATGTCGACTTGTCTGAGT 151
Db 178 ThrArgThrGlnTyrHisAsnProSerPheGlnValIleThr 191

RESULT 6
VL2_HPV49
ID_VL2_HPV49 STANDARD; PRT; 521 AA.
AC P36762;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS Human papillomavirus type 49.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10616;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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CC -----
DR EMBL; X74467; CA52504.1; -.
DR PIR; S36471; S36471.
DR InterPro; IPR000784; Late L2.
DR Pfam; PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 519 AA; 56873 MW; 52E21620474CD1E8 CRC64;

Alignment Scores:
Pred. No.: 6.83 Length: 519
Score: 71.00 Matches: 16
Percent Similarity: 50.00% Conservative: 11
Best Local Similarity: 29.63% Mismatches: 23
Query Match: 19.67% Indels: 4
DB: 1 Gaps: 1

US-09-830-144-3_COPY_1338_1541 (1-204) x VL2_HPV14 (1-519)
QY 2 AAGCCCGCACTTAACCTGCAGTCCACCAACA-----CGCACAGCAGACA 49
Db 138 GluValHisProGlyProSerArgProThrAspThrProValThrSerThrGly 157
QY 50 GCAGCTCCAGCTCAGCAGGAGCTTCGCTCCGCGCGCGCAGCTGCTCCGCTG 109
Db 158 GlySerSerAlaIleLeuGluValAlaProGluProThrProSerArgValArgVal 177
QY 110 GCAGCAGCTGCTGTTGAGCCCTATGTCGACTTGTCTGAGT 151
Db 178 ThrArgThrGlnTyrHisAsnProSerPheGlnValIleThr 191

RESULT 7
DSBD_PANCI
ID_DSBD_PANCI STANDARD; PRT; 578 AA.
AC Q9XDB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiol:disulfide interchange protein dsbD precursor (EC 1.8.1.8)
DE (Protein-disulfide reductase) (Disulfide reductase).
GN DSBD.
OS Pantoea citrea.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=53336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1056R;
RX MEDLINE=20200361; PubMed=10735866;
RA Fujol C.J., Kado C.I.;
RT "Genetic and biochemical characterization of the pathway in Pantoea
citrea leading to pink disease of pineapple.";
RL J. Bacteriol. 182:2230-2237(2000).
CC -!- FUNCTION: Required to facilitate the formation of correct
disulfide bonds in some periplasmic proteins and for the assembly
of the periplasmic c-type cytochromes. Acts by transferring
electrons from cytoplasmic thioredoxin to the periplasm. This
transfer involves a cascade of disulfide bond formation and
reduction steps (By similarity).
CC -!- CATALYTIC ACTIVITY: Protein dithiol + NAD(P)+ = protein disulfide
+ NAD(P)H.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(BY similarity).
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. DSBD SUBFAMILY.
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CC -----
DR EMBL; AF102175; AAD38449.1; -.
DR HAMAP; MF_00399; 1
DR InterPro; IPR003834; Cytococh_TM.
DR InterPro; IPR006662; Thioredo.
DR Pfam; PF02683; DsbD; 1.

```

DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Oxidoreductase; Redox-active center; Electron transport; NAD;
 KW Transmembrane; Inner membrane; Cytochrome c-type biogenesis; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 578
 FT DOMAIN 23 180
 FT TRANSMEM 181 201
 FT DOMAIN 202 216
 FT TRANSMEM 217 237
 FT DOMAIN 238 253
 FT TRANSMEM 254 274
 FT DOMAIN 275 306
 FT TRANSMEM 307 327
 FT DOMAIN 328 336
 FT TRANSMEM 337 357
 FT DOMAIN 358 367
 FT TRANSMEM 368 388
 FT DOMAIN 389 394
 FT TRANSMEM 395 415
 FT DOMAIN 416 428
 FT TRANSMEM 429 449
 FT DOMAIN 450 578
 FT DISULFID 125 131
 FT DISULFID 193 315
 FT DISULFID 492 495
 SQ SEQUENCE 578 AA; 62547 MW; 383B32797B7FA0B4 CRC64;

Alignment Scores:
 Pred. No.: 6.89 Length: 578
 Score: 71.00 Matches: 23
 Percent Similarity: 45.61% Conservativeness: 3
 Best Local Similarity: 40.35% Mismatches: 13
 Query Match: 19.67% Indels: 18
 DB: 1 Gaps: 4

US-09-830-144-3_COPY_1338_1541 (1-204) x DSDP_PANCI (1-578)

QY 20 TGCAGTCCACCA---ACACGC-----ACACGCAGCAGCA 52
 Db 131 CysTyProProGluThrArgGluValProLeuSerGlnValSerThrArgSerGlu 150
 QY 53 GTCCTGAGCTGTACGAGGAGCTCTCCGCTCCCGGCGCC-----CCCACT 97
 Db 151 AlaProAlaThrAlaAlaThrProAlaProValProGluProGlnSerGlyProAla 170
 QY 98 CGCTCCCGCTGCGAGGAGCGTGTGAGCCCTATGTGACTTGTGTG 148
 Db 171 ValSerArgLeuPro-----PheSerProLeuTrpAlaLeuLeu 183

RESULT 8
 VL2 HPV12
 ID VL2 HPV12 STANDARD; PRT; 518 AA.
 AC P36748;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Minor capsid protein L2.
 GN L2.
 OS Human papillomavirus type 12.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10604;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X74466; CAA52500.1; -;
 DR PIR; S36542; S36542.
 DR InterPro; IPR000784; Late L2.
 DR Pfam; PF00513; late protein L2; 1.
 KW Coat protein; late protein.
 SQ SEQUENCE 518 AA; 56776 MW; BFDFOB9BED22A9B CRC64;

Alignment Scores:
 Pred. No.: 7.73 Length: 518
 Score: 70.50 Matches: 20
 Percent Similarity: 56.36% Conservativeness: 11
 Best Local Similarity: 36.36% Mismatches: 21
 Query Match: 19.53% Indels: 3
 DB: 1 Gaps: 2

US-09-830-144-3_COPY_1338_1541 (1-204) x VL2 HPV12 (1-518)

QY 23 AGTCCACCAACACGACGACGACGACGCTCCAGCTCTGAGGAGGCTCTTCGCT 82
 Db 150 SerProValValThrThrSerArgGlySerSer---AlaLeuGluValAlaProAsp 169
 QY 83 CCGGCGCGCCCACTCGCTCCGCTCCGCTGGGAGGAGCGTGTGTGAGCCCTATGTGGACT 142
 Db 169 ProIleProProThrArgValArgValAlaArgThrGlnTyrHisAsnProAlaPheGln 188
 QY 143 TTGCTG-----AGTTTACCGCTCTGGAGCGTGACCATGGCG 181
 Db 189 IleIleThrGluSerThrProAlaGlnGlyGluThrSerLeuAla 203

RESULT 9
 GSCL MOUSE
 ID GSCL MOUSE STANDARD; PRT; 198 AA.
 AC P56916;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein goosecoid-like (GSC-2).
 GN GSCL
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97189340; PubMed=9037598;
 RA Gallili N., Baldwin H.S., Lund J., Reeves R., Gong W., Wang Z.,
 RA Roe B.A., Emanuel B.S., Nayak S., Mickanin C., Budarf M.L., Buck C.A.;
 RT "A region of mouse chromosome 16 is syntenic to the DiGeorge,
 RT velocardiofacial syndrome minimal critical region.";
 RL Genome Res. 7:17-26(1997).
 RN [2]
 RP ERRATUM.
 RX MEDLINE=97264346; PubMed=9110179;
 RA Gallili N., Baldwin H.S., Lund J., Reeves R., Gong W., Wang Z.,
 RA Roe B.A., Emanuel B.S., Nayak S., Mickanin C., Budarf M.L., Buck C.A.;
 RL Genome Res. 7:399-399(1997).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98110571; PubMed=9441739;
 RA Funke B., St Jore B., Puech A., Sirotkin H., Edelman L., Carlson C.,
 RA Raft S., Pandita R.K., Kucherlapati R., Skoultschi A., Morrow B.E.;
 RT "Characterization and mutation analysis of goosecoid-like (GSCL), a
 RT homeodomain-containing gene that maps to the critical region for
 RT VCFS/DGS on 22q11.";
 RL Genomics 46:364-372(1997).
 CC -----
 CC -!- FUNCTION: MAY HAVE A ROLE IN DEVELOPMENT. MAY REGULATE ITS OWN
 CC -!- TRANSCRIPTION. MAY BIND THE BICOID CONSENSUS SEQUENCE TAATCC.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTIS.

DR	SMART; SMO0147; RasGEF; 1.
DR	SMART; SMO0229; RasGFEN; 1.
DR	PROSITE; PS00720; RASGEF; 1.
DR	PROSITE; PS02000; RA; 1.
DR	PROSITE; PS50009; RASGEF_CAT; 1.
DR	PROSITE; PS0212; RASGEF_NTER; 1.
KW	Guanine-nucleotide releasing factor; 3D-structure.
FT	DOMAIN 112 237 N-TERMINAL RAS-GEF.
FT	DOMAIN 367 629 RAS-GEF.
FT	DOMAIN 779 866 RAS-ASSOCIATING.
FT	STRAND 779 787
FT	STRAND 796 801
FT	TURN 802 803
FT	STRAND 805 805
FT	HELIX 806 815
FT	TURN 816 818
FT	HELIX 824 826
FT	STRAND 827 834
FT	TURN 835 836
FT	STRAND 837 840
FT	TURN 843 844
FT	STRAND 846 846
FT	HELIX 847 850
FT	TURN 853 854
FT	STRAND 858 863
SQ	SEQUENCE 895 AA; 98869 MW; 43E1674675A4E1C9 CRC64;

Alignment Scores:

Pred. No.:	11.7	Length:	895
Score:	69.00	Matches:	14
Percent Similarity:	51.43%	Conservative:	4
Best Local Similarity:	40.00%	Mismatches:	9
Query Match:	19.11%	Indels:	8
DB:	1	Gaps:	1

US-09-830-144-3_COPY_1338_1541 (1-204) x GNDS_RAT (1-895)

QY	6	CCCGACCTTAACCTGCAGTCCACCAACGACGACGACGACGACGACGACTCCAGCTCTGA	65
Dd	321	ProGluLeuAspProThrValSerGlnSerLeuHisLeuGlu-----	334
QY	66	CGGAGGCCCTTCCTCCGCTCCGGCCGCCGACCTCGCTCCGCCCTGG	110
Dd	335	-----ProAlaProValProAlaProAlaLeuGluProSerTrp	347

RESULT 13

RGSK_MOUSE	ID	RGSK_MOUSE	STANDARD;	PRT;	239 AA.
AC	Q9QZB1; Q9CUV8				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Regulator of G-protein signaling 20 (RGS20) (Regulator of G-protein signaling Z1).				
DE	RGS20 OR RGSZ1.				
GN	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NB	NCBI_taxID=10090;				
NRN	[1]				
NRN	SEQUENCE FROM N.A., AND VARIANT ARG-32.				
RRP	STRAIN=129/B6, and BALB/c;				
RC	Barker S.A., Wang J., Ross E.M.;				
RC	"A mouse ortholog of RGSZ1."				
RC	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
RC	[2]				
RRP	SEQUENCE OF 5-239 FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Hippocampus;				
RC	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,				

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momabaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y., et al.

Functional annotation of a full-length mouse cDNA collection."

Nature 409:685-690(2001).

-!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. BINDS SELECTIVELY TO G(Z)-ALPHA AND IS INHIBITED BY THE PHOSPHORYLATION AND PALMITOYLATION OF THE G-PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).

-!- PTM: FATTY ACYLATED. HEAVILY PALMITOYLATED IN THE CYSTEINE STRING MOTIF (BY SIMILARITY). Contains 1 RGS domain.

-!- SIMILARITY: Contains 1 RGS domain.

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EMBL; AF191554; AAF05757.1; --
EMBL; AF191552; AAF05756.1; --
EMBL; AK013773; BAB28987.1; --
HSSP; P49795; 1CMZ.
MGD; MGI:1929866; Rgs20.
InterPro; IPR000342; Regl_Gprotein.
Pfam; PF00615; RGS; 1.
PRINTS; PR01301; RGSPROTEIN.
ProDom; PD001580; Regl_Oproteins; 1.
SMART; SM00315; RGS; 1.
PROSITE; PS50132; RGS; 1.
Signal transduction inhibitor; Membrane; Lipoprotein; Palmitate; Polymorphism.
FT DOMAIN 59 71 POLY-CYS.
FT DOMAIN 113 229 RGS.
FT VARIANT 32 32 M -> R (IN BALB/C).
SQ SEQUENCE 239 AA; 26986 MW; F383923163A44D18 CRC64;

Alignment Scores:
Pred. No.: 12 Length: 239
Score: 68.50 Matches: 20
Percent Similarity: 40.00% Conservative: 8
Best Local Similarity: 28.57% Mismatches: 25
Query Match: 18.22% Indels: 17
DB: 1 Gaps: 3

US-09-830-144-3_COPY_1338_1541 (1-204) x RGS_K_MOUSE (1-239)

QY 190 CGCTCGTCGCCATGGTCACGCTCCAGAGCGGTAAACT----- 149
Db 2 ArgThrAlaAsnGlyGlyProArgAlaArgAlaSerProSerAlaSerProAlaAspPro 21
QY 148 -----CAGCAAAAGTCACATAGGGCTCAACACGACCGCTCTCGCACGCGGAGCGAGT 95
Db 22 GlyLeuProGlnGlySerGluArgThrGluMetArgMetArgGlnMetCysGlyGlySer 41
QY 94 -----GGCGGGCGGGAGCGGAAGAGCCCTCGTCAGAGC----- 59
Db 42 GluThrGlnGlyProAlaProSerGlnGlnGlyArgGlySerAsnAlaCysCysPhe 61


```

FT METAL      556      CALCIUM (BY SIMILARITY)
FT METAL      561      CALCIUM (BY SIMILARITY)
SQ SEQUENCE  824 AA;  90769 MW;  A7D81C148CEFD938 CRC64;

Alignment Scores:
Pred. No.:      13.1      Length:      824
Score:          68.50     Matches:    18
Percent Similarity: 40.35% Conservative:   5
Best Local Similarity: 31.58% Mismatches:   21
Query Match:      18.22% Indels:     13
DB:              1       Gaps:       3

US-09-830-144-3_COPY_1338_1541 (1-204) x TGM1_RAT (1-824)

QY      175  GTCCACGCTCCAGAGCGGTAA-----
Db      3   GlyProArgSerAspValGlyArgTrpGlyArgSerProTrpGln

QY      139  CCACATAGGCGTCAACACGACCGTCTCCGCCAGCGCGAGCGAGTGT
Db      23  ProGluProGluProGluProGluProAspArgSerSerArgSer

QY      79   GGAGAGGCGCTCGTCAGAGCTGGAGC-----TGCTGCTCTCGCGTGT
Db      43  -----ArgSerPheTrpAlaArgCysCysGlyCysCys

Search completed: December 4, 2003, 09:03:42
Job time : 7.82432 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 00:51:52 ; Search time 944.878 Seconds
(without alignments) 8932.421 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 204

Sequence: 1 caaagccgacaccttaaccct.....agagcgtggtgacagcaccg 204

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

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26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

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37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	1515	6	E31041 Method for
2	204	100.0	1560	6	AR058299 Sequence
3	204	100.0	1560	6	AR058302 Sequence
4	204	100.0	1560	6	AR088273 Sequence
5	204	100.0	1560	6	AR088276 Sequence
6	204	100.0	1560	6	AR088276 Sequence
7	204	100.0	1560	6	AR116881 Sequence
8	204	100.0	1560	6	AR116884 Sequence
9	204	100.0	1560	6	AR231191 Sequence
10	204	100.0	1560	6	AR307972 Sequence
11	204	100.0	1568	6	E14752 Human mRNA
12	204	100.0	1568	6	AR231223 Sequence
13	204	100.0	1568	6	AR308004 Sequence
14	204	100.0	1569	6	AR231195 Sequence
15	204	100.0	1569	6	AR307976 Sequence
16	204	100.0	3096	9	HSU49928
17	204	100.0	3253	9	BC050554
18	204	100.0	3290	9	BC038582
19	204	100.0	6960	9	HS407F17
20	204	100.0	17118	2	AC141444
21	164.6	80.7	1784	10	AB088136
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24	159.8	78.3	182516	2	AC140267
25	159.8	78.3	288805	2	AC127784
26	96.8	47.5	1926	5	AC127924
27	40	19.6	1926	5	U92031 Xenopus lae
28	37.4	18.3	53121	2	SC0939115
29	37.4	18.3	53121	2	AC136331
30	37.2	18.2	181545	10	AL626774
31	37.2	18.2	1485	6	E15521
32	37.2	18.2	1491	6	AR073849
33	37.2	18.2	1491	9	BT006992
34	37.2	18.2	1491	12	BT007934
35	37.2	18.2	1505	6	E16553
36	37.2	18.2	1648	6	E04413
37	37.2	18.2	1653	9	HUMAAAT
38	37.2	18.2	1871	9	BC018207
39	37.2	18.2	10622	1	AE004819
40	36.2	17.7	36792	3	LMFL3747
41	36	17.6	301700	1	AP005028
42	35.8	17.5	41630	9	AP005948
43	35.8	17.5	57075	2	AC110746
44	35.8	17.5	162090	10	AL805921
45	35.8	17.5	174678	9	AL450332

ALIGNMENTS

RESULT 1
E31041
LOCUS E31041 Method for screening substance inhibiting binding to XIAP. PAT 18-JUN-2001
DEFINITION E31041
ACCESSION E31041
VERSION E31041.1 GI:13017306
KEYWORDS JP 199326328-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1515)
AUTHORS Kunihiko, M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 199326328-A 1 26-NOV-1999;
KUNIHICO MATSUMOTO

ORGANISM					
Unknown.					
Unclassified.					
REFERENCE					
1 (bases 1 to 1560)					
AUTHORS					
Matsumoto,K. and Nishida,E.					
TITLE					
TAB1 protein and DNA coding therefore					
JOURNAL					
Patent: US 6140042-A 1 31-OCT-2000;					
FEATURES					
Location/Qualifiers					
1..1560					
BASE COUNT					
332 a 469 c 480 g 279 t					
ORIGIN					
Query Match					
100.0%; Score 204; DB 6; Length 1560;					
Best Local Similarity 100.0%; Pred.No.1.6e-37;					
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy					
1 CAAGGCCGACCTTAAACCTCGAGTCCTCCAAACAGCACGACGAGCAGCAGCTCCAGC 60					
Db					
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Qy					
61 TCTGACGGAGGCCTCTTCGGCTCCCGGCCCGCCACTCGCTCCCGCTGTGGAGGACGGT 120					
Db					
1398 TCTGACGGAGGCCTCTTCGGCTCCCGGCCCGCCACTCGCTCCCGCTGTGGAGGACGGT 1457					
Qy					
121 CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGCTCTGGAGCGTGGACCATTGCC 180					
Db					
1458 CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGCTCTGGAGCGTGGACCATTGCC 1517					
Qy					
181 GAGCAGAGCGTGGTGACAGCACCG 204					
Db					
1518 GAGCAGAGCGTGGTGACAGCACCG 1541					
RESULT 7					
AR116884					
LOCUS					
AR116884 1560 bp DNA linear PAT 16-MAY-2001					
DEFINITION					
Sequence 5 from patent US 6140042.					
ACCESSION					
AR116884					
VERSION					
AR116884.1 GI:14097790					
KEYWORDS					
Source					
Unknown.					
ORGANISM					
Unknown.					
Unclassified.					
REFERENCE					
1 (bases 1 to 1560)					
AUTHORS					
Matsumoto,K. and Nishida,E.					
TITLE					
TAB1 protein and DNA coding therefore					
JOURNAL					
Patent: US 6140042-A 5 31-OCT-2000;					
FEATURES					
Location/Qualifiers					
1..1560					
BASE COUNT					
333 a 468 c 480 g 279 t					
ORIGIN					
Query Match					
100.0%; Score 204; DB 6; Length 1560;					
Best Local Similarity 100.0%; Pred.No.1.6e-37;					
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Db					
1338 CAAAGCCGACCTTAAACCTCGAGTCCTCCAAACAGCACGACGAGCAGCAGCTCCAGC 1397					
Qy					
61 TCTGACGGAGGCCTCTTCGGCTCCCGGCCCGCCCACTCGCTCCCGCTGTGGAGGACGGT 120					
Db					
1398 TCTGACGGAGGCCTCTTCGGCTCCCGGCCCGCCCACTCGCTCCCGCTGTGGAGGACGGT 1457					
Qy					
121 CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGCTCTGGAGCGTGGACCATTGCC 180					
Db					
1458 CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGCTCTGGAGCGTGGACCATTGCC 1517					
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181 GAGCAGAGCGTGGTGACAGCACCG 204					
Db					
1518 GAGCAGAGCGTGGTGACAGCACCG 1541					

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RESULT 8
LOCUS AR231191 1560 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6451617.
ACCESSION AR231191
VERSION AR231191.1 GI:27272079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
TITLE Method of screening TGF-beta-inhibitory substances
JOURNAL Patent: US 6451617-A 1 17-SEP-2002;
FEATURES
Location/Qualifiers
1..1560
/organism="unknown"
BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN
Query Match 100.0%; Score 204; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 60
Db 1338 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397

QY 61 TCTGACGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 120
Db 1398 TCTGACGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 1457

QY 121 CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db 1458 CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517

QY 181 GACGAGCGGTGGTGACGACCG 204
Db 1518 GACGAGCGGTGGTGACGACCG 1541

RESULT 9
LOCUS AR307972 1560 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6551840.
ACCESSION AR307972
VERSION AR307972.1 GI:31698729
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Ono,K., Ohtomo,T. and Tsuchiya,M.
TITLE Method of screening TGF-beta-inhibiting substances
JOURNAL Patent: US 6551840-A 1 22-APR-2003;
FEATURES
Location/Qualifiers
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/organism="unknown"
BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN
Query Match 100.0%; Score 204; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 60
Db 1338 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397

QY 61 TCTGACGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 120
Db 1398 TCTGACGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 1457

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QY 121 CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db 1458 CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517

QY 181 GACGAGCGGTGGTGACGACCG 204
Db 1518 GACGAGCGGTGGTGACGACCG 1541

RESULT 10
LOCUS E14752 1560 bp DNA linear PAT 28-JUL-1999
DEFINITION Human mRNA for the TAB1 protein.
ACCESSION E14752
VERSION E14752.1 GI:5709435
KEYWORDS JP 1998004976-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1560)
AUTHORS Matsumoto,K. and Nishida,E.
TITLE TAB1 PROTEIN AND DNA CODING THE SAME
JOURNAL Patent: JP 1998004976-A 1 13-JAN-1998;
COMMENT
UENO NAOTO
OS Homo sapiens (human)
FN JP 1998004976-A/1
PD 13-JAN-1998
PF 28-OCT-1996 JP 1996300856
PR 24-APR-1996 JP 96P 126282
PI MATSUMOTO KUNIHICO, NISHIDA EISUKE
PC C12N15/09, C07H21/04, C07K14/47, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, G01N33/53, (C12N1/19, C12P1/865), (C12N1/21, C12P1/19),
PC C12N5/10, (C12P21/02, C12P1/865), (C12P21/02, C12P1/91); CC
strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..1560
/organism="Homo sapiens"
/ tissue_type="kidney"
FT CDS 30..1544
/product="the TAB1 protein"
FT unsure 185
FT Location/Qualifiers
FT source 1..1560
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 332 a 469 c 480 g 279 t
ORIGIN
Query Match 100.0%; Score 204; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 60
Db 1338 CAAAGCCGACCTTAAACCTTGCAGTCCACCAACGACGACGAGCAGCTCCAGC 1397

QY 61 TCTGAGGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 120
Db 1398 TCTGAGGGAGGCTCTTCGCTCCCGCCGCCCACTCGCTCCCGCTCGGAGGACGGT 1457

QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db 1458 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517

QY 181 GACGAGCGGTGGTGACGACCG 204

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Db      1518 GAGCAGAGCGTGTGACAGCAGCG 1541
|||||
RESULT 11
LOCUS      AR2311223
DEFINITION Sequence 42 from patent US 6451617.
ACCESSION AR2311223
VERSION    AR2311223.1 GI:27272111
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1568)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6451617-A 42 17-SEP-2002;
FEATURES    Location/Qualifiers
            source          1..1568
            /organism="unknown"
BASE COUNT 339 a 472 c 477 g 280 t
ORIGIN
Query Match      100.0%; Score 204; DB 6; Length 1568;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
Db      1346 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1405
QY      61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 120
Db      1406 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 1465
QY      121 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db      1466 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
QY      181 GAGCAGAGCGTGTGACAGCAGCG 204
Db      1526 GAGCAGAGCGTGTGACAGCAGCG 1549
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1568)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6451617-A 42 17-SEP-2002;
FEATURES    Location/Qualifiers
            source          1..1568
            /organism="unknown"
BASE COUNT 339 a 472 c 477 g 280 t
ORIGIN
Query Match      100.0%; Score 204; DB 6; Length 1568;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
Db      1346 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1405
QY      61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 120
Db      1406 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 1465
QY      121 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db      1466 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
QY      181 GAGCAGAGCGTGTGACAGCAGCG 204
Db      1526 GAGCAGAGCGTGTGACAGCAGCG 1549
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1568)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6551840-A 42 22-APR-2003;
FEATURES    Location/Qualifiers
            source          1..1568
            /organism="unknown"
BASE COUNT 339 a 472 c 477 g 280 t
ORIGIN
Query Match      100.0%; Score 204; DB 6; Length 1568;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
Db      1346 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1405

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QY      61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 120
Db      1406 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 1465
QY      121 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db      1466 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
QY      181 GAGCAGAGCGTGTGACAGCAGCG 204
Db      1526 GAGCAGAGCGTGTGACAGCAGCG 1549
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1569)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6451617-A 10 17-SEP-2002;
FEATURES    Location/Qualifiers
            source          1..1569
            /organism="unknown"
BASE COUNT 343 a 466 c 476 g 284 t
ORIGIN
Query Match      100.0%; Score 204; DB 6; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
Db      1315 CAAAGCCGACCTTAACCTCTGCAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1374
QY      61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 120
Db      1375 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 1434
QY      121 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db      1435 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1494
QY      181 GAGCAGAGCGTGTGACAGCAGCG 204
Db      1495 GAGCAGAGCGTGTGACAGCAGCG 1518
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1569)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6551840-A 10 22-APR-2003;
FEATURES    Location/Qualifiers
            source          1..1569
            /organism="unknown"
BASE COUNT 343 a 466 c 476 g 284 t
ORIGIN
QY      61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 120
Db      1375 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCGTGGCGAGGACGGT 1434
QY      121 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db      1435 CGTGTGAGCGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1494
QY      181 GAGCAGAGCGTGTGACAGCAGCG 204
Db      1495 GAGCAGAGCGTGTGACAGCAGCG 1518
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1569)
AUTHORS     Ono,K., Ohmoto,T. and Tsuchiya,M.
TITLE       Method of screening TGF-.beta. inhibitory substances
JOURNAL     Patent: US 6551840-A 10 22-APR-2003;
FEATURES    Location/Qualifiers
            source          1..1569
            /organism="unknown"
BASE COUNT 343 a 466 c 476 g 284 t
ORIGIN

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Query Match      100.0%; Score 204; DB 6; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCCGAGCTTAAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 60
DB 1315 CAAAGCCCGAGCTTAAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1374

QY 61 TCTGACGAGGAGCTTCTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGT 120
DB 1375 TCTGACGAGGAGCTTCTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGT 1434

QY 121 CGTGTGAGCCCTATGTGAGCTTCTCGAGTCTTACCGCTCTGAGAGCTGACCATGGC 180
DB 1435 CGTGTGAGCCCTATGTGAGCTTCTCGAGTCTTACCGCTCTGAGAGCTGACCATGGC 1494

QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
DB 1495 GAGCAGAGCGTGGTGACAGCACCG 1518
  
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RESULT 15
HSU49928
LOCUS      3096 bp mRNA linear PRI 06-APR-1998
DEFINITION Homo sapiens TAK1 binding protein (TAK1) mRNA, complete cds.
ACCESSION U49928
VERSION U49928.1 GI:1401125
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  
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1 (bases 1 to 3096)
Shibuya,H., Yamaguchi,K., Shirakabe,K., Tonegawa,A., Gotoh,Y.,
Ueno,N., Irie,K., Nishida,E. and Matsumoto,K.
TAB1: an activator of the TAK1 MAPKK in TGF-beta signal
transduction
Science 272 (5265), 1179-1182 (1996)
96216294
8638164
PUBMED
REFERENCE 2 (bases 1 to 3096)
AUTHORS Shibuya,H.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1996) Hiroshi Shibuya, Faculty of Pharmaceutical
Sciences, Hokkaido University, Nishi 6-chome, Kita 12, Kita-ku,
Sapporo, Hokkaido 060, Japan
FEATURES
Location/Qualifiers
1..3096
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..3096
/gene="TAB1"
21..1535
/gene="TAB1"
/note="activator for TAK1"
/codon_start=1
/product="TAK1 binding protein"
/protein_id="AAC12660.1"
/db_xref="GI:1401126"
/translation="WAAORSLQEQPQSDTDDPLCHLGVGSASNRYSADCKGT
ESHPPEDSWLKFERNFLGVNGVDFNVAORLSAELLGLGNAEAEADV
REVLQAQDVVERSFLEDDALAEKASLSQSLPGVPHQLPPQYQKILERLKTLE
EISGAMAVVLLNNKLYVANVINRALLCKSTVDGLQVTLNVDHTTENEDELFR
SGLGDAGIKQVGRIGCGSTRIGDYKYGYTDIDLLSAKSPKPIIAPEIHGAQ
PLDGVTFGLVMSGLYKALEAHGFGQANIEAAMIDTEFAKQTSIDAQAQVVDV
KRIHSDTARFGGERARFCPRHEDMTLLVNFYPLGMSQPTSPAPAGGRVPVS
PYSSAQSTSKTSVTLVMPVSGOMVNGAHSATLDEATPTLTNOSPILTLQSTWHT
QSSSSSDGGLFRSPALSLPFGEDGRVEFYDFAEFRLMSVDHGQSVTAP"
  
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642 a 936 c 952 g 566 t
BASE COUNT
ORIGIN
  
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Query Match      100.0%; Score 204; DB 9; Length 3096;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCCGAGCTTAAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 60
DB 1329 CAAAGCCCGAGCTTAAACCTCGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 1388

QY 61 TCTGACGAGGAGCTTCTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGT 120
DB 1389 TCTGACGAGGAGCTTCTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGT 1448

QY 121 CGTGTGAGCCCTATGTGAGCTTCTCGAGTCTTACCGCTCTGAGAGCTGACCATGGC 180
DB 1449 CGTGTGAGCCCTATGTGAGCTTCTCGAGTCTTACCGCTCTGAGAGCTGACCATGGC 1508

QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
DB 1509 GAGCAGAGCGTGGTGACAGCACCG 1532
  
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Search completed: December 4, 2003, 06:11:26
Job time : 950.378 secs

1	204	100.0	1515	21	AAZ48861	Human TAB1 coding
2	204	100.0	1560 <td>18</td> <td>AAAT91175</td> <td>Human TAB1 (TAK1) b</td>	18	AAAT91175	Human TAB1 (TAK1) b
3	204	100.0	1560 <td>18</td> <td>AAAT91178</td> <td>Human TAB1 (TAK1) b</td>	18	AAAT91178	Human TAB1 (TAK1) b
4	204	100.0	1560	20	AAAX56278	Human TAB1 encodin
5	204	100.0	1560	21	AAA39106	Human TAB-1 nucleo
6	204	100.0	1568	20	AAAX58310	Human TAB1 encodin
7	204	100.0	1569	20	AAAX56282	Human TAB1-FLAG en
8	204	100.0	3450	25	ABX34568	Human mdt1 cDNA se

X

XX

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein
 XX
 PS Claim 2; Page 25-26; 43pp; Japanese.

XX This sequence encodes the human TAB1 protein.

CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocytic migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.

XX Sequence 1515 BP; 323 A; 457 C; 463 G; 272 T; 0 other;

Query Match 100.0%; Score 204; DB 21; Length 1515;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACGACGACGACGACGACG 60
 Db 1309 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACGACGACGACGACG 1368
 QY 61 TCTGACGGAGGCTTTCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGGAGGCGGT 120
 Db 1369 TCTGACGGAGGCTTTCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGGAGGCGGT 1428
 QY 121 CGTGTTCGAGCCCTATGTGGACTTTGTGAGTTTACCGCCCTCTGGAGCGTGGACATGGC 180
 Db 1429 CGTGTTCGAGCCCTATGTGGACTTTGTGAGTTTACCGCCCTCTGGAGCGTGGACATGGC 1488
 QY 181 GAGCAGAGCGTGTGACAGCACCG 204
 Db 1489 GAGCAGAGCGTGTGACAGCACCG 1512

RESULT 2
 AAT91175
 ID AAT91175 standard; cDNA; 1560 BP.

AC AAT91175;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-APR-1998 (first entry)
 XX
 DE Human TAB1 (TAK1 binding protein) cDNA.

XX TAB1; TAK1 binding protein; transforming growth factor-beta;
 KW signal transduction; human; ds.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 30..1544
 FT /*tag= a
 FT variation 185
 FT /*tag= b
 FT /note= "another clone has adenine at position 185,
 FT with codon AGC (Ser) altered to AGA (Arg)"

XX EP803571-A2.

XX 29-OCT-1997.

XX 24-APR-1997; 97EP-0302808.

XX 20-NOV-1996; 96US-0752891.

PR 24-APR-1996; 96JP-0126282.
 PR 28-OCT-1996; 96JP-0300856.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX Matsumoto K, Nishida E;
 XX WPI: 1997-515318/48.
 DR P-PSDB; AAN26706.
 XX
 XX DNA encoding TAK1 binding protein TAB1 - member of transforming
 PT growth factor beta receptor signal production pathway, which
 PT activates TAK-1 kinase activity upon binding
 XX
 XX Claim 1; Page 17-19; 30pp; English.
 XX This cDNA clone codes for human TAB1 (see AAN26706), a novel member
 CC of the transforming growth factor-beta receptor signal transduction
 CC pathway, which activates TAK-1 kinase activity upon binding. To
 CC obtain the full-length TAB1 coding sequence, a human kidney cDNA
 CC library was screened using as a probe a partial TAB1 cDNA obtained
 CC from a yeast two-hybrid assay for proteins that interacted with
 CC TAK1. The 5' terminus was identified by 5'RACE. 2 Different
 CC clones were sequenced, with cytosine and adenine (see AAT91178) as
 CC the 185th nucleotide, respectively, and deposited as FERM BP-5599
 CC and FERM BP-5508, respectively. Also claimed are: isolated DNA
 CC encoding a protein modified by a substitution, deletion and/or
 CC addition of 1 or more amino acids of the 504-residue TAB1 sequence;
 CC (2) DNA which can hybridize with the 1560 bp nucleic acid sequence;
 CC (3) isolated DNA encoding a protein comprising amino acids 21-579
 CC or 437-504 of the 504 TAB1 sequence; (4) DNA encoding a fusion
 CC protein comprising an above protein or polypeptide; (5) expression
 CC vector comprising an above DNA; and (6) host cell, preferably a
 CC mammalian or yeast cell, transformed by the expression vector.
 CC Cells expressing TAB1 and TAK1 can be used to screen for TGF-beta
 CC signalling pathway inhibitors by contacting the cells with a test
 CC compound, and measuring the TAK1 kinase activity.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 1560 BP; 332 A; 469 C; 480 G; 279 T; 0 other;

Query Match 100.0%; Score 204; DB 18; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACGACGACGACGACGACG 60
 Db 1338 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACGACGACGACGACG 1397
 QY 61 TCTGACGGAGGCTTTCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGGAGGCGGT 120
 Db 1398 TCTGACGGAGGCTTTCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGGAGGCGGT 1457
 QY 121 CGTGTTCGAGCCCTATGTGGACTTTGTGAGTTTACCGCCCTCTGGAGCGTGGACATGGC 180
 Db 1458 CGTGTTCGAGCCCTATGTGGACTTTGTGAGTTTACCGCCCTCTGGAGCGTGGACATGGC 1517
 QY 181 GAGCAGAGCGTGTGACAGCACCG 204
 Db 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 3
 AAT91178
 ID AAT91178 standard; cDNA; 1560 BP.

XX AAT91178;

XX 25-MAR-2003 (updated)

XX 14-APR-1998 (first entry)

XX Human TAB1 (TAK1 binding protein) cDNA.

KW TAB1; TAK1 binding protein; transforming growth factor-beta;
 XX signal transduction; human; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 30..1544
 FT /*tag= a
 FT variation 185
 FT /*tag= b
 FT /note= "another clone has cytosine at position 185,
 FT with codon AGA (Arg) altered to AGC (Ser)."
 XX
 PN EP803571-A2.
 XX
 PD 29-OCT-1997.
 XX
 PF 24-APR-1997; 97EP-0302808.
 XX
 PR 20-NOV-1996; 96US-0752891.
 PR 24-APR-1996; 96JP-0126282.
 PR 28-OCT-1996; 96JP-0300856.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Matsumoto K, Nishida E;
 XX
 DR WPI; 1997-515318/48.
 DR P-PSDB; AAW26707.
 XX
 XX
 PT DNA encoding TAK1 binding protein TAB1 - member of transforming
 PT growth factor beta receptor signal production pathway, which
 PT activates TAK-1 kinase activity upon binding
 XX
 PS Example 5; Page 19-21; 30pp; English.
 XX
 CC This cDNA clone codes for human TAB1 (see AAW26707), a novel member
 CC of the transforming growth factor-beta receptor signal transduction
 CC pathway, which activates TAK-1 kinase activity upon binding. To
 CC obtain the full-length TAB1 coding sequence, a human kidney cDNA
 CC library was screened using as a probe a partial TAB1 cDNA obtained
 CC from a yeast two-hybrid assay for proteins that interacted with
 CC TAK1. The 5' terminus was identified by 5'RACE. 2 Different
 CC clones were sequenced, with cytosine (see AAT91175) and adenine as
 CC the 185th nucleotide, respectively, and deposited as FERM BP-5599
 CC and FERM BP-5508, respectively.
 CC encoding a protein modified by a substitution, deletion and/or
 CC addition of 1 or more amino acids of the 504-residue TAB1 sequence;
 CC (2) DNA which can hybridize with the 1560 bp nucleic acid sequence;
 CC (3) isolated DNA encoding a protein comprising amino acids 21-579
 CC or 437-504 of the 504 TAB1 sequence; (4) DNA encoding a fusion
 CC vector comprising an above protein or polypeptide; (5) expression
 CC mammalian or yeast cell, transformed by the expression vector.
 CC Cells expressing TAB1 and TAK1 can be used to screen for TGF-beta
 CC signalling pathway inhibitors by contacting the cells with a test
 CC compound, and measuring the TAK1 kinase activity.
 CC (Updated on 25-MAR-2003 to correct FA field.)
 XX
 SQ Sequence 1560 BP; 333 A; 468 C; 480 G; 279 T; 0 other;
 Query Match 100.0%; Score 204; DB 18; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGAGAGCAGCTCCAGC 60
 DB 1338 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGAGAGCAGCTCCAGC 1397
 QY 61 TCTGACGAGGAGCTCTTCCGCTCCCGCGCCGCGCCACTCGCTCCCGCTGCGGAGACGGT 120
 DB 1398 TCTGACGAGGAGCTCTTCCGCTCCCGCGCCGCGCCACTCGCTCCCGCTGCGGAGACGGT 1457

QY 121 CGTGTGAGCCCTATGTGGACTTTCGTGAGTTTACCGCTCTGGAGCGTGACCAATGGC 180
 DB 1458 CGTGTGAGCCCTATGTGGACTTTCGTGAGTTTACCGCTCTGGAGCGTGACCAATGGC 1517
 QY 181 GAGCAGAGCGTGTGACAGCACC 204
 DB 1518 GAGCAGAGCGTGTGACAGCACC 1541
 RESULT 4
 AAX56278
 ID AAX56278 standard; DNA; 1560 BP.
 XX
 AC AAX56278;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TAB1 encoding DNA.
 XX
 KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 30..1544
 FT /*tag= a
 XX
 PN WO9921010-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-JP04796.
 XX
 PR 22-OCT-1997; 97JP-0290188.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Ono K, Tsuchiya M;
 DR WPI; 1999-312645/26.
 DR P-PSDB; AAY09541.
 XX
 PT Screening for TGF- beta inhibitory substances, which are useful as
 PT drugs for treatment of diseases relating to its disorder
 XX
 PS Example 1; Page 143-147; 195pp; Japanese.
 XX
 CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors, or activators, or cell proliferation prevention inhibitors or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes human TAB1.
 XX
 SQ Sequence 1560 BP; 332 A; 469 C; 480 G; 279 T; 0 other;
 Query Match 100.0%; Score 204; DB 20; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGAGAGCAGCTCCAGC 60
 DB 1338 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGAGAGCAGCTCCAGC 1397

CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes human TAB1.
 XX
 SQ Sequence 1568 BP; 339 A; 472 C; 477 G; 280 T; 0 other;
 Query Match 100.0%; Score 204; DB 20; Length 1568;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCCGACCTTAACTTACCTTGAAGTCCACCAACGACGACGAGCAGCTCCAGC 1405
 Db 1346 CAAAGCCCGACCTTAACTTGAAGTCCACCAACGACGACGAGCAGCTCCAGC 1405
 QY 61 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTCGGAGGACGCT 120
 Db 1406 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTCGGAGGACGCT 1465
 QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
 Db 1466 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525
 QY 181 GAGCAGAGCGTGTGACAGCACCG 204
 Db 1526 GAGCAGAGCGTGTGACAGCACCG 1549

RESULT 7
 AAX56282
 ID AAX56282 standard; DNA; 1569 BP.
 XX
 AC AAX56282;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TAB1-FLAG encoding DNA.
 XX
 KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..1560
 FT /*tag= a
 XX
 PN WO9921010-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-JP04796.
 XX
 PF 22-OCT-1997; 97JP-0290188.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Ono K, Tsuchiya M;
 XX
 DR WPI; 1999-312645/26.
 DR P-PSDB; AAY09546.
 XX

Screening for TGF- beta inhibitory substances, which are useful as
 drugs for treatment of diseases relating to its disorder
 XX
 PS Example 1; Page 159-163; 195pp; Japanese.
 XX
 CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for

CC indications e.g. as TGF-beta signal transmission inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes TAB1-FLAG from an example of
 CC the present invention.
 XX

SQ Sequence 1569 BP; 343 A; 466 C; 476 G; 284 T; 0 other;

Query Match 100.0%; Score 204; DB 20; Length 1569;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCCGACCTTAACTTACCTTGAAGTCCACCAACGACGACGAGCAGCTCCAGC 60
 Db 1315 CAAAGCCCGACCTTAACTTGAAGTCCACCAACGACGACGAGCAGCTCCAGC 1374
 QY 61 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTCGGAGGACGCT 120
 Db 1375 TCTGACGGAGGCTCTTCCGCTCCCGCCGCGCCACTCGCTCCGCTCGGAGGACGCT 1434
 QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
 Db 1435 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1494
 QY 181 GAGCAGAGCGTGTGACAGCACCG 204
 Db 1495 GAGCAGAGCGTGTGACAGCACCG 1518

RESULT 8
 ABX34568
 ID ABX34568 standard; cDNA; 3450 BP.
 XX
 AC ABX34568;
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human mddt cDNA SEQ ID 129.
 XX
 KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US09944.
 XX

28-MAR-2001; 2001US-279619P.
 29-MAR-2001; 2001US-280067P.
 29-MAR-2001; 2001US-280068P.
 16-MAY-2001; 2001US-291280P.
 17-MAY-2001; 2001US-291829P.
 17-MAY-2001; 2001US-291849P.
 19-JUN-2001; 2001US-299428P.
 20-JUN-2001; 2001US-299776P.
 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX

PR 25-SEP-2000; 2000US-0234398.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249266.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251038.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX Disclosure; SEQ ID NO 12825; 1701pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABAI1004-ABA21534) and proteins
 CC (ABAI4678-ABAI8001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 16977 BP; 3563 A; 4508 C; 4516 G; 4290 T; 0 other;
 SQ
 Query Match 100.0%; Score 204; DB 22; Length 16877;
 Best Local Similarity 100.0%; Pred. No. 5.3e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCGACCTTAACCTTGAGTCCACCAACGACGACGACGACGACGACGACGACG 60
 Db 15011 CAAAGCCGACCTTAACCTTGAGTCCACCAACGACGACGACGACGACGACGACG 15070
 QY 61 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCTCCGCGAGGACGGT 120
 Db 15071 TCTGACGAGGCGCTCTTCGCTCCGCGCGCGCCACTCGCTCCGCTCCGCGAGGACGGT 15130
 QY 121 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACGCTCTGGAGCGTGGACCAATGGC 180
 Db 15131 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACGCTCTGGAGCGTGGACCAATGGC 15190
 QY 181 GAGCAGAGCGTGTGACAGCACCG 204
 Db 15191 GAGCAGAGCGTGTGACAGCACCG 15214
 RESULT 10
 AAL36984
 ID AAL36984 standard; DNA; 16877 BP.
 XX AAL36984;
 XX AC AAL36984;
 XX XX
 DT 08-JAN-2002 (first entry)
 XX Human musculoskeletal system related polynucleotide SEQ ID NO 3349.
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system; ds.
 XX Homo sapiens.
 OS

XX	WO200155367-A1.	PR	27-SEP-2000;	2000US-0235836.
PN		PR	29-SEP-2000;	2000US-0236327.
XX		PR	29-SEP-2000;	2000US-0236367.
PD	02-AUG-2001.	PR	29-SEP-2000;	2000US-0236368.
XX		PR	29-SEP-2000;	2000US-0236369.
PF		PR	29-SEP-2000;	2000US-0236370.
XX		PR	02-OCT-2000;	2000US-0236802.
XX	17-JAN-2001; 2001WO-US01338.	PR	02-OCT-2000;	2000US-0237037.
PR	31-JAN-2000;	PR	02-OCT-2000;	2000US-0237038.
PR	04-FEB-2000;	PR	02-OCT-2000;	2000US-0237039.
PR	24-FEB-2000;	PR	02-OCT-2000;	2000US-0237040.
PR	02-MAR-2000;	PR	13-OCT-2000;	2000US-0239935.
PR	16-MAR-2000;	PR	13-OCT-2000;	2000US-0239937.
PR	17-MAR-2000;	PR	20-OCT-2000;	2000US-0240960.
PR	18-APR-2000;	PR	20-OCT-2000;	2000US-0241221.
PR	19-MAY-2000;	PR	20-OCT-2000;	2000US-0241785.
PR	07-JUN-2000;	PR	20-OCT-2000;	2000US-0241786.
PR	28-JUN-2000;	PR	20-OCT-2000;	2000US-0241808.
PR	30-JUN-2000;	PR	20-OCT-2000;	2000US-0241809.
PR	07-JUL-2000;	PR	20-OCT-2000;	2000US-0241826.
PR	07-JUL-2000;	PR	01-NOV-2000;	2000US-0244617.
PR	11-JUL-2000;	PR	08-NOV-2000;	2000US-0246474.
PR	14-JUL-2000;	PR	08-NOV-2000;	2000US-0246475.
PR	26-JUL-2000;	PR	08-NOV-2000;	2000US-0246476.
PR	26-JUL-2000;	PR	08-NOV-2000;	2000US-0246477.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246478.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246523.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246524.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246525.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000;	PR	08-NOV-2000;	2000US-0246611.
PR	18-AUG-2000;	PR	08-NOV-2000;	2000US-0246613.
PR	22-AUG-2000;	PR	17-NOV-2000;	2000US-0249207.
PR	22-AUG-2000;	PR	17-NOV-2000;	2000US-0249208.
PR	23-AUG-2000;	PR	17-NOV-2000;	2000US-0249209.
PR	30-AUG-2000;	PR	17-NOV-2000;	2000US-0249210.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249211.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	PR	17-NOV-2000;	2000US-0249215.
PR	05-SEP-2000;	PR	17-NOV-2000;	2000US-0249216.
PR	05-SEP-2000;	PR	17-NOV-2000;	2000US-0249217.
PR	06-SEP-2000;	PR	17-NOV-2000;	2000US-0249218.
PR	06-SEP-2000;	PR	17-NOV-2000;	2000US-0249219.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249244.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249264.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249265.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000;	PR	17-NOV-2000;	2000US-0249300.
PR	12-SEP-2000;	PR	01-DEC-2000;	2000US-0250160.
PR	14-SEP-2000;	PR	01-DEC-2000;	2000US-0250391.
PR	14-SEP-2000;	PR	05-DEC-2000;	2000US-0251030.
PR	14-SEP-2000;	PR	05-DEC-2000;	2000US-0251988.
PR	14-SEP-2000;	PR	06-DEC-2000;	2000US-0256719.
PR	14-SEP-2000;	PR	06-DEC-2000;	2000US-0251473.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251856.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251868.
PR	14-SEP-2000;	PR	08-DEC-2000;	2000US-0251869.
PR	21-SEP-2000;	PR	08-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	PR	08-DEC-2000;	2000US-0251990.
PR	25-SEP-2000;	PR	11-DEC-2000;	2000US-0254097.
PR	25-SEP-2000;	PR	05-JAN-2001;	2001US-0259678.
PR	26-SEP-2000;	XX		
PR	27-SEP-2000;	XX		
			(HUNA-) HUMAN GENOME SCI INC.	

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 XX Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 XX
 XX Example 2; SEQ ID NO 3349; 781pp + Sequence Listing; English.
 PS
 XX
 XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (AB03087-AB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 16877 BP; 3563 A; 4508 C; 4516 G; 4290 T; 0 other;
 Query Match 100.0%; Score 204; DB 22; Length 16877;
 Best Local Similarity 100.0%; Pred. No. 5.3e-45;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAAGCCGACCTTAACTGAGCTTCCAGTCCACCAACGACGACGAGCAGCTCCAGC 60
 Db 15011 CAAAGCCGACCTTAACTGAGCTTCCAGTCCACCAACGACGACGAGCAGCTCCAGC 15070
 QY 61 TCTGACGAGGCTTCTCCGCTCCGCGCCGCGCCACTCGCTCCGCTCCGCGAGGAGCGT 120
 Db 15071 TCTGACGAGGCTTCTCCGCTCCGCGCCGCGCCACTCGCTCCGCTCCGCGAGGAGCGT 15130
 QY 121 CGTGTTCAGCCCTATGAGCTTGTGAGCTTTACCGCTCTCGAGGCTGACCATGGC 180
 Db 15131 CGTGTTCAGCCCTATGAGCTTGTGAGCTTTACCGCTCTCGAGGCTGACCATGGC 15190
 QY 181 GAGCAGAGCGTGTGACGACGACCG 204
 Db 15191 GAGCAGAGCGTGTGACGACGACCG 15214
 RESULT 11
 ABX59972
 ID ABX59972 standard; cDNA; 16877 BP.
 XX
 AC ABX59972;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 XX cDNA encoding novel human musculoskeletal system antigen #2316.
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height;
 KW
 KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biorhythm; circadian rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.
 XX
 OS Homo sapiens.
 XX
 PN US2002147140-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 17-JAN-2001; 2001US-0764877.
 XX
 PR 31-JAN-2000; 2000US-179065P.
 PR 04-FEB-2000; 2000US-180628P.
 PR 28-JUN-2000; 2000US-214886P.
 PR 07-JUL-2000; 2000US-216647P.
 PR 07-JUL-2000; 2000US-216880P.
 PR 11-JUL-2000; 2000US-217487P.
 PR 11-JUL-2000; 2000US-217496P.
 PR 14-JUL-2000; 2000US-218290P.
 PR 26-JUL-2000; 2000US-220963P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 14-AUG-2000; 2000US-224518P.
 PR 14-AUG-2000; 2000US-224519P.
 PR 14-AUG-2000; 2000US-225267P.
 PR 14-AUG-2000; 2000US-225268P.
 PR 14-AUG-2000; 2000US-225270P.
 PR 14-AUG-2000; 2000US-225477P.
 PR 14-AUG-2000; 2000US-225757P.
 PR 22-AUG-2000; 2000US-226868P.
 PR 30-AUG-2000; 2000US-228924P.
 PR 01-SEP-2000; 2000US-229287P.
 PR 01-SEP-2000; 2000US-229343P.
 PR 01-SEP-2000; 2000US-229344P.
 PR 01-SEP-2000; 2000US-229345P.
 PR 05-SEP-2000; 2000US-229509P.
 PR 05-SEP-2000; 2000US-229511P.
 PR 08-SEP-2000; 2000US-231413P.
 PR 21-SEP-2000; 2000US-234223P.
 PR 21-SEP-2000; 2000US-234274P.
 PR 25-SEP-2000; 2000US-234997P.
 PR 27-SEP-2000; 2000US-235834P.
 PR 29-SEP-2000; 2000US-236327P.
 PR 29-SEP-2000; 2000US-236367P.
 PR 29-SEP-2000; 2000US-236368P.
 PR 29-SEP-2000; 2000US-236369P.
 PR 29-SEP-2000; 2000US-236370P.
 PR 02-OCT-2000; 2000US-236802P.
 PR 02-OCT-2000; 2000US-237037P.
 PR 02-OCT-2000; 2000US-237038P.
 PR 02-OCT-2000; 2000US-237039P.
 PR 13-OCT-2000; 2000US-237040P.
 PR 20-OCT-2000; 2000US-239935P.
 PR 20-OCT-2000; 2000US-240960P.
 PR 20-OCT-2000; 2000US-241785P.
 PR 20-OCT-2000; 2000US-241809P.
 PR 01-NOV-2000; 2000US-244617P.
 PR 17-NOV-2000; 2000US-249299P.
 PR 08-DEC-2000; 2000US-251856P.
 PR 08-DEC-2000; 2000US-251868P.
 XX
 (ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.
 Rosen CA, Ruben SM, Barash SC;

ABQ56072
 ID ABQ56072 standard; cDNA; 670 BP.
 XX AC ABQ56072;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HPDWT55 cDNA, SEQ ID NO:1952.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 XX 07-JUN-2001; 2001WO-US18569.
 XX
 PF 07-JUN-2000; 2000US-209467P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Birse CE, Rosen CA;
 XX
 PI WPI; 2002-147878/19.
 XX
 DR P-PSDB; ABP42995.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer); immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 1; SEQ ID No 1952; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 670 BP; 103 A; 210 C; 226 G; 126 T; 5 other;
 XX
 Query Match 18.2%; Score 37.2; DB 24; Length 670;
 Best Local Similarity 50.0%; Pred. No. 1.2;
 Matches 93; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
 XX
 QY 14 TAACCTGTCAGTCCACCAACAGCAGCAGCAGCAGCAGCTTCCAGCTTCTGACGAGGCC 73
 Db 190 TCACCGAGCAGGTCTTCAATGAGGCTCTTGCCATCAGCTGCAACCCAGTGCAGGCGGCCA 249
 QY 74 TCTTCCGCTCCGCGCCGCCACTGCTCCCGCTGCGCAGCAGCGTCTGTGAGCCCT 133
 Db 250 TGTACTCTCTCCCGCGGTGCGAGTGCCTCCCGCGCGGTGCGCGGCTCAGGAGCTGG 309
 QY 134 ATGTGGACTTTGCTGAGTTTACCGCTCTTGAGCGCTTGACCATGGCGCAGCAGCGTGG 193
 Db 310 GCCTGGCCCCGATATGTTCTTCTGCTGCGCTCTTGAGGACCGGCATCTGCGTGG 369
 QY 194 TGACAG 199
 Db 370 TGCCAG 375
 XX
 RESULT 14
 AAV16790
 ID AAV16790 standard; cDNA; 1485 BP.
 XX AC AAV16790;
 XX
 DT 24-JUN-1998 (first entry)
 XX
 DE cDNA encoding a human mutant alanine aminotransferase.
 XX KW Alanine aminotransferase; mutation; human; ss.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1485
 FT /*tag= a
 FT /note= "no stop codon given"
 XX
 PN JPI0075787-A.
 XX
 PD 24-MAR-1998.
 XX
 PF 02-SEP-1996; 96JP-0231540.
 XX
 PR 02-SEP-1996; 96JP-0231540.
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 1998-244361/22.
 DR P-PSDB; AAW46904.
 XX
 PT Recombinant mutant of human alanine aminotransferase - in which at
 PT least five N-terminal residues are deleted
 XX
 PS Claim 1; Pages 7-9; lipp; Japanese.
 XX
 CC The present sequence encodes a human mutant alanine aminotransferase
 CC (HALT) in which at least 5 amino acids at the N-terminus are deleted.
 CC The mutant enzyme retains HALT activity. The mutant HALT can be used
 CC to identify individuals carrying the mutant form and to investigate
 CC the consequences of carrying this mutation.
 XX
 SQ Sequence 1485 BP; 257 A; 469 C; 503 G; 256 T; 0 other;
 XX
 Query Match 18.2%; Score 37.2; DB 19; Length 1485;
 Best Local Similarity 50.0%; Pred. No. 1.4;
 Matches 93; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 14 TAAACCTGCAGTCCACCAACGACACGACGAGCAGCTCCAGCTCTGACGGAGGCC 73
Db 1172 TCACCGAGCAGGTCTTCAATGAGGCTTCCTGGCATCAGCTGCAACCCAGTGCAGGGCGCCA 1231
QY 74 TCTTCCGCTCCCGGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGTCTGTTGAGCCCT 133
Db 1232 TGTACTCTTCCCGCGGTGCAGCTGCCCGCGGGCGGTGGAGCGGCTCAGGAGCTGG 1291
QY 134 ATGTGACATTTGCTGAGTTTACCGCTCTGAGCGCTGACCAATGGCGGAGCAGAGCTGG 193
Db 1292 GCCTGGCCCCGATATGTTCTTCTGCTGGCGCTCTCTGGAGGAGACCGGCATCTGCGTGG 1351
QY 194 TGACAG 199
Db 1352 TGCCAG 1357

RESULT 15

AAV39457
ID AAV39457 standard; cDNA; 1505 BP.

XX AAV39457;

XX AC

XX DT

XX 15-OCT-1998 (first entry)

XX DE Modified human alanine aminotransferase encoding cDNA.

XX KW Human; alanine aminotransferase; ALT; modified; liver disease;

XX OS viral hepatitis; hepatic cirrhosis; gene therapy; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key

XX CDS Location/Qualifiers

XX FT 9..1499

XX FT /*tag= a

XX FT /product= "modified alanine aminotransferase"

XX PA WO9830703-A1.

XX PD 16-JUL-1998.

XX PF 19-SEP-1997; 97WO-JP03339.

XX PR 09-JAN-1997; 97JP-0013282.

XX PA (ORF1) ORIENTAL YEAST CO LTD.

XX PI Eto A, Funatsu M, Matsuo Y, Nakamura A, Tanaka T;

XX PI Tanase S;

XX WPI; 1998-399148/34.

XX DR P-PSDB; AAW62267.

XX PT Gene for modified human alanine amino-transferase with improved

XX PT activity - and production of enzyme by culture of Escherichia coli

XX PT transformed with gene

XX PS Claim 1; Page 13-16/1; 37pp; Japanese.

XX CC The present sequence encodes a modified human alanine aminotransferase

XX CC (ALT) which has improved activity over the wild-type enzyme, and in

XX CC which the following five changes have been made: 4-SER, 5-THR, 7-ASP,

XX CC 39-GLY and 222-ALA. ALT is an enzyme which is depleted or absent from

XX CC serum in patients with liver diseases such as viral hepatitis and

XX CC hepatic cirrhosis. The recombinant modified ALT may be used in treatment

XX CC of these diseases, and the DNA (with a suitable vector) as gene therapy.

XX SQ Sequence 1505 BP; 266 A; 466 C; 507 G; 266 T; 0 other;

Query Match 18.2%; Score 37.2; DB 19; Length 1505;

Best Local Similarity 50.0%; Pred. No. 1.4;

Matches 93; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 14 TAAACCTGCAGTCCACCAACGACACGACGAGCAGCTCCAGCTCTGACGGAGGCC 73
Db 1183 TCACCGAGCAGGTCTTCAATGAGGCTTCCTGGCATCAGCTGCAACCCAGTGCAGGGCGCCA 1242
QY 74 TCTTCCGCTCCCGGGCCCGCCCACTCGCTCCCGCTGGCGAGGACGGTCTGTTGAGCCCT 133
Db 1243 TGTACTCTTCCCGCGGTGCAGCTGCCCGCGGGCGGTGGAGCGGCTCAGGAGCTGG 1302
QY 134 ATGTGACATTTGCTGAGTTTACCGCTCTGAGCGCTGACCAATGGCGGAGCAGAGCTGG 193
Db 1303 GCCTGGCCCCGATATGTTCTTCTGCTGGCGCTCTCTGGAGGAGACCGGCATCTGCGTGG 1362
QY 194 TGACAG 199
Db 1363 TGCCAG 1368

Search completed: December 4, 2003, 05:02:29
Job time : 107.986 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:36:53 : Search time 25.2703 Seconds
(without alignments)
3563.166 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 204

Sequence: 1 caaagccgacctaaccct.....agacgtggtagacagaccg 204

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	1560	2	US-08-752-891-1 Sequence 1, Appli
2	204	100.0	1560	2	US-08-752-891-5 Sequence 5, Appli
3	204	100.0	1560	2	US-09-144-178-1 Sequence 1, Appli
4	204	100.0	1560	2	US-09-144-178-5 Sequence 5, Appli
5	204	100.0	1560	3	US-09-406-854-1 Sequence 1, Appli
6	204	100.0	1560	3	US-09-406-854-5 Sequence 5, Appli
7	204	100.0	1560	4	US-09-529-279-1 Sequence 1, Appli
8	204	100.0	1560	4	US-10-158-895-1 Sequence 1, Appli
9	204	100.0	1568	4	US-09-529-279-42 Sequence 42, Appli
10	204	100.0	1568	4	US-10-158-895-42 Sequence 42, Appli
11	204	100.0	1569	4	US-09-529-279-10 Sequence 10, Appli
12	204	100.0	1569	4	US-10-158-895-10 Sequence 10, Appli
13	37.2	18.2	1278	4	US-09-252-991A-4932 Sequence 4932, Ap
14	37.2	18.2	1491	2	US-08-941-647A-4 Sequence 4, Appli
15	37.2	18.2	1505	4	US-09-142-481-1 Sequence 1, Appli
16	37.2	18.2	1878	4	US-09-252-991A-4933 Sequence 4933, Ap
17	37.2	18.2	2211	4	US-09-252-991A-4927 Sequence 4927, Ap
18	35.4	17.4	762	4	US-09-252-991A-3481 Sequence 3481, Ap
19	35.4	17.4	1203	4	US-09-252-991A-3468 Sequence 3468, Ap
20	35.4	17.4	1269	4	US-09-252-991A-3470 Sequence 3470, Ap
21	33.8	16.6	47981	4	US-09-679-279-1 Sequence 1, Appli
22	33.6	16.5	81001	4	US-09-679-279-1 Sequence 1, Appli
23	31.2	15.3	4403765	3	US-09-750-580-1 Sequence 1, Appli
24	31.2	15.3	4411529	3	US-09-103-840A-2 Sequence 2, Appli
25	31	15.2	1101	4	US-09-103-840A-1 Sequence 1, Appli
26	31	15.2	1173	3	US-09-152-060-23 Sequence 23, Appli
27	31	15.2	1473	4	US-08-706-216-5 Sequence 5, Appli
					Sequence 43, Appli

28	31	15.2	4092	2	US-08-469-537A-106 Sequence 106, App
29	30.8	15.1	408	4	US-09-252-991A-16497 Sequence 16497, A
c 30	30.8	15.1	417	4	US-09-252-991A-16104 Sequence 16104, A
c 31	30.8	15.1	753	4	US-09-252-991A-16000 Sequence 16000, A
c 32	30.8	15.1	855	4	US-09-252-991A-16209 Sequence 16209, A
c 33	30.8	15.1	4411529	3	US-09-103-840A-1 Sequence 1, Appli
34	30.6	15.0	540	4	US-09-252-991A-7104 Sequence 7104, Ap
35	30.6	15.0	1041	2	US-08-580-545B-5 Sequence 5, Appli
36	30.6	15.0	1041	3	US-09-262-653A-5 Sequence 5, Appli
c 37	30.6	15.0	1494	4	US-09-252-991A-7049 Sequence 7049, Ap
c 38	30.6	15.0	4236	4	US-09-252-991A-7057 Sequence 7057, Ap
c 39	30.6	15.0	10023	3	US-09-252-991A-6997 Sequence 6997, Ap
c 40	30.6	15.0	44377	2	US-08-804-227C-7 Sequence 7, Appli
c 41	30.6	15.0	44377	2	US-08-804-198-1 Sequence 1, Appli
c 42	30.6	15.0	4403765	3	US-09-103-840A-2 Sequence 2, Appli
c 43	30.4	14.9	507	4	US-09-252-991A-15900 Sequence 15900, A
c 44	30.4	14.9	639	4	US-09-252-991A-15846 Sequence 15846, A
45	30.4	14.9	1063	3	US-09-077-675A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-752-891-1
; Sequence 1, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION: - ~~16209~~ 11/17/98
; APPLICANT: MATSUMOTO, Kunihiro
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1541
; FEATURE:
; NAME/KEY: mat_peptide

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; LOCATION: 30..1541
US-08-752-891-1

Query Match          100.0%; Score 204; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGCCGACCTTAAACCTTGAGTCCACCAACACGACACGACAGCAGCAGCTCCAGC 60
Db 1338 CAAGCCGACCTTAAACCTTGAGTCCACCAACACGACACGACAGCAGCAGCTCCAGC 1397

Qy 61 TCTGACGGAGGCGCTTTCCGCTCCCGCGCCGCCACTCGCTCCCGCTGCGGAGGACGT 120
Db 1398 TCTGACGGAGGCGCTTTCCGCTCCCGCGCCGCCACTCGCTCCCGCTGCGGAGGACGT 1457

Qy 121 CGTGTTCAGCGCCATATGTGGACTTTTGTCTGAGTTTTACCGCCTCTGGAGCGTGGACCATGGC 180
Db 1458 CGTGTTCAGCGCCATATGTGGACTTTTGTCTGAGTTTTACCGCCTCTGGAGCGTGGACCATGGC 1517

Qy 181 GACGACAGCGTGGTGACAGCACCG 204
Db 1518 GACGACAGCGTGGTGACAGCACCG 1541

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RESULT 2
US-08-752-891-5
: Sequence 5, Application US/08752891
: Patent No. 5837819
: GENERAL INFORMATION:
: APPLICANT: MATSUMOTO, Kunihiro
: APPLICANT: NISHIDA, Eisuke
: TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/752,891
: FILING DATE: 20-NOV-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 8-300856
: FILING DATE: 28-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 8-126282
: FILING DATE: 24-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 17981/111
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1560 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 30..1541
: FEATURE:

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; NAME/KEY: mat_peptide
; LOCATION: 30..1541
US-08-752-891-5

Query Match      100.0%; Score 204; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db    1338 CAAAGCCGACCTTAACCCTGGAGTCCACCAACAGCACGAGCAGCGACTCCAGC 1397

Qy    61   TCTGAGGGAGGCCTCTTCGGCTCCCGGCCCGGCCACTCGTCCCGGCTCGCGAGGACGGT 120
      |||
Db    1398 TCTGAGGGAGGCCTCTTCGGCTCCCGGCCCGGCCACTCGTCCCGCTCGCGAGGACGGT 1457

Qy    121  CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGGCTCTGGAGCGCTGGACCATGGC 180
      |||
Db    1458 CGTGTTGAGCCCTATGTGACATTTCGTGAGTTTACCGGCTCTGGAGCGCTGGACCATGGC 1517

Qy    181  GAGCAGAGCGTGGTGACAGCACCG 204

Db    1518 GAGCAGAGCGTGGTGACAGCACCG 1541
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RESULT 3
US-09-144-178-1
; Sequence 1, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:

102e

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; NAME/KEY: CDS
; LOCATION: 30..1541
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 30..1541
US-09-144-178-1

Query Match      100.0%; Score 204; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 3e-45; 0; Indels 0; Gaps 0;
Matches 204; Conservative 0; Mismatches 0;

QY      1  CAAGGCCGACCTTAACCTCGAGTCCACCAACACGACACACGACGACGAGTCCAGC 60
      |||
Db      1338  CAAGGCCGACCTTAACCTCGAGTCCACCAACGACACGACGACGAGTCCAGC 1397
      |||

QY      61  TCTGACGGAGGCGCTCTTCGCTCCCGGCGCGCCACTCGCTCCGCTCCGCGAGGACGTT 120
      |||
Db      1398  TCTGACGGAGGCGCTCTTCGCTCCCGGCGCGCCACTCGCTCCGCGAGGACGTT 1457
      |||

QY      121  CGTGTTGAGCCCTATGCGACCTTTGCTGAGTTTTACGCGCTCTGGAGCGTGGACCATGGC 180
      |||
Db      1458  CGTGTTGAGCCCTATGCGACCTTTGCTGAGTTTTACGCGCTCTGGAGCGTGGACCATGGC 1517
      |||

QY      181  GAGCAGAGCGTGGTGACAGCACCG 204
      |||
Db      1518  GAGCAGAGCGTGGTGACAGCACCG 1541
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; Sequence 5, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs

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1022

RESULT 12
US-10-158-895-10
; Sequence 10, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895

	Query Match	Best Local Similarity	Matches	18.2%;	Score 37.2;	DB 4;	Length 1278;			
			66;	Conservative	0;	Mismatches	48;	Indels	Gaps	0;
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QY	124	GTTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCTCTGGAGCGTGGACCAT	177							
Db	631	GCGGGAACCGGCTCTCGCGCTTTGAGCAGCAGCGGCACGTCCGCGCGCTAGACCTT	578							

RESULT 15
US-09-142-481-1
; Sequence 1, Application US/09142481
; Patent No. 6316238
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Atsuo
; APPLICANT: TANAKA, Toshio
; APPLICANT: MATSUO, Yushi
; APPLICANT: TANASE, Sumio
; APPLICANT: FUNATSU, Masahiko
; APPLICANT: ETO, Akira
; TITLE OF INVENTION: PROCESS FOR PRODUCING ACTIVE HUMAN ALT
; FILE REFERENCE: NAKAMURA=14
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/03339
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: JP 9-13282
; PRIOR FILING DATE: 1997-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1496)
US-09-142-481-1

Query Match 18.2%; Score 37.2; DB 4; Length 1505;
Best Local Similarity 50.0%; Pred. No. 0.3;
Matches 93; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 14 TAACCTGAGTCCACCAACGACGACGAGCAGAGCAGCTCCAGCTTCAGCGAGGCC 73
Db 1183 TCACCGAGCAGTCTTCAATGAGGCTCTCTGGCATCAGCTGCAACCCAGTGCAGGGCGCCA 1242
QY 74 TCTTCGGCTCCCGCGCGCCCACTCGCTCCCGCTGGCGAGGACGCTCGTTGAGCCCT 133
Db 1243 TGTACTCTCTCCCGCGCGTGCAGCTGCCCGCGCGGTGGAGCGGCTCAGGAGCTGG 1302
QY 134 ATGTGAGCTTTGCTGAGTTTACCGCTCTGAGGCGTGGACCATGGCGAGCAGAGCGTGG 193
Db 1303 GCCTGGCCCCCATATGTTCTCTGCTGCGCTCTCTGGAGGAGACCGGCATCTGCGTGG 1362
QY 194 TGACAG 199
Db 1363 TGCCAG 1368
Search completed: December 4, 2003, 07:06:45
Job time : 34.2703 secs

RESULT 14
US-08-941-647A-4
; Sequence 4, Application US/08941647A
; Patent No. 5952211
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, ATSUO
; APPLICANT: TANAKA, TOSHIO
; APPLICANT: MATSUO, YUSHI
; APPLICANT: TANASE, SUMIO
; APPLICANT: FUNATSU, MASAHIKO
; APPLICANT: ETO, AKIRA
; TITLE OF INVENTION: METHOD FOR PRODUCING ACTIVE HUMAN
; TITLE OF INVENTION: ALANINE AMINOTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,647A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/533,717
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 6-269119
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7335-001-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-941-647A-4

Query Match 18.2%; Score 37.2; DB 2; Length 1491;
Best Local Similarity 50.0%; Pred. No. 0.3;
Matches 93; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 14 TAACCTGAGTCCACCAACGACGACGAGCAGCTCCAGCTTCAGCGAGGCC 73
Db 1175 TCACCGAGCAGTCTTCAATGAGGCTCTCTGGCATCAGCTGCAACCCAGTGCAGGGCGCCA 1234
QY 74 TCTTCGGCTCCCGCGCGCCCACTCGCTCCCGCTGGCGAGGACGCTCGTTGAGCCCT 133
Db 1235 TGTACTCTCTCCCGCGGTGAGTGGCGCGGTGGAGCGGCTCAGGAGCTGG 1294
QY 134 ATGTGAGCTTTGCTGAGTTTACCGCTCTGAGGCGTGGACCATGGCGAGCAGAGCGTGG 193
Db 1295 GCCTGGCCCCCATATGTTCTCTGCTGCGCTCTCTGGAGGAGACCGGCATCTGCGTGG 1354
QY 194 TGACAG 199
Db 1355 TGCCAG 1360

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 06:12:04 ; Search time 304.392 Seconds
(without alignments)
2227.439 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 204

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	1560	12	US-10-384-743-1
2	204	100.0	1560	13	Sequence 1, Appli
3	204	100.0	1560	13	Sequence 1, Appli
4	204	100.0	1560	13	Sequence 5, Appli
5	204	100.0	1568	12	Sequence 1, Appli
6	204	100.0	1568	13	Sequence 42, Appli
7	204	100.0	1568	13	Sequence 10, Appli
8	204	100.0	1569	13	Sequence 10, Appli
9	204	100.0	16877	10	Sequence 3349, Ap
10	203.6	99.8	696	10	Sequence 330, App
11	199.2	97.6	409	11	Sequence 32946, A
12	36.8	18.0	2036	10	Sequence 17, Appli
13	36.4	17.8	591	14	Sequence 289, App
14	36.4	17.8	2380	14	Sequence 864, App
15	36.2	17.7	2922	14	Sequence 1749, Ap
16	36.2	17.7	9025608	14	Sequence 1, Appli

c 17	35.4	17.4	975	12	US-10-027-632-10526	Sequence 10526, A
c 18	35.4	17.4	975	13	US-10-027-632-10526	Sequence 10526, A
c 19	35.2	17.3	14643	14	US-10-156-761-931	Sequence 931, App
c 20	35	17.2	5811	13	US-10-002-600-15	Sequence 15, Appl
c 21	34.8	17.1	1275	14	US-10-156-761-5872	Sequence 5872, Ap
c 22	34.4	16.9	1089	14	US-10-156-761-6553	Sequence 6553, Ap
c 23	34.4	16.9	1287	10	US-09-887-576-806	Sequence 806, Appli
c 24	34.4	16.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 25	33.8	16.6	1011	12	US-10-259-165-521	Sequence 521, App
c 26	33.6	16.5	1128	14	US-10-156-761-6376	Sequence 6376, Ap
c 27	33.6	16.5	547	12	US-10-029-386-12487	Sequence 12487, A
c 28	33.6	16.5	933	14	US-10-156-761-6779	Sequence 6779, Ap
c 29	33.6	16.5	81001	10	US-09-751-877-1	Sequence 1, Appli
c 30	33.6	16.5	81001	11	US-09-842-364-1	Sequence 1, Appli
c 31	33.6	16.5	1691139	14	US-10-067-514-1	Sequence 1, Appli
c 32	33	16.2	460	10	US-09-896-791B-1	Sequence 1, Appli
c 33	33	16.2	28066	12	US-10-017-161-2395	Sequence 2395, Ap
c 34	32.8	16.1	1125	14	US-10-156-761-6007	Sequence 6007, Ap
c 35	32.4	15.9	2640	12	US-09-814-353-19681	Sequence 19681, A
c 36	32.4	15.9	14654	9	US-09-764-860-1054	Sequence 1054, Ap
c 37	32.4	15.9	14654	12	US-10-212-872-1054	Sequence 1054, Ap
c 38	32.4	15.9	14654	14	US-10-074-095-1054	Sequence 1054, Ap
c 39	32.2	15.8	1737	14	US-10-156-761-3579	Sequence 3579, Ap
c 40	31.8	15.6	566	10	US-09-917-800A-960	Sequence 960, App
c 41	31.8	15.6	693	14	US-10-156-761-6496	Sequence 6496, Ap
c 42	31.6	15.5	2838	14	US-10-156-761-6936	Sequence 6936, Ap
c 43	31.4	15.4	1740	14	US-10-156-761-1087	Sequence 1087, Ap
c 44	31.2	15.3	858	12	US-10-027-632-28569	Sequence 28569, A
c 45	31.2	15.3	858	13	US-10-027-632-28569	Sequence 28569, A

ALIGNMENTS

RESULT 1

US-10-384-743-1
; Sequence 1, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MAGAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278 US/10/384,743
; CURRENT APPLICATION NUMBER: 2003-03-11
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)...(1541)
US-10-384-743-1

Query Match 100.0%; Score 204; DB 12; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGAGCAGCTCCAGC	60
DB	1338	CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGAGCAGCTCCAGC	1397
QY	61	TCTGACGAGGCTTCTCGCTCCGCGCCGCCACTCGCTCCCGGAGGACCGT	120

Db 1398 TCTGACGAGCGCTCTTCCGCTCCCGCGCCGACCTCGCTCCCGCTGGCGAGGACGGT 1457
QY 121 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 180
Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 1517
QY 181 GAGCAGAGCGTGTGGTACAGCACCG 204
Db 1518 GAGCAGAGCGTGTGGTACAGCACCG 1541

RESULT 2

US-10-123-427-1
; Sequence 1, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/123,427
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE: <Unknown>
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-123-427-1

Query Match 100.0%; Score 204; DB 13; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAAGCCGACCTTAACCTGCTCCAGTCCACACGACGACGAGCAGCAGCTCCAGC 60

Db 1338 CAAAGCCGACCTTAACCTGCTCCAGTCCACACGACGACGAGCAGCAGCTCCAGC 1397
QY 61 TCTGACGAGCGCTCTTCCGCTCCCGCGCCGACCTCGCTCCCGCTGGCGAGGACGGT 120
Db 1398 TCTGACGAGCGCTCTTCCGCTCCCGCGCCGACCTCGCTCCCGCTGGCGAGGACGGT 1457
QY 121 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 180
Db 1458 CGTGTTCAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTCGAGCGTGGACCATGGC 1517
QY 181 GAGCAGAGCGTGTGGTACAGCACCG 204
Db 1518 GAGCAGAGCGTGTGGTACAGCACCG 1541

RESULT 3

US-10-123-427-5
; Sequence 5, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/123,427
FILING DATE: 17-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE: <Unknown>
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:

NAME/KEY: mat_peptide
LOCATION: 30..1541
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-123-427-5

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Query Match      100.0%; Score 204; DB 13; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
DB 1338 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1397

QY 61 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 120
DB 1398 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 1457

QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
DB 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517

QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
DB 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 4
US-10-158-895-1
; Sequence 1, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1541)
US-10-158-895-1

Query Match      100.0%; Score 204; DB 13; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
DB 1338 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1397

QY 61 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 120
DB 1398 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 1457

QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
DB 1458 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1517

QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
DB 1518 GAGCAGAGCGTGGTGACAGCACCG 1541

RESULT 5
US-10-384-743-42
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; Sequence 42, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 1568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(1549)
US-10-384-743-42

Query Match      100.0%; Score 204; DB 12; Length 1568;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 60
DB 1346 CAAGCCCGACCTTAAACCTTGAGTCCACCAACGACGACGACGAGCAGCTCCAGC 1405

QY 61 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 120
DB 1406 TCTGACGAGGCGCTTCCGCTCCCGGCCCGCCCACTCGCTCCCGCTGGCGAGGACCGT 1465

QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
DB 1466 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525

QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
DB 1526 GAGCAGAGCGTGGTGACAGCACCG 1549

RESULT 6
US-10-158-895-42
; Sequence 42, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 1568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (11)..(1549)
US-10-158-895-42

Query Match 100.0%; Score 204; DB 13; Length 1568;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 60
Db 1346 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 1405

QY 61 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 120
Db 1406 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 1465

QY 121 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 180
Db 1466 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1525

QY 181 GAGCAGAGCGTGGTGACGACCG 204
Db 1526 GAGCAGAGCGTGGTGACGACCG 1549

RESULT 7

US-10-384-743-10
; Sequence 10, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-10-384-743-10

Query Match 100.0%; Score 204; DB 12; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 60
Db 1315 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 1374

QY 61 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 120
Db 1375 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 1434

QY 121 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 180
Db 1435 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1494

QY 181 GAGCAGAGCGTGGTGACGACCG 204
Db 1495 GAGCAGAGCGTGGTGACGACCG 1518

RESULT 8

US-10-158-895-10
; Sequence 10, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-10-158-895-10

Query Match 100.0%; Score 204; DB 13; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 60
Db 1315 CAAAGCCGACCTTAACCTGAGTCCAGTCCACCAACGACGACGAGAGAGAGTCCAGC 1374

QY 61 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 120
Db 1375 TCTGACGAGGCGCTTCCGCTCCCGCCGCGCCCACTCGCTCCCGCTGGGAGGAGCGT 1434

QY 121 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 180
Db 1435 CGTGTGAGCCCTAATGAGTCTTGGTCTGAGTTTACCGCCCTCTGGAGCGTGGACCATGGC 1494

QY 181 GAGCAGAGCGTGGTGACGACCG 204
Db 1495 GAGCAGAGCGTGGTGACGACCG 1518

RESULT 9

US-09-764-877-3349
; Sequence 3349, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3349

Query Match 100.0%; Score 204; DB 10; Length 16877;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;

	Matches	204;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CAAAGCCCGACCTTAA	CCCTGCA	GTCCAA	CAACACACAGCAGCAGCAGCTCCAGC	60				
Db	15011	CAAAGCCCGACCTTAA	CCCTGCA	GTCCAA	CAACACACAGCAGCAGCAGCTCCAGC	15070				
Qy	61	TCGTGCGGAGGCGCTCT	CCGCTC	CCGGCGCGGCCA	CTGCCTCCGCGCTGGCGAGACCGT	120				
Db	15071	TCGTGCGGAGGCGCTCT	CCGCTC	CCGGCGCGGCCA	CTGCCTCCGCGCTGGCGAGACCGT	15130				
Qy	121	CGTGTTGAGCCCTATG	TGGACT	TTCCTGAG	TTTACCGCCTCTGGAGCGTGGACCATGGC	180				
Db	15131	CGTGTTGAGCCCTATG	TGGACT	TTCCTGAG	TTTACCGCCTCTGGAGCGTGGACCATGGC	15190				
Qy	181	GAGCAGAGCGTG	TGACAG	CACCG	CCG	204				
Db	15191	GAGCAGAGCGTG	TGACAG	CACCG	CCG	15214				

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RESULT 10
US-09-925-300-330
; Sequence 330, Application US/09925300
; Patent NO. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (657)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (685)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-330

```

```

RESULT 11
US-09-918-995-32946
; Sequence 32946, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32946
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-32946

Query Match      97.6%; Score 199.2; DB 11; Length 409;
Best Local Similarity 98.5%; Pred. No. 4.4e-50;
Matches 201; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CAAAGCCCGACCTTAAACCTCGAGTCACCAACGACGACGACGACGACGCTCCAGC 60
Db      48  CAAAGCCCGACCTTAAACCTGCGAGCCACCAACACGACGACGACGCTCCAGC 107

Qy      61  TCTGACGGAGGCGCTTTCGCGTCCTCCGCGCCGCGCCACTCGCTCCCGCTGCGGAGGACGT 120
Db      108  TCTGACGGAGGCGCTTTCGCGTCCTCCGCGCCGCGCCACTCGCTCCCGCTGCGGAGGACGT 167

Qy      121  CGTGTTGAGCCCTATGTGGAATTGTGAGTTTACGCCCTCTGGAGCGTGAGCATGGC 180
Db      168  CGTGTTGAGCCCTATGTGGAATTGTGAGCTTTACGCCCTCTGGAGCGTGGACCATGGC 227

Qy      181  GAGCAGAGCGTGGTGACGACCG 204
Db      228  GAGCAGAGCGGTTGACGACCG 251

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```

RESULT 12
US-09-866-582-17
; Sequence 17, Application US/09866582
; Patent No. US20020127620A1
; GENERAL INFORMATION:
; APPLICANT: Witman, George B.
; APPLICANT: Pazour, Gregory J.
; APPLICANT: Rosenbaum, Joel L.
; APPLICANT: Cole, Douglas G.
; TITLE OF INVENTION: INTRAFAGELLAR TRANSPORT
; FILE REFERENCE: 07917-145001
; CURRENT APPLICATION NUMBER: US/09/866,582
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,923
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1517)
US-09-866-582-17

Query Match      18.0%; Score 36.8; DB 10; Length 2036;
Best Local Similarity 54.4%; Pred. No. 0.16;
Matches 74; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 51 CAGCTCCAGCTCTGACGGAGCGCTCTTTCGCTCCCGCGCCACTGCTCCGCGCTGG 110

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Db 812 CTGCATCAACTGGCGGCGCCCTTCATCCGCTCTCTCGTCACTCGAGCACCTGCCGCT 871
Qy 111 CGAGGAGCGTGTGTGAGCCCTATGTGACTTTGTGAGTTTACCGCTCTGGAGCGT 170
Db 872 GGTGGAGTTTGTAGCTGGAGCGGCGGTGTGACGAGGAGGCGGCGGCTGTGGGCGA 931
Qy 171 GGACCATGGGAGCAG 186
Db 932 GGAGCGGGCATGGAG 947

RESULT 13
US-10-101-464A-289
; Sequence 289, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-289

Query Match 17.8%; Score 36.4; DB 14; Length 591;
Best Local Similarity 50.6%; Pred. No. 0.19;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 30 CAACACGACACGAGGAGCAGCTCAGCTCTGACGAGGCGCTCTTCGCTCCCGGCC 89
Db 364 CAAGTCCACCCCGGAGCTTCGACGCTCCGTCGAGGCGACCCCTCTCTTCAGCTGGC 423
Qy 90 CGGCCACTCGCTCCCGCTGGCGAGGAGCGTGTGAGCCCTATGTGACTTTGTCTGA 149
Db 424 CTCCTCCGCTCCCGCTCCCGCTCCGTCGAGGCGGCGGCTCTCTTCAGCTTTTCGC 483
Qy 150 GTTTTACCGCTCTGGAGCGTGGACCATGCGGAGGAGCGGTGTGACAGCACC 203
Db 484 CTTCTCCGCGAGCGGAGCGGAGCGTGTCTCTTACAGCATGCGGAGCGGCTGG 537

RESULT 14
US-10-101-464A-864
; Sequence 864, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
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; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 864
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-864

Query Match 17.8%; Score 36.4; DB 14; Length 2380;
Best Local Similarity 50.6%; Pred. No. 0.21;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 30 CAACACGACACGAGGAGCAGCTTCAGCTCTGACGAGGCGCTTCGCTCCCGGCC 89
Db 364 CAAGTCCACCCCGGAGCTTCGACGCTCCGTCGAGGCGACCCCTCTCTTCAGCTGGC 423
Qy 90 CGGCCACTCGCTCCCGCTGGCGAGGAGCGTGTGAGCCCTATGTGACTTTGTCTGA 149
Db 424 CTCCTCCGCTCCCGCTCCCGCTCCGTCGAGGCGGCGGCTCTCTTCAGCTTTTCGC 483
Qy 150 GTTTTACCGCTCTGGAGCGTGGACCATGCGGAGGAGCGGTGTGACAGCACC 203
Db 484 CTTCTCCGCGAGCGGAGCGGAGCGTGTCTCTTACAGCATGCGGAGCGGCTGG 537

RESULT 15
US-10-156-761-1749
; Sequence 1749, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1749
; LENGTH: 2922
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; LOCATION: (1)...(2922)
US-10-156-761-1749

Query Match 17.7%; Score 36.2; DB 14; Length 2922;
Best Local Similarity 49.7%; Pred. No. 0.24;
Matches 92; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 11 CTTTACCTTCGAGTCCACCAACGACGACGAGGAGGAGCTTCAGCTTCAGCGAG 70
Db 194 CTTGGACCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
Qy 71 GCCTTTTCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 130
Db 254 GAGAGTTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 313
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Qy	131	CCTATGTGGACTTTGCTGAGTTTACCGCCTCTGGAGCGTGGACCAATGGCGAGCAGCG	190
Db	314	ACGTCCCGCGGAGTGGCGGACCGCGGTGCTCTCCGGTGGGCCCGCGAGAGCG	373
Qy	191	TGGTG	195
Db	374	TGCTG	378

Search completed: December 4, 2003, 09:00:10
Job time : 314.892 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:08:45 ; Search time 23.2027 Seconds
(without alignments)
465.179 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPITLTLQSTNTHQTSSSSS.....AEFYELWSVDHGEQSWVTAP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	359	100.0	504	18	AAW26706 Human TAB1 (TAK1 b
2	359	100.0	504	18	AAW26707 Human TAB1 (TAK1 b
3	359	100.0	504	20	AAV09541 Human TAB1 protein
4	359	100.0	504	21	AAV91001 Human TAB-1 protein
5	359	100.0	504	21	AAV94450 Human TAB1 protein
6	359	100.0	513	20	AAV09550 Human TAB1 protein
7	359	100.0	516	24	ABU11578 Human MDDT polypep
8	359	100.0	517	20	AAV09546 Human TAB1-FLAG pr
9	352	98.1	84	21	AAB56692 Human prostate can

10	77	21.4	16	20	AAV09549 Human TAB1 peptide
11	70	19.5	1162	22	ABB70838 Drosophila melanog
12	69.5	19.4	199	22	AAW77804 Human HT4SG64 seri
13	68.5	19.1	113	22	AAU47075 Propionibacterium
14	67.5	18.8	739	22	ABG16477 Novel human diago
15	67.5	18.8	739	22	ABG16477 Atrophin-1 interac
16	67.5	18.8	739	24	ABR41097 Human atrophin-1 i
17	67.5	18.8	739	24	AAE32720 Atrophin-1 interac
18	67.5	18.8	852	20	AAV30948 Human E3 ubiquitin
19	66	18.4	16	20	AAV09548 Human TAB1 peptide
20	64.5	18.0	116	22	AAU32515 Novel human secret
21	64.5	18.0	244	21	AAV86525 Human gene 72-enco
22	63.5	17.7	187	21	AAV86525 Arabidopsis thalia
23	63.5	17.7	219	21	AAV86525 Arabidopsis thalia
24	63.5	17.7	240	19	AAW75243 Fragment of human
25	63.5	17.7	240	23	AAE27007 Human gene 13 enco
26	63.5	17.7	240	23	AAE27145 Human gene 13 enco
27	63.5	17.7	240	24	ABU65018 Human secreted pro
28	63.5	17.7	241	22	ABG01626 Novel human diago
29	63.5	17.7	243	21	AAV35653 Arabidopsis thalia
30	63.5	17.7	335	19	AAW75208 Human secreted pro
31	63.5	17.7	335	23	AAE26971 Human gene 13 enco
32	63.5	17.7	335	23	AAE27109 Human gene 13 enco
33	63.5	17.7	335	24	ABU64982 Human secreted pro
34	63.5	17.7	391	22	ABG36176 Human D1B2 protein
35	63.5	17.7	824	22	AAV20251 Human ADAM8. Homo
36	63.5	17.7	824	23	AAU86156 Human PRO1686 poly
37	63.5	17.7	10431	24	ABU54861 Human CA125 amino
38	63	17.5	66	22	AAV86430 Human immune/haema
39	63	17.5	2112	22	ABB60403 Drosophila melanog
40	62.5	17.4	92	21	AAV2825 Human ORF2589
41	62.5	17.4	675	22	AAU50204 Propionibacterium
42	62.5	17.4	1945	22	ABB64947 Drosophila melanog
43	62	17.3	527	19	AAW48419 Amino acid sequenc
44	62	17.3	727	24	ABB84668 Human SECP-20 prot
45	62	17.3	734	22	AAV82316 Human immunoglobul

ALIGNMENTS

RESULT 1

AAW26706

ID AAW26706 standard; Protein; 504 AA.

XX AC AAW26706;

XX AC AAW26706;

XX DT 25-MAR-2003 (updated)

XX DT 14-APR-1998 (first entry)

XX XX

DE Human TAB1 (TAK1 binding protein).

XX XX

XX KW TAB1; TAK1 binding protein; transforming growth factor-beta;

XX KW signal transduction; human.

XX OS Homo sapiens.

XX XX

XX FH Key Location/Qualifiers

XX FT Misc-difference 52

XX FT note= "variant has Arg as residue 52"

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX


```

XX (CHUS ) CHUGAI SEIYAKU KK.
PA Ohtomo T, Ono K, Tsuchiya M;
XX WPI; 1999-312645/26.
DR N-PSDB; AAY56278.
XX Screening for TGF- beta inhibitory substances, which are useful as
PT drugs for treatment of diseases relating to its disorder
PS Claim 3; Page 147-149; 195pp; Japanese.
XX A method has been developed for screening for substances which inhibit
CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
CC comprises: (a) contacting the polypeptide in the presence of a sample;
CC and (b) detecting the amount of bound polypeptide, in which the sample
CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
CC indications e.g. as TGF-beta signal transduction inhibitors or
CC activators, or extracellular matrix protein production enhancement
CC inhibitors or activators, or cell proliferation prevention inhibitors or
CC activators, or monocyte migration inhibitors or activators, or
CC physiological activity induction inhibitors or activators, or
CC immunosuppression inhibitors or activators, or amyloid beta protein
CC precipitation inhibitors or activators, and such substances can also be
CC inhibitors of the TAK1 polypeptide function, particularly kinase
CC activity. The present sequence represents human TAB1.
XX Sequence 504 AA;
SQ
Query Match 100.0%; Score 359; DB 20; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
DB 437 QSPFTLTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496
QY 61 EQSVVTAP 68
DB 497 EQSVVTAP 504

RESULT 4
AAY91001
ID AAY91001 standard; Protein; 504 AA.
XX
AC AAY91001;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human TAB-1 protein sequence SEQ ID NO:4.
XX
KW Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;
KW screening; signal transduction; inhibition; inflammatory cytokine;
KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;
KW antiinflammatory; suppression.
XX
OS Homo sapiens.
XX
PN WO200023610-A1.
XX
PD 27-APR-2000.
XX
PF 21-OCT-1999; 99WO-JP05817.
XX
PR 21-OCT-1998; 98JP-0299962.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
FI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;
XX

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DR WPI; 2000-339707/29.
DR N-PSDB; AAA39106.
XX Method for screening inhibitors of TAK1 signal transduction for
PT suppression of inflammatory cytokine production and use as
PT antiinflammatory agents -
XX Disclosure; Page 90-94; 100pp; Japanese.
XX The present invention describes a method for screening compounds for
CC inhibition of inflammatory cytokine signal transduction by contacting
CC the sample with TAK1 and its receptor TAB1 and selecting for inhibition
CC of TAK1/TAB1 binding. Also described is a method for screening compounds
CC for inhibition of inflammatory cytokine signal transduction in which the
CC inhibition of inflammatory cytokine signal transduction containing as
CC compositions for the treatment of inflammatory disorders containing as
CC active component an inflammatory cytokine signal transduction inhibitor.
CC TAK1 is an essential component of the signalling process which results
CC in release of inflammatory cytokines such as interleukin-1 (IL-1),
CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used
CC for the selection of effective antiinflammatory agents. The present
CC sequence represents human TAB-1, which is used in the exemplification of
CC the present invention.
XX Sequence 504 AA;
SQ
Query Match 100.0%; Score 359; DB 21; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
DB 437 QSPFTLTQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496
QY 61 EQSVVTAP 68
DB 497 EQSVVTAP 504

RESULT 5
AAY59450
ID AAY59450 standard; Protein; 504 AA.
XX
AC AAY59450;
XX
DT 24-MAR-2000 (first entry)
XX
DE Human TAB1 protein sequence.
XX
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta.
XX
OS Homo sapiens.
XX
PN JP11326328-A.
XX
PD 26-NOV-1999.
XX
PF 13-MAY-1998; 98JP-0130378.
XX
PR 13-MAY-1998; 98JP-0130378.
XX
PA (MATS/) MATSUMOTO K.
XX
DR WPI; 2000-078337/07.
DR N-PSDB; AAZ48861.
XX
PT Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein -
XX

```

PS	Claim 2; Page 25-26; 43pp; Japanese.	
XX	This sequence represents the human TAB1 protein.	
CC	The invention relates to a method for screening a substance inhibiting	
CC	the formation of a complex between XIAP and TAB1, in which X-linked	
CC	inhibitor of apoptosis protein (XIAP), transforming growth factor-beta	
CC	activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be	
CC	tested are contacted with each other and then the presence or formation	
CC	of a complex between XIAP and TAB1 is detected. The substance can be used	
CC	as a drug for extracellular matrix protein production enhancement, cell	
CC	growth inhibition, monocyte migration, physiologically active substance	
CC	induction, immunosuppression, and beta-amyloid protein deposition. A	
CC	substance inhibiting the formation of a complex between TAB1 and XIAP as	
CC	well as between XIAP and TGF-beta (Transforming growth factor-beta) type	
CC	I and/or type II receptor is useful as a drug.	
XX		
Sequence	504 AA;	
Query Match	100.0%; Score 359; DB 21; Length 504;	
Best Local Similarity	100.0%; Pred. No. 3.6e-37;	
Matches	68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QSPTLTQSTNTHQTQSSSSDGLFRSRPAHSLPPGDCGRVEPYVDFAEFYRLWSVDHG 60	
Db	437 QSPTLTQSTNTHQTQSSSSDGLFRSRPAHSLPPGDCGRVEPYVDFAEFYRLWSVDHG 496	
QY	61 EQSVVTAP 68	
Db	497 EQSVVTAP 504	
RESULT 6		
AAAY09550		
ID	AAAY09550 standard; Protein; 513 AA.	
AC	AAAY09550;	
XX		
DT	21-JUL-1999 (first entry)	
XX		
DE	Human TAB1 protein SEQ ID NO:43.	
XX		
KW	Human; TAB1; TAK1; screening; inhibition; TGF-beta;	
KW	transforming growth factor beta.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9921010-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	22-OCT-1998; 98WO-JP04796.	
XX		
PR	22-OCT-1997; 97JP-0290188.	
XX		
PA	(CHUS) CHUGAI SEIYAKU KK.	
XX		
PI	Ohtomo T, Ono K, Tsuchiya M;	
XX		
DR	WPI; 1999-312645/26.	
DR	N-PSDB; AAX56310.	
XX		
PT	Screening for TGF- beta inhibitory substances, which are useful as	
PT	drugs for treatment of diseases relating to its disorder	
XX		
PS	Example 13; Page 186-188; 195pp; Japanese.	
XX		
CC	A method has been developed for screening for substances which inhibit	
CC	the binding of TAK1 polypeptide to TAB1 polypeptide. The method	
CC	comprises: (a) contacting the polypeptide in the presence of a sample;	
CC	and (b) detecting the amount of bound polypeptide, in which the sample	
CC	can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming	
CC	growth factor (TGF)-beta inhibitory substances can be used in drugs for	
CC	indications e.g. as TGF-beta signal transmission inhibitors or	

CC	activators, or extracellular matrix protein production enhancement	
CC	inhibitors or activators; or cell proliferation prevention inhibitors or	
CC	activators, or monocyte migration inhibitors or activators, or	
CC	physiological activity induction inhibitors or activators, or	
CC	immunosuppression inhibitors or activators, or amyloid beta protein	
CC	precipitation inhibitors or activators, and such substances can also be	
CC	inhibitors of the TAK1 polypeptide function, particularly kinase	
CC	activity. The present sequence represents human TAB1.	
XX		
Sequence	513 AA;	
Query Match	100.0%; Score 359; DB 20; Length 513;	
Best Local Similarity	100.0%; Pred. No. 3.6e-37;	
Matches	68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QSPTLTQSTNTHQTQSSSSDGLFRSRPAHSLPPGDCGRVEPYVDFAEFYRLWSVDHG 60	
Db	446 QSPTLTQSTNTHQTQSSSSDGLFRSRPAHSLPPGDCGRVEPYVDFAEFYRLWSVDHG 505	
QY	61 EQSVVTAP 68	
Db	506 EQSVVTAP 513	
RESULT 7		
ABU11578		
ID	ABU11578 standard; Protein; 516 AA.	
XX		
AC	ABU11578;	
XX		
DT	12-FEB-2003 (first entry)	
XX		
DE	Human MDDT polypeptide SEQ ID 525.	
XX		
KW	MDDT; human; disease detection and treatment molecule polypeptide;	
KW	anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;	
KW	haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;	
KW	gene therapy; protein replacement therapy; cell proliferative disorder;	
KW	cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;	
KW	anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;	
KW	Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;	
XX	psoriasis; hepatitis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200279449-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	27-MAR-2002; 2002WO-US09944.	
XX		
PR	28-MAR-2001; 2001US-279619P.	
PR	29-MAR-2001; 2001US-280067P.	
PR	29-MAR-2001; 2001US-280068P.	
PR	16-MAY-2001; 2001US-291280P.	
PR	17-MAY-2001; 2001US-291829P.	
PR	17-MAY-2001; 2001US-291849P.	
PR	19-JUN-2001; 2001US-293428P.	
PR	20-JUN-2001; 2001US-299776P.	
PR	20-JUN-2001; 2001US-300001P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
PI	Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;	
PI	Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;	
PI	Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;	
PI	Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;	
PI	Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;	
XX		
XX	WPI; 2003-058431/05.	
DR	N-PSDB; ABX34568.	
XX		
PT	New purified disease detection and treatment molecule proteins and	

PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis

PS Claim 27; SEQ ID NO 525; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukemia, lymphoma, melanoma, myeloma or sarcoma), anemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 516 AA;

Query Match 100.0%; Score 359; DB 24; Length 516;
 Best Local Similarity 100.0%; Pred. No. 3.7e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPILTLQSTNTHQTQSSSSDGGGLFRSRPAHSLPPGEGRVEPYVDFAEFRLMSVDHG 60
 |||||
 DB 449 QSPILTLQSTNTHQTQSSSSDGGGLFRSRPAHSLPPGEGRVEPYVDFAEFRLMSVDHG 508

QY 61 EQSVVTAP 68
 |||||

DB 509 EQSVVTAP 516

RESULT 8

AA09546
 ID AA09546 standard; Protein; 517 AA.

AC AA09546;

XX 21-JUL-1999 (first entry)

DE Human TAB1-FLAG protein.

XX Human; TAB1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta.

XX Homo sapiens.

OS Synthetic.

XX WO9921010-A1.

XX 29-APR-1999.

XX 22-OCT-1998; 98WO-JP04796.

XX 22-OCT-1997; 97JP-0290188.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ohtomo T, Ono K, Tsuchiya M;

XX WPI; 1999-312645/26.

XX N-PSDB; AAX56282.

XX Screening for TGF- beta inhibitory substances, which are useful as
 PT drugs for treatment of diseases relating to its disorder
 PT
 XX

PS Example 1; Page 163-166; 195pp; Japanese.

XX A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production inhibitors or
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence represents TAB1-FLAG from an example of
 CC the present invention.

XX Sequence 517 AA;

Query Match 100.0%; Score 359; DB 20; Length 517;
 Best Local Similarity 100.0%; Pred. No. 3.7e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPILTLQSTNTHQTQSSSSDGGGLFRSRPAHSLPPGEGRVEPYVDFAEFRLMSVDHG 60
 |||||
 DB 437 QSPILTLQSTNTHQTQSSSSDGGGLFRSRPAHSLPPGEGRVEPYVDFAEFRLMSVDHG 496

QY 61 EQSVVTAP 68
 |||||

DB 497 EQSVVTAP 504

RESULT 9

AA56692
 ID AA56692 standard; Protein; 84 AA.

XX AA56692;

XX 13-MAR-2001 (first entry)

XX Human prostate cancer antigen protein sequence SEQ ID NO:1270.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05988.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

XX N-PSDB; AAF15895.

XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -
 XX

PS Claim 11; Page 1693; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated

CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

CC The prostate cancer antigens can have neuroprotective, cytostatic,

CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,

CC nephrotropic, antineoplastic, gynaecological and antibacterial activities,

CC and can be used in gene therapy. The prostate cancer antigen

CC polynucleotides may be used for detection of prostate cancer, chromosome

CC identification, as chromosome markers, and for numerous other diagnostic

CC or research purposes. The prostate cancer antigens may be used to treat

CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to

CC AAB57303 represent sequences used in the exemplification of the present

XX invention.

SQ Sequence 84 AA;

Query Match 98.1%; Score 352; DB 21; Length 84;

Best Local Similarity 98.5%; Pred. No. 2.7e-37;

Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSDGLFPRPAHSLPGEDGRVPEYVDFAEFYRLWSVDHG 60

DB 17 QSPFTLQSTNTHTQSSSSDGLFPRPAHSLPGEDGRVPEYVDFAEFYRLWSVDHG 76

QY 61 EQSVVTAP 68

DB 77 EQSVVTAP 84

RESULT 10

AAV09549

ID AAV09549 standard; peptide; 16 AA.

XX AAV09549;

AC AAV09549;

DT 21-JUL-1999 (first entry)

XX Human TAB1 peptide TAB1C-2.

DE Human; TAB1; TAK1; screening; inhibition; TGF-beta;

XX transforming growth factor beta.

KW Homo sapiens.

XX WO9921010-A1.

EN 29-APR-1999.

PD 22-OCT-1998; 98WO-JP04796.

XX 22-OCT-1997; 97JP-0290188.

ER (CHUS) CHUGAI SEIYAKU KK.

XX Ohtomo T, Ono K, Tsuchiya M;

PI WPI; 1999-312645/26.

XX Screening for TGF- beta inhibitory substances, which are useful as

PT drugs for treatment of diseases relating to its disorder

XX Example 13; Page 182; 195pp; Japanese.

PS A method has been developed for screening for substances which inhibit

CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method

CC comprises: (a) contacting the polypeptide in the presence of a sample;

CC and (b) detecting the amount of bound polypeptide, in which the sample

CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming

CC growth factor (TGF)-beta inhibitory substances can be used in drugs for

CC indications e.g. as TGF-beta signal transmission inhibitors or

CC activators, or extracellular matrix protein production enhancement

CC inhibitors or activators, or cell proliferation prevention inhibitors or

CC activators, or monocyte migration inhibitors or activators, or

CC physiological activity induction inhibitors or activators, or

CC immunosuppression inhibitors or activators, or amyloid beta protein

CC precipitation inhibitors or activators, and such substances can also be

CC inhibitors of the TAK1 polypeptide function, particularly kinase

CC activity. The present sequence represents a peptide from an example

CC of the present invention.

XX Sequence 16 AA;

SQ Query Match 21.4%; Score 77; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQ 15

DB 2 QSPFTLQSTNTHTQ 16

RESULT 11

ABB70838

ID ABB70838 standard; Protein; 1162 AA.

XX ABB70838;

AC ABB70838;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 39306.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

KW Drosophila melanogaster.

XX WO200171042-A2.

EN 27-SEP-2001.

PD 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

FA Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL14941.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

PS Disclosure; SEQ ID NO 39306; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1162 AA;

SQ Query Match 19.5%; Score 70; DB 22; Length 1162;

quantitate the presence of similar nucleic acids in samples. The PSPase polypeptides may be used as antigens in the production of antibodies against the PSPase polypeptides and in assays to identify modulators of PSPase expression and activity. The anti-PSPase antibodies and antagonists may also be used to down regulate expression and activity, the anti-PSPase antibodies may also be used as diagnostic agents for detecting the presence of PSPase polypeptides in samples. Disorders that may be prevented, diagnosed and/or treated by the invention are: immune/autoimmune disorders (e.g. Wiscott-Aldrich syndrome, Chediak-Higashi syndrome, Hashimoto's thyroiditis and multiple sclerosis); inflammatory conditions (e.g. Crohn's disease, inflammatory bowel disease, appendicitis and rheumatoid arthritis); cellular proliferative disorders (e.g. lymphoma, lung and intestinal cancers); and cardiovascular disorders (e.g. Scimitar syndrome, Ebstein's anomaly and aneurysm).

Query Match 19.4%; Score 69.5; DB 22; Length 199;
Best Local Similarity 41.9%; Pred. No. 1.3;
Matches 18; Conservative 3; Mismatches 17; Indels 5; Gaps 5;

1 QSTFLTLQSTNNHTQSSSSDGG-----LFRSRFAHSLPPGE 38
119 QSTFLTDQTRIHSRDAFSSISGCSKFTAVRKRMADKLPPVGQ 161

RESULT 13
AAU47075
ID AAU47075 standard; Protein; 113 AA.
AC AAU47075;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #7971.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN W0200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
XX
PR 02-JUN-2000; 2000US-208841P.
XX
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI: 2001-616774/71.
XX
XX N-PSDB; AAS59536.
XX
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX
XX Example 1; SEQ ID No 8270; 1069pp; English.
XX
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at www.int/pub/published/pct/sequences.

AA	Sequence	739 AA;
AA	Sequence	739 AA;

Query Match 18.8%; Score 67.5; DB 22; Length 739;
Best Local Similarity 31.1%; Pred. No. 13;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 48

DB 119 SSAGSELPINININISGAIGGELIFHIDGGGGCINLEAYVQGLKLEKLEKLEKLE
QY 49 AEFYRLWSVDHGEG 62
 | | |

RESULT 15
MAC68173

ID AAG66173 standard, 1000000; 1000000; 1000000;
 XX
 AC AAG66173;
 vv

XX
XX
DE Atrophin-1 interacting protein (AIP4) SEQ ID NO:89.
XX
XX 25-JAN-2002 (first entry)
XX
XX human high basic mass. URM gene. Zmavl gene. chromosome 11: 11q13.3.

KW sequence tagged site; STS; osteoporosis; osteoporosis; gene therapy
KW antisense therapy; vaccine; bone disorder; Paget's disease;
KW sclerostosis; osteomalacia; fibrous dysplasia.

OS Homo sapiens.
XX
PN WO200177327-A1.

PD 18-OCT-2001.
XX
PF 21-JUN-2000; 2000WO-US16951.

PR 05-APR-2000; 2000US-0543771.
PR 05-APR-2000; 2000US-0544398.
XX XX

XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX

XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis -
PT

PS Claim 76; Page 392-394; 443pp; English.

XX

CC The present invention describes the human Zmax1 gene and the high bone

CC HBM genes have osteopathic activities. The genes can be used in gene
CC therapy, antiseize therapy and in the production of vaccines. They
CC can be used in the diagnosis and treatment of bone disorders including
CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous
CC dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent

CC sequences used in the exemplification of the present invention.

XX SQ Sequence 739 AA;
Query Match 18.8%; Score 67.5; DB 22; Length 739;
Best Local Similarity 31.1%; Pred. No. 13;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;
QY 2 SPTLTQSTNTHTQSSSSSDG-----GLFRSRPAH-----SLPPGEDGRVEFYVDF 48
Db 119 SSGSLPPTNTNTNTSEGAISGLIIPLTISGGSGRPLNPNVTQAPLPQWEQRVD----- 173
QY 49 AEFYRLMSVDHGEQ 62
Db 174 -QHGRVYVDHVEK 186

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Job time : 24.2027 secs

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Run on: December 4, 2003, 07:04:49 ; Search time 57.3851 Seconds
(without alignments)
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Title: US-09-830-144-1_COPY_408_1091

Perfect score: 1252

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Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -TRANS=human40.cdi
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1252	100.0	567	20	AAZ28998	Human TGF-beta act
2	1252	100.0	579	18	AAW27092	Mouse transforming
3	1252	100.0	579	18	AAW27093	Human transforming
4	1252	100.0	579	20	AAZ28996	Human TGF-beta act
5	1252	100.0	579	20	AAZ28995	Human TAK1 protein
6	1252	100.0	579	21	AAZ28994	Human TAK1 protein
7	1252	100.0	579	23	AAZ28993	Human TAK1-1 protei
8	1252	100.0	579	23	AAZ28992	Pain regulated pro
9	1252	100.0	590	20	AAZ28991	Human TAK1-6xHis p
10	700	55.9	678	22	ABZ5061	Human TGF-beta act
11	414	33.1	252	22	ABZ5061	Drosophila melanog
12	374	29.9	367	21	ABZ5061	Drosophila melanog
13	374	29.9	369	21	ABZ5061	Arabidopsis thalia
14	374	29.9	407	21	ABZ5061	Arabidopsis thalia
15	373	29.8	369	21	ABZ5061	Arabidopsis thalia
16	373	29.8	374	21	ABZ5061	Arabidopsis thalia
17	373	29.8	412	21	ABZ5061	Arabidopsis thalia
18	371	29.6	349	22	ABZ5061	Human colon cancer
19	371	29.6	455	21	ABZ5061	A human regulator
20	371	29.6	455	21	ABZ5061	Human survival reg
21	371	29.6	455	21	ABZ5061	A human cardioasc
22	371	29.6	473	22	ABZ5061	Human protein sequ
23	371	29.6	800	22	ABZ5061	Human TGF-beta rec
24	371	29.6	800	22	ABZ5061	Novel protein kina
25	371	29.6	800	23	ABZ5061	Motif zipper conta
26	363.5	29.0	394	24	ABZ5061	Human protein kina
27	363.5	29.0	1020	22	ABZ5061	Drosophila melanog
28	359.5	28.7	1024	23	ABZ5061	Human NOV7, a mixe
29	355.5	28.4	1021	23	ABZ5061	Novel human protei
30	355	28.4	719	22	ABZ5061	Human protein kina
31	355	28.4	1036	23	ABZ5061	Novel human protei
32	355	28.4	1036	24	ABZ5061	Amino acid sequenc
33	355	28.4	1036	24	ABZ5061	Human kinase and p
34	353.5	28.2	859	16	ABZ5061	Human leucine zipp
35	353.5	28.2	859	18	ABZ5061	Human leucine zipp
36	353.5	28.2	859	24	ABZ5061	Polypeptide sequen
37	352.5	28.2	888	23	ABZ5061	Mouse ischaemic co
38	351.5	28.1	977	22	ABZ5061	Drosophila melanog
39	350	28.0	589	21	ABZ5061	Arabidopsis thalia
40	350	28.0	732	21	ABZ5061	Arabidopsis thalia
41	350	28.0	760	21	ABZ5061	Arabidopsis thalia
42	349.5	27.9	1046	22	ABZ5061	Human kinase (PKIN
43	349.5	27.9	1097	23	ABZ5061	Human PKIN-12 prot
44	348	27.8	319	21	ABZ5061	Arabidopsis thalia
45	348	27.8	341	21	ABZ5061	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAZ28998
ID AAZ28998 standard; Protein; 567 AA.

XX AAZ28998;

XX AAZ28998;

DT 29-OCT-1999 (first entry)

DE Human TGF-beta activated kinase (TAK) 1c amino acid sequence.

XX Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
XX TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
XX intractable disease; atrophic dermatitis; psoriasis; viral infection;
XX endotoxin shock; septicemia; human; hTAK1c.

XX Homo sapiens.

XX OS

XX WO9940202-A1.

XX PD 12-AUG-1999.

XX PF 02-FEB-1999; 99WO-JP00422.

XX PR 30-OCT-1998; 98JP-0309316.

XX PR 06-FEB-1998; 98JP-0026003.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Hasegawa K, Kageyama N, Sakurai H, Sugita T;

XX DR WPI; 1999-494298/41.

XX DR N-PSDB; AAX99698.

XX PT Nuclear factor kappa B activation inhibitors, useful as preventives

XX PT for, e.g. autoimmune diseases

XX PS Examples; Page 43-46; 49pp; Japanese.

XX CC The invention provides a method for identifying or screening a nuclear

XX CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a

XX CC test substance on modulating the function(s) of TGF-beta activated kinase

XX CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to

XX CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),

XX CC intractable diseases with inflammation (such as atrophic dermatitis and

XX CC psoriasis), viral infection, endotoxin shock, septicemia and others. The

XX CC present sequence represents the amino acid sequence of human TAK1c

XX CC (hTAK1c) protein.

XX SQ Sequence 567 AA;

Alignment Scores:

Pred. No.: 7.32e-134 Length: 567

Score: 1252.00 Matches: 228

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 20 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x AAY28998 (1-567)

QY 1 GTAGAGCTCGGAGTATCCGCTGCAACATCCCTTAATTTGTAAGCTTTATGAGCC 60

DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnLeuValLysLeuTyrGlyAla 95

QY 61 TGCTTGAATCCAGTGCTCTTGTCATGGAATATGCTCAAGGGGCTCTTATATATG 120

DB 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115

QY 121 CTGCAGTCTGCAACCATGTCATATATATGCTGCTGCCCAAGCAATGAGTTGGTGT 180

DB 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135

QY 181 CAGTGTTCCCAAGAGTGGTTACTCTACAGATGCAACCCAAAGCGCTAAATTCACAGG 240

DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArg 155

QY 241 GACCTGAACACCAAACTTACTCTGCTGTCAGGGGGAGCAGTTCTAAATAATTTGTAT 300

DB 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175

QY 301 TTGGTTCAGCTGTGACATTCAGACACACATGACCAATACAGGGAGTGGCTGGTGG 360

DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLysGlySerAlaAlaTyr 195

QY 361 ATGCACCTCAAGTTTGTAGGTAGTAAATACAGTGAATAATCTGACGTTCTCAGCTGG 420

DB 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215

QY 421 GGTATTATCTTTGGGAGTGGATACCGCTCGGAACCTTTGATGAGATTTGGGCCA 480

DB 216 GlyIleIleLeuTyrGluValIleThrArgLysProPheAspGluIleGlyGlyPro 235

QY 481 GCTTTCCGATCATGTGGGCTGTTTCATATGCTACTCGACCACTGATAAAAAATT 540

DB 236 AlaPheArgIleMetTyrPalaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255

QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTCGTTTGTCTTAAAGATCTTCCAGCCCT 600

DB 256 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275

QY 601 TCAATGGAGAAATTTGTAATATGACTCATCTTGTATCGGTACTTTCAGGAGCAGAT 660

DB 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295

QY 661 GAGCATTACAGTATCTTGTCTGAG 684

DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 2

AAW27092

ID AAW27092 standard; Protein; 579 AA.

XX AC AAW27092;

XX DT 19-NOV-1997 (first entry)

XX DE Mouse transforming growth factor-beta activated kinase TAK-1.

XX KW TGF-beta; signal transduction; TGF-beta activated kinase; BMP;

XX KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;

XX KW protein kinase.

XX OS Mus musculus.

XX XX JP09163990-A.

XX PD 24-JUN-1997.

XX PF 27-SEP-1996; 96JP-0256747.

XX PR 24-JUL-1996; 96US-0685625.

XX PR 29-SEP-1995; 95JP-0253549.

XX (CHUS) CHUGAI PHARM CO LTD.

XX PA (UENO) UENO N.

XX DR WPI; 1997-380171/35.

XX DR N-PSDB; AAT85094.

XX PT DNA encoding transforming growth factor-beta-activated kinase, TAK-1

XX PT - useful for studying the TGF-beta signal transduction system

XX PS Claim 14; Page 10-12; 20pp; Japanese.

XX CC The present sequence represents mouse transforming growth factor-beta

XX CC (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the

XX CC TAK-1 protein which is involved in the TGF-beta family signal

XX CC transduction system. TAK-1, also known as activator of MAPK Kinase

XX CC (AMK-1), is an enzyme which is activated by TGF-beta and bone

XX CC morphogenetic protein (BMP) and activates MAPK kinase by

XX CC phosphorylation.

XX SQ Sequence 579 AA;

Alignment Scores:

Pred. No.: 7.38e-134 Length: 579

Score: 1252.00 Matches: 228

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 18 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x AAW27092 (1-579)

QY 1 GTAGAGCTCGCAGTATCCCGTGTGAACCATCTTAATATTGAAAGCTTTATGAGCC 60
 Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
 QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
 QY 121 CTGCATCGTGTGAACCATCTCCCATATTATATCTGCTGCCACGCAATGAGTGTGTTA 180
 Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
 QY 181 CAGTGTTCACAGAGTGTCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
 Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
 QY 241 GACCTGAAACCAACACTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
 QY 301 TTTGTTACAGCTGTGACATTCACACACATGACCAATACACAGGGGAGTGTCTGTTG 360
 Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
 QY 361 ATGCACTGAGTGTGTTTGAAGTAGTAATACAGTGAAGAAATGTGACGTCTTCAGCTGG 420
 Db MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
 QY 421 GGTATTATCTTTGGGAGTGTATACCGGTGCGAAGCCCTTTGATGAGTGTGCGCCA 480
 Db GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
 QY 481 GCTTTCCGAATCATGTGGCTGTTCATAATGTGTACTGACACACACCTGATATAAAATTTA 540
 Db AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCCCATTCAGAGCCTGTGATCGTGTGCTTAAAGATCCTTCCAGCGCCT 600
 Db ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGAGAAATTCGTAATTAATGACTCCTGATCGGTACTTTCAGAGCAGAT 660
 Db SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTCTCTCAG 684
 Db GluProLeuGlnTyrProCysGln 303

RESULT 3

AAW27093
 ID AAW27093 standard; Protein; 579 AA.

XX AC AAW27093;

XX DT 19-NOV-1997 (first entry)

XX DE Human transforming growth factor-beta activated kinase TAK-1.

XX DE TGF-beta; signal transmission; TGF-beta activated kinase;

XX KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;

XX KW protein kinase.

XX OS Homo sapiens.

XX PN JF09163990-A.

XX PD 24-JUN-1997.

XX PF 27-SEP-1996; 96JP-0256747.

XX PR 24-JUL-1996; 96US-0685625.

XX PR 29-SEP-1995; 95JP-0253549.

XX

(CHUS) CHUGAI PHARM CO LTD.
 (UENO/) UENO N.
 DR WPI; 1997-380171/35.
 XX N-ESDB; AAT85095.
 PT DNA encoding transforming growth factor-beta-activated kinase, TAK-1
 - useful for studying the TGF-beta signal transmission system
 XX
 FS Claim 15; Page 13-15; 20pp; Japanese.

XX The present sequence represents human transforming growth factor-beta
 (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the
 CC TAK-1 protein which is involved in the TGF-beta family signal
 CC transmission system. TAK-1, also known as activator of MAPK Kinase
 CC (AMK-1), is an enzyme which is activated by TGF-beta and bone
 CC morphogenetic protein (BMP) and activates MAPK kinase by
 CC phosphorylation.

XX Sequence 579 AA;

Alignment Scores:

Pred. No.: 7.38e-134 Length: 579
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x AAW27093 (1-579)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGAAAGCTTTATGAGCC 60
 Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
 QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
 QY 121 CTGCATCGTGTGACATTCACACACATGACCAATACACAGGGGAGTGTCTGTTA 180
 Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
 QY 181 CAGTGTTCACAGAGTGTGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
 Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
 QY 241 GACCTGAAACCAACACTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
 QY 301 TTTGTTACAGCTGTGACATTCACACACATGACCAATACACAGGGGAGTGTCTGTTG 360
 Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
 QY 361 ATGCACTGAGTGTGTTTGAAGTAGTAATACAGTGAAGAAATGTGACGTCTTCAGCTGG 420
 Db MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
 QY 421 GGTATTATCTTTGGGAGTGTATACCGGTGCGAAGCCCTTTGATGAGTGTGCGCCA 480
 Db GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
 QY 481 GCTTTCCGAATCATGTGGCTGTTCATAATGTGTACTGACACACACCTGATATAAAATTTA 540
 Db AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCCCATTCAGAGCCTGTGATCGTGTGCTTAAAGATCCTTCCAGCGCCT 600
 Db ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGAGAAATTCGTAATTAATGACTCCTGATCGGTACTTTCAGAGCAGAT 660

Db 276 SerMetGluGluLeuValValValValMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTGTCAG 684
 Db 296 GluProLeuGlnTyrProCysGln 303
 RESULT 4
 ID AAY28996 standard; Protein; 579 AA.
 AC AAY28996;
 XX 29-OCT-1999 (first entry)
 DT Human TGF-beta activated kinase (TAK) 1a amino acid sequence.
 XX Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
 KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
 KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
 KW endotoxin shock; septicemia; human; hTAK1a.
 XX Homo sapiens.
 OS
 XX
 XX WO9940202-A1.
 XX 12-AUG-1999.
 XX 02-FEB-1999; 99WO-JP00422.
 XX 30-OCT-1998; 98JP-0309316.
 PR 06-FEB-1998; 98JP-0026003.
 XX (TANA) TANABE SEIYAKU CO.
 XX Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 PI WPI; 1999-494298/41.
 DR N-PSDB; AAX39696.
 XX Nuclear factor kappa B activation inhibitors, useful as preventives
 PT for, e.g. autoimmune diseases
 XX Examples; Page 35-39; 49pp; Japanese.
 CC The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NPKB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the amino acid sequence of human TAK1a
 CC (hTAK1a) protein.
 XX
 SQ Sequence 579 AA;
 Alignment Scores:
 Pred. No.: 7,38e-134 Length: 579
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-830-144-1_COPY_408_1091 (1-684) x AAY28996 (1-579)
 QY 1 GTACAGCTCGCGAGTATCCGCTGTAACCATCTCTAATATGTAAAGCTTTATGGAGCC 60
 Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnLeuValValysLeuTyrGlyAla 95
 QY 61 TGCTTGATCCAGTGTGCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115

QY 121 CTGCGATGGTGGTGAACCATTTGCCATATTACTGTCTGCCCGCCCAATGAGTTGGTGTTA 180
 Db 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
 QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
 Db 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArg 155
 QY 241 GACCTGAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTCTTAAATAATTCGTGAT 300
 Db 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
 QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAAGGGGAGTGTGCTTGG 360
 Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
 QY 361 ATGGCACCTGAAGTGTGAAAGTAGTAAATTACAGTGAAGAAATGTGACGTCTTCAGCTGG 420
 Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
 QY 421 GGTATTATTCTTTGGGAAGTGTAAACGCTCGGAAACCCCTTTCATGAGATTGTTGGCCCA 480
 Db 216 GlyIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
 QY 481 GCTTTCCGAATCATGTGGGCTGTTCATAATGTGTACTCGACCCACTGTATAAAATTTA 540
 Db 236 AlaPheArgIleMetTyrPalaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCCCATTCAGAGCCTGATGACTCGTGTGTGTCTAAAGATCCTTCCCGAGCGCCT 600
 Db 256 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGGAGAAATTCGAAATTAATGACTCACTGATCGGTACTTCCAGGAGCAGAT 660
 Db 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTGTCAG 684
 Db 296 GluProLeuGlnTyrProCysGln 303
 RESULT 5
 AAY09542
 ID AAY09542 standard; Protein; 579 AA.
 XX
 AC AAY09542;
 XX 21-JUL-1999 (first entry)
 DT Human TAK1 protein.
 DE
 XX Human, TAK1; TAK1; screening; inhibition; TGF-beta;
 XX transforming growth factor beta.
 KW
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT CDS 183...1922 /*tag= a
 FT
 XX WO9921010-A1.
 XX 29-APR-1999.
 PD 22-OCT-1998; 98WO-JP04796.
 XX 22-OCT-1997; 97JP-0290188.
 PR (CHUS) CHUGAI SEIYAKU KK.
 PA Ohtomo T, Ono K, Tsuchiya M;
 FI WPI; 1999-312645/26.
 XX DR

DR N-PSDB; AAX56279.

PT Screening for TGF- β inhibitory substances, which are useful as

PT drugs for treatment of diseases relating to its disorder

XX

PS Claim 4; Page 155-157; 195pp; Japanese.

XX

CC A method has been developed for screening for substances which inhibit

CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method

CC comprises: (a) contacting the polypeptide in the presence of a sample;

CC and (b) detecting the amount of bound polypeptide, in which the sample

CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming

CC growth factor (TGF)- β inhibitory substances can be used in drugs for

CC indications e.g. as TGF- β signal transduction inhibitors or

CC activators, or extracellular matrix protein production enhancement

CC inhibitors or activators, or cell proliferation prevention inhibitors or

CC activators, or monocyte migration inhibitors or activators, or

CC physiological activity induction inhibitors or activators, or

CC immunosuppression inhibitors or activators, or amyloid β protein

CC precipitation inhibitors or activators, and such substances can also be

CC inhibitors of the TAK1 polypeptide function, particularly kinase

CC activity. The present sequence represents human TAK1.

XX

SQ Sequence 579 AA;

Alignment Scores:

Pred. No.:	7.38e-134	Length:	579
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-830-144-1_COPY_408_1091 (1-684) x AAY09542 (1-579)

QY 1 GTAGAGCTGGCGAGTTATCCGTTGAGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60

DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95

QY 61 TGCTTGATCCAGTGTCTGTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120

DB 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115

QY 121 CTGATGTGTGACCACTTCCCATATTATATCTGCTGCCAGCAATGAGTTGTGTTA 180

DB 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135

QY 181 CAGTGTTCCTCCAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG 240

DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155

QY 241 GACCTGAACCAACCAACTTACTGCTGCTGAGGGGGGAGAGTCTTAAATTTGTGAT 300

DB 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175

QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATACAGGGAGGCTGCTGG 360

DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195

QY 361 ATGCACCTGAAGTTTGTGAAGGTAGTAATTTACAGTGAAGAAATGTGCTTCAGCTGG 420

DB 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 215

QY 421 GGTATTATCTTGGGAGTGTATACCGCTGCGAAACCCCTTTGATGAGATTGGTGCCCA 480

DB 216 GlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 235

QY 481 GCTTTCGAATCATGTGGCTGTTTCAATAATGGTACTGACCAACCACTGATATAAATTTA 540

DB 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255

QY 541 CCTAAGCCCATTTGAGAGCTGATGACTGCTTGTGGTCTTAAGATCCTTCCAGCGCCT 600

DB 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275

QY 601 TCAATGGAGGAAATGTGAAATAATGACTCACTGATGCGGTACTTCCAGGACAGAT 660

DB 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295

QY 661 GAGCCATTACAGTATCCCTGTGTCAG 684

DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 6

ID AAY91000

XX AAY91000 standard; Protein; 579 AA.

AC AAY91000;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human TAK-1 protein sequence SEQ ID NO:2.

XX

KW Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;

KW screening; signal transduction; inhibition; inflammatory cytokine;

KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;

KW antiinflammatory; suppression.

XX

OS Homo sapiens.

XX

PN WO200023610-A1.

XX

PD 27-APR-2000.

XX

PF 21-OCT-1999; 99WO-JP05817.

XX

PR 21-OCT-1998; 98JP-0299962.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;

XX

DR WPI; 2000-339707/29.

DR N-PSDB; AAA39105.

XX

PT Method for screening inhibitors of TAK1 signal transduction for

PT suppression of inflammatory cytokine production and use as

PT antiinflammatory agents -

XX

PS Example 1; Page 80-84; 100pp; Japanese.

XX

CC The present invention describes a method for screening compounds for

CC inhibition of inflammatory cytokine signal transduction by contacting

CC the sample with TAK1 and its receptor TAB1 and selecting for inhibition

CC of TAK1/TAB1 binding. Also described is a method for screening compounds

CC for inhibition of inflammatory cytokine signal transduction in which the

CC inhibition of TAK1 phosphorylation is selected for; and drug

CC compositions for the treatment of inflammatory disorders containing as

CC active component an inflammatory cytokine signal transduction inhibitor.

CC TAK1 is an essential component of the signalling process which results

CC in release of inflammatory cytokines such as interleukin-1 (IL-1),

CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used

CC for the selection of effective antiinflammatory agents. The present

CC sequence represents human TAK-1, which is used in the exemplification of

CC the present invention.

XX

SQ Sequence 579 AA;

Alignment Scores:

Pred. No.:	7.38e-134	Length:	579
Score:	1252.00 <td>Matches:</td> <td>228</td>	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-830-144-1_COPY_408_1091 (1-684) x AAY91000 (1-579)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGGCAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
 DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
 QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAATGTG 120
 DB 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
 QY 121 CTGCATGGTCTGAACCATTCGCATATATATCTGCTGCCACGCAATGAGTTGGTGT 180
 DB 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
 QY 181 CAGTGTTCACAGGAGTGGCTTCTCTCAGAGTCAGCATGCAACCCAAAGCGCTTAATCCACAGG 240
 DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
 QY 241 GACCTGAAACCCACCAACTTACTGCTGCTGGTTCGAGGGGGGACAGTTCTAAAAATTTGTGAT 300
 DB 156 AspLeuIysProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp 175
 QY 301 TTGGTACACCTGTGATTCAGACACACATGACCAATACAAAGGGAGTGTGCTGTGG 360
 DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 195
 QY 481 GCTTTCCGATCATGTGGTGTCTTCAATATGAGTGTGCTGACCAACCTGATGATAAAATTTA 540
 DB 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCCCATTTGAGAGCCTGATCAGCTGTGTGGTCTTAAGATCCTCCAGCGCCT 600
 DB 256 ProIysProIleGluSerLeuMetThrArgCysTrpSerIysAspProSerGlnArgPro 275
 QY 601 TCAATGAGGAGAAATTTGTAATAATGACTCAGTGTGATGGGTACTTTCCAGGAGCAGAT 660
 DB 276 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTGAG 684
 DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 7

ABB85033
 ID ABB85033 standard; Protein; 579 AA.

AC ABB85033;

DT 16-MAY-2002 (first entry)

DE Pain regulated protein sequence 28.

KW Pain; analgesic; gene therapy; neurological disorder;

KW neurodegenerative disease.

OS Homo sapiens.

PN WO200012338-A2.

PD 14-FEB-2002.

PF 03-AUG-2001; 2001WO-EP09011.

PR 03-AUG-2000; 2000DE-1037759.

XX

(CHEF) GRUENENTHAL GMBH.

XX Gallen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;

XX WPI; 2002-257469/30.

DR N-PSDB; ABL88437.

XX Identifying pain-regulating compounds, useful for treating chronic pain
 PT and for diagnosis, by measuring binding of compounds to specific
 PT peptides and proteins

XX Claim 1; Fig 44; 213pp; German.

XX The invention relates to identifying pain-regulating substances (A)

CC comprises (i) incubating a test substance with a cell (or preparation
 CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
 CC either binding of the test substance to (B) or some functional parameter
 CC that is altered by this binding. The method is useful for identifying
 CC pain-regulating substances (A) with analgesic activity. (A) along with
 CC nucleic acid (ABL88437-ABL88441) that encode proteins (B,

CC ABB85006-ABB85037) that interact with (A); (B); vectors containing the
 CC nucleic acid; antibodies against (B); cells that express (B) and agents
 CC that bind to (B), are all useful for treating pain, particularly chronic

CC pain, including use in gene therapy. The same materials can also be used
 CC for diagnosis, e.g. of neurological and neurodegenerative diseases. The
 CC present sequence is that of a polypeptide of the invention.

XX SQ Sequence 579 AA;

Alignment Scores:

Pred. No.: 7,38e-134 Length: 579
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x ABB85033 (1-579)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGGCAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
 DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
 QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAATGTG 120
 DB 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
 QY 121 CTGCATGGTCTGAACCATTCGCATATATATCTGCTGCCACGCAATGAGTTGGTGT 180
 DB 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
 QY 181 CAGTGTTCACAGGAGTGGCTTCTCTCAGAGTCAGCATGCAACCCAAAGCGCTTAATCCACAGG 240
 DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
 QY 241 GACCTGAAACCCACCAACTTACTGCTGCTGGTTCGAGGGGGGACAGTTCTAAAAATTTGTGAT 300
 DB 156 AspLeuIysProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp 175
 QY 301 TTGGTACACCTGTGATTCAGACACACATGACCAATACAAAGGGAGTGTGCTGTGG 360
 DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 195
 QY 361 ATGGCAGCTGAAAGTTTGTGAAGGTAGTAATTCAGTGAATAAATGTCAGCTCTTCAGCTGG 420
 DB 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTrp 215
 QY 421 GGTATTATCTTTGGGAAGTCAATAACCGTCGGAAACCTTTGATGAGATTTGGTGGCCCA 480
 DB 216 GlyIleIleLeuTyrGluValIleThrArgArgIysProPheAspGluIleGlyGlyPro 235
 QY 481 GCTTTCCGATCATGTGGTGTCTTCAATATGAGTGTGCTGACCAACCTGATGATAAAATTTA 540

PD 12-AUG-1999.
 XX
 PF 02-FEB-1999; 99WO-JP00422.
 XX
 PR 30-OCT-1998; 98JP-0309316.
 PR 06-FEB-1998; 98JP-0026003.
 XX
 XX (TANA) TANABE SEIYAKU CO.
 PA
 Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 XX WPI; 1999-494298/41.
 DR N-PSDB; AAX99697.
 XX
 PT Nuclear factor kappa B activation inhibitors, useful as preventives
 PT for, e.g. autoimmune diseases
 XX
 PS Examples; Page 39-43; 49pp; Japanese.
 XX
 CC The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the amino acid sequence of human TAK1b
 CC (hTAK1b) protein.
 XX
 SQ Sequence 606 AA;

Alignment Scores:
 Pred. No.: 7,51e-134 Length: 606
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 200.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-830-144-1_COPY_408_1091 (1-684) x AAY28997 (1-606)

QY 1 GTAGAGCTTCGGCAGTTCATCCGCTGCAACCATCTAATATTTAAAGCTTTATGAGCC 60
 Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnLeuValLysLeuTyrGlyValA 95
 QY 61 TGCTTGAATCCAGTGTCTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
 Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
 QY 121 CTGCATGCTGTGAACCATTCGCCATATATATCTGCTGCCACGCAAGAGTGTGTGTTA 180
 Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
 QY 181 CAGTGTTCACCAAGGAGTGGCTTACTTTCACAGCATGCAACCAAGCGCTTAATTCACAGG 240
 Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuLeuHisArg 155
 QY 241 GACCTGAACACCAAACTTACTGCTGTGTCAGGGGGCAGCTTCTAAATAATTTGTGAT 300
 Db AspleuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysLeuCysAsp 175
 QY 301 TTTGGTACAGCTGTGACATTCACACATGACCATACCAATACAGGGGAGTGTGCTGG 360
 Db PheGlyThrAlaCysAspLeuGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
 QY 361 ATGGCAGCTGAAGTTTTTGAAGGTAGTAATACAGTGAATAATGTGACGCTCTTCAGCTGG 420
 Db MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 215
 QY 421 GGTATTTATCTTGGGAGTGAATACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
 Db GlyLeuLeuLeuTrpGluValLeuThrArgArgLysProPheAspGluLeuGlyGlyPro 235

QY 481 GCTTTCGAATCATGTGGGCTGTTTCAATGTTACTCGACCCACTGATAAAAAATTTA 540
 Db AlpheArgIleMetTrpAlaValHisAsnGlyThrArgProLeuLeuLeuLysAsnLeu 255
 QY 541 CCTAAGCCCATTCAGAGCCCTGATGACTCGTGTGTGGTCTAAAGATCTTCCACGCGCCT 600
 Db ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGGAGAAATTTGAAAAATATGATCATCTGATGCGGTACTTCCAGGAGCAGAT 660
 Db SerMetGluGluLeuValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
 Db GluProLeuGlnTyrProCysGln 303
 RESULT 10
 ABB58061
 ID ABB58061 standard; Protein; 678 AA.
 XX
 AC ABB58061;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 975.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 XX
 XX Drosophila melanogaster.
 XX
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL02164.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 975; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published/pct_sequences.
 XX
 SQ Sequence 678 AA;
 Alignment Scores:
 Pred. No.: 9.5e-71 Length: 678
 Score: 700.00 Matches: 130
 Percent Similarity: 73.01% Conservative: 35
 Best Local Similarity: 57.52% Mismatches: 57
 Query Match: 55.91% Indels: 4

[illegible]

PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138647.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.

PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161320.
 PR 28-OCT-1999; 99US-0161392.
 PR 28-OCT-1999; 99US-0161393.
 PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 1,36e-33 Length: 369
 Score: 374.00 Matches: 86
 Percent Similarity: 57.80% Conservative: 40
 Best Local Similarity: 39.45% Mismatches: 70
 Query Match: 29.87% Indels: 22
 DB: 21 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x AAG32052 (1-369)

QY 4 GAGCTTGGGAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGCGCTGC 63
 DB 137 GluValSerMetLeuAlaAsnLeuLysHisProAsnIleValArgPheIleGlyAlaCys 156
 QY 64 TTGAATCCAGT-----TGCTTTGTGATGATATGCTGAAGGGGCTCTTTATATAAT 117
 DB 157 ArgLysProMetValTrpCysIleValThrGluTyrAlaLysGlyGlySerValArgGln 176
 QY 118 GTGCTG-----CATGTGTCTGAACCATTTGCCATATTATATCTGCTGCCACGCA 165
 DB 177 PheLeuThrArgArgGlnAsnArgAlaValProLeuLysLeu-----Ala 191
 QY 166 ATGAGTTGGTGTTCACAGTGTCCCAAGGAGTGGCTTTATCTACAGCATGCAACCCAAA 225
 DB 192 ValLysGlnAlaLeuAspValAlaArgGlyMetAlaTyrValHisGly-----Arg 208
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 DB 268 LysValAspValTyrSerPheGlyIleValLeuTrpGluLeuIleThrGlyLeuLeuPro 287
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RESULT 14

AAG32051

ID AAG32051 standard; Protein; 407 AA.

XX AAG32051;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38595.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

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Best Local Similarity: 39.45%
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XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 24999.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX FD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity: 39.91%
Query Match: 29.79%
DB: 21
Length: 369
Matches: 87
Conservative: 39
Mismatch: 70
Indels: 22
Gaps: 9

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Job time : 63.3851 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 08:37:54 ; Search time 30.0405 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 566616

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1252	100.0	606	JC5956	transforming growt
4	392.5	31.3	954	S68178	mixed-lineage prot
5	374	29.9	407	G84635	probable protein k
6	373	29.8	412	T10671	protein kinase hom
7	363.5	29.0	394	TJ0229	mixed-lineage prot
8	362	28.9	1338	T18287	protein-tyrosine k
9	356	28.4	462	S29851	protein kinase 6 (
10	355.5	28.4	370	T46150	protein kinase ATN
11	353.5	28.2	668	JC2363	protein kinase [EC
12	353.5	28.2	888	AS5318	serine/threonine p
13	351.5	28.1	888	JC5399	dual leucine zippe
14	350	28.0	546	D84555	probable protein k

15	348	27.8	391	2	T48115	protein kinase ATM
16	347	27.7	475	2	T12955	probable protein k
17	346	27.6	328	2	T16747	hypothetical prote
18	346	27.6	1030	2	F96763	hypothetical prote
19	345.5	27.6	553	2	T04683	hypothetical prote
20	345.5	27.6	847	1	A53800	mixed-lineage prot
21	344	27.5	390	2	T01451	protein kinase hom
22	341	27.2	410	2	B35670	protein-tyrosine k
23	340	27.2	387	2	T22511	hypothetical prote
24	336	26.8	356	2	S61786	protein kinase ATN
25	329.5	26.3	357	2	C84856	probable protein k
26	329.5	26.3	545	2	T05675	hypothetical prote
27	328.5	26.2	377	2	T46149	protein kinase ATN
28	328.5	26.2	736	2	T05137	protein kinase hom
29	324	25.9	982	2	T08576	probable protein k
30	323	25.8	356	2	T48206	protein kinase ATN
31	323	25.8	821	2	T48400	serine/threonine-p
32	321.5	25.7	364	2	G71410	probable protein k
33	320	25.6	829	2	T07406	probable protein k
34	319.5	25.5	438	2	C86273	protein kinases ho
35	319.5	25.5	445	2	T31581	hypothetical prote
36	315.5	25.2	1064	1	S57450	protein-tyrosine k
37	314	25.1	406	2	T52626	probable mitogen-a
38	313	25.0	1015	2	T00726	probable serine/th
39	308.5	24.6	848	2	B87950	protein F33E2.2 [i
40	308.5	24.6	855	2	T20082	hypothetical prote
41	307.5	24.6	1115	1	S29926	protein-tyrosine k
42	304.5	24.3	402	2	B34735	protein-tyrosine k
43	304.5	24.3	435	2	JN0290	protein-tyrosine k
44	304.5	24.3	477	2	JN0291	protein-tyrosine k
45	304.5	24.3	801	4	TVHURE	transforming prote

ALIGNMENTS

RESULT 1

JC5957
transforming growth factor-beta activated kinase (BC 2.7.-.-) 1c - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Mar-2000
C;Accession: JC5957
R;Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
Biochem. Biophys. Res. Commun. 243, 545-549, 1998
A;Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
A;Reference number: JC5955; MUID:98153801; PMID:9480845
A;Accession: JC5957
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-567 <SAK>
A;Cross-references: DDBJ,AB009358
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: phosphotransferase

Alignment Scores:
Pred No.: 3.96e-73 Length: 567
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x JC5957 (1-567)

Qy	1	GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC	60
Db	76	ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla	95
Qy	61	TGCTTGAATCCAGTGTGTCTTGTCATGCATATCTGACGGGCTCTTTATAATG	120
Db	96	CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal	115
Qy	121	CTGCATGTGTGACCACTTCCCATATTATCTGTCTGCCACGCAATGAGTTGTGTTTA	180

Db 116 LeuHisGlyAlaGluProLeuProTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCACAGGAGTGGCTTATCTTCACAGATGCAACCCCAAGCGCTTAATTCACAGG 240
Db 136 GlnCysSerGlnGlyValAlaIatYrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCCCAACTTACTGCTGGTTCAGGGGGGAGCAGTCTTAAATAATTTGTGAT 300
Db 156 AspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTCTGTGG 360
Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCACCTGAAGTTTTGAAGGTAGTAATTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTGG 420
Db 196 MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
QY 421 GGTATTATTCTTTGGGAAGTGAATACGCGTTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 216 GlyIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
QY 481 GCTTTCCGATCATGTGGCTGTTCATATGCTACCTGACCAACCATGATAAAAAATTTA 540
Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CCTAACCCATTCAGAGCCTGATGACTCGTGTGCTTAAAGATCTTCCAGAGCCCT 600
Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGGAGAAATTTGTAATAATGACTCACTTGTGCTTAAAGATCTTCCAGAGCAGAT 660
Db 276 SerMetGluGluValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCTTGTCTAG 684
Db 296 GluProLeuGlnTyrProCysGln 303

RESULT 2
JC5955
transforming growth factor-beta activated kinase (EC 2.7.-.-) 1a - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5955
R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
Biochem. Biophys. Res. Commun. 243, 545-549, 1998
A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
A:Reference number: JC5955; MUID:98153801; PMID:9480845
A:Accession: JC5955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-579 <SAK>
A:Cross-references: DBJ:AB009356; NID:92924623; PID:BAA25025.1; PID:g2924624
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase

Alignment Scores:
Pred. No.: 3 94e-73 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x JC5955 (1-579)

QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60
Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
QY 61 TGCTTGAATCCAGTGTGCTTGTGATGGAATGCTGAGGGGCTCTTTATATAATGTG 120
Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115

QY 121 CTGATGCTGCTGAAACCAATTCATATTAATCTGCTCCCAACCAAGTGGTGTGTTA 180
Db 116 LeuHisGlyAlaGluProLeuProTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCACAGGAGTGGCTTATCTTCACAGATGCAACCCCAAGCGCTTAATTCACAGG 240
Db 136 GlnCysSerGlnGlyValAlaIatYrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCCCAACTTACTGCTGGTTCAGGGGGGAGCAGTCTTAAATAATTTGTGAT 300
Db 156 AspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTCTGTGG 360
Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCACCTGAAGTTTTGAAGGTAGTAATTCAGTCAAGTCAAGTCAAGTCAAGTGG 420
Db 196 MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
QY 421 GGTATTATTCTTTGGGAAGTGAATACGCGTTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 216 GlyIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
QY 481 GCTTTCCGATCATGTGGCTGTTCATATGCTACCTGACCAACCATGATAAAAAATTTA 540
Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CCTAACCCATTCAGAGCCTGATGACTCGTGTGCTTAAAGATCTTCCAGAGCCCT 600
Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
QY 601 TCAATGGAGAAATTTGTAATAATGACTCACTTGTGCTTAAAGATCTTCCAGAGCAGAT 660
Db 276 SerMetGluGluValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCTTGTCTAG 684
Db 296 GluProLeuGlnTyrProCysGln 303

RESULT 3
JC5956
transforming growth factor-beta activated kinase (EC 2.7.-.-) 1b - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5956
R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
Biochem. Biophys. Res. Commun. 243, 545-549, 1998
A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
A:Reference number: JC5955; MUID:98153801; PMID:9480845
A:Accession: JC5956
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-606 <SAK>
A:Cross-references: DBJ:AB009357; NID:92924625; PID:BAA25026.1; PID:g2924626
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase

Alignment Scores:
Pred. No.: 3 9e-73 Length: 606
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x JC5956 (1-606)

QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60
Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95

QY 61 TGCTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATGTC 120
 Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
 QY 121 CTGCATGCTGCTGAACCATTCATATATATCTGCTGCCACGCAATGAGTTGGTGTTA 180
 Db 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
 QY 181 CAGTGTTCCTCCAGAGTGGCTTATCTTCACAGCATGCCAACCCAAAGCGCTAATTCACAGG 240
 Db 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisarg 155
 QY 241 GACCTGAACCCACCAACTTACTGCTGGTGGAGGGGACAGTCTTAAATAATTTGTGAT 300
 Db 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysileCysAsp 175
 QY 301 TTTTGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGGAGTGTGCTTGG 360
 Db 176 PheGlyThrAlaCysaspGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
 QY 361 ATGGCACCTCGAAGTTTGAAGTAGTAATTAACAGTGAATAATGTGACGCTCTTCAGCTGG 420
 Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysaspValPheSerTyr 215
 QY 421 GGTATTAATCTTTGGGAAGTATAACGCTGCGAAACCTTTTGCATGAGATTGTGGCCCA 480
 Db 216 GlyIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
 QY 481 GCTTTCCGAATCATGGGCTGTTCATATGTTACTCGACCCACCTGATGATAAAATTTA 540
 Db 236 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAACCCCATTCAGAGCCCTGATGACTCGTGTGGTGTGTTAAAGATCTTCCAGCGCCCT 600
 Db 256 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGAGGAATTTGAAATAATGACTTCATCTGATGGGTACTTCCAGGAGCAGAT 660
 Db 276 SerMetGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACGATCTCTCTCAG 684
 Db 296 GluProLeuGlnTyrProCysGln 303

RESULT 4
 S68178
 mixed-lineage protein kinase 2 (EC 2.7.1.-) - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
 C/Accession: S68178; I38044; S32468
 R/Dorow, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simpa
 Eur. J. Biochem. 234, 492-500, 1995
 A/Title: Complete nucleotide sequence, expression, and chromosomal localisation of human
 A/Reference number: S68178; MUID:96128179; PMID:8536694
 A/Accession: S68178
 A/Molecule type: mRNA
 A/Residues: 1-954 <DOR>
 A/Cross-references: EMBL:X90846; NID:9971419; PIDN:CAA62351.1; PID:9971420
 R/Katoh, M.; Hirai, M.; Sugimura, T.; Terada, M.
 Oncogene 10, 1447-1451, 1995
 A/Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase
 A/Reference number: I38044; MUID:95249256; PMID:7731697
 A/Accession: I38044
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
 A/Cross-references: EMBL:Z48615; NID:g758592; PIDN:CAA88531.1; PID:g758593
 R/Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
 Eur. J. Biochem. 213, 701-710, 1993
 A/Title: Identification of a new family of human epithelial protein kinases containing
 A/Reference number: S32467; MUID:93238756; PMID:8477742
 A/Accession: S32468
 A/Molecule type: mRNA

A/Residues: 244-464, 'AQAAGRRQPHQPALWL' <DO2>
 C/Genetics:
 A/Gene: GDB:MLK2; GDB:MST
 A/Cross-references: GDB:362654; GDB:624810; OMIM:600137
 A/Map position: 19q13.1-19q13.2
 C/Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology
 C/Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein ki
 F:23-76/Domain: SH3 homology <SH3>
 F:96-364/Domain: protein kinase homology <KIN>
 F:104-112/Region: protein kinase ATP-binding motif
 F:384-405/Region: leucine zipper motif
 F:419-440/Region: leucine zipper motif
 F:449-463/Region: basic
 F:125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Alignment Scores:
 Pred. No.: 3,948-18 Length: 954
 Score: 392.50 Matches: 88
 Percent Similarity: 56.68% Conservative: 35
 Best Local Similarity: 40.55% Mismatches: 77
 Query Match: 31.35% Indels: 17
 DB: 6 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x S68178 (1-954)

QY 4 GAGCTCGCAGTATTCCTCGTGTGAACCATCTCTAATATTGTAAAGCTTTATGGAGCTGC 63
 Db 145 GluAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleAlaLeuArgGlyAlaCys 164
 QY 64 TTGAATCCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
 Db 165 LeuAsnProProHisLeuCysLeuValMetGluTyrAlaArgGlyGlyAlaLeuSerArg 184
 QY 118 GTGCTCATGCTGCTGAACCATGCTCATATATTACTGCTGCCACGCAATGAGTGTGT 177
 Db 185 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnTyrPala 200
 QY 178 TTAACGTGTTCCTCAAGGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGCTAATTCAC 237
 Db 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleIleHis 220
 QY 238 AGGACCTGAACCCACCAACTTACTGCTGGT-----GCGGG 276
 Db 221 ArgAspLeuLysSerIleAsnIleLeuLeuGluAlaIleGluAsnHisAsnLeuAla 240
 QY 277 GGGACAGTCTCAAAATTTGTGATTTTGTACAGCTGTGCAC---ATTCAGACACACATG 333
 Db 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGluTyrHisLysThrThrLys 260
 QY 334 ACCAATAACAAGGGAGTGTGCTTGGATGCGACCTCAAGTTTTTGAAGGTAGTAATTCAC 393
 Db 261 MetSerAlaAlaGlyThrTyrAlaTyrMetAlaProGluValIleArgLeuSerLeuPhe 280
 QY 394 AGTGAAATAATGTGACGCTTTTCAGCTGGGGTATTATTCTTTGGGAAGTGAATACCGCTGG 453
 Db 281 SerLysSerSerAspValTyrSerPheGlyValLeuLeuTyrGluLeuLeuThrGlyGlu 300
 QY 454 AAACCTTTTGTAGATGTTGGTGGCCAGCTTCCGAATCATGTGGGCTGT---CATAAT 510
 Db 301 ValProTyrArgGluIle-----AspAlaLeuAlaValAlaTyrGlyValAlaMetAsn 318
 QY 511 GGTACTCGACCCACCATGATAAAATTTTACCTAAGCCCATTTGAGCGCTGATGACTCGT 570
 Db 319 LysLeuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuLeuGluGlu 338
 QY 571 TGTGGTCTAAAGATCTCTCCAGCGCCCTTCAATGGAGGAAATGTGAAA 621
 Db 339 CysTyrAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355

RESULT 5
 G84635
 probable protein kinase [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)


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RESULT 7
JU0229
mixed-lineage protein kinase 1 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C/Accession: S32467; JU0229
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
A:Title: Identification of a new family of human epithelial protein kinases containing b
A:Reference number: S32467; MUID:93238756; PMID:8477742
A:Accession: S32467
A:Molecule type: mRNA
A:Residues: 1-394 <DO2>
C:Genetics:
A:Gene: GDB:MLK1
A:Cross-references: GDB:141921; OMIM:600136
A:Map position: 14q24.3-14q31
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F;1-269/Domain: protein kinase homology <KIN>
F;1-269/Domain: catalytic <CAT>
F;9-17/Region: protein kinase ATP-binding motif
F;289-310/Region: leucine zipper motif
F;324-345/Region: leucine zipper motif
F;354-368/Region: basic

Alignment Scores:
Pred. No.: 3,49e-16 Length: 394
Score: 363.50 Matches: 83
Percent Similarity: 54.09% Conservative: 36
Best Local Similarity: 37.73% Mismatches: 84
Query Match: 29.03% Indels: 17
DB: 2 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x JU0229 (1-394)
QY 4 GAGCTTCGGAGTTATCCGTTGGTGAACATCTTAATATTGTAAGCTTTATGGAGCTGC 63
Db 50 GluAlaLysLeuPheAlaMetLeuLysHisProAsnIleAlaLeuArgGlyValCys 69
QY 64 TTGAATCCA-----GTGTGCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 70 LeuLysGluProAsnLeuCysLeuValMetGluPheAlaArgGlyGlyProLeuAsnArg 89
QY 118 GTGCTGCATGCTGTGAACCATTCCTCATATTATATCTGCTGCCACCAATGAGTTGGTGT 177
Db 90 ValLeuSerGlyLysArgGlyProProAspIle-----LeuValAsnTIPAla 105
QY 178 TTACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCAC 237
Db 106 ValGlnIleAlaArgGlyMetAsnTyrLeuHisAspGluAlaIleValProIleIleHis 125
QY 238 AGGACCTGAAACCAACCAACTTACTGCTGTT-----GCAGGG 276
Db 126 ArgAspLeuLysSerSerAsnIleLeuLeuGlnLysValGluAsnGlyAspLeuSer 145
QY 277 GGGACAGTCTTAAATAATTGTGATTTTGGTACGCTGTGAC---ATTACAGACACATG 333
Db 146 AsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTyrHisArgThrThrLys 165
QY 334 ACCAATAACAAGGAGTGGCTTGGATGGACCTGAAGTTTGAAGGTAGTAAATTAC 393
Db 166 MetSerAlaAlaGlyThrTyrAlaTyrMetAlaProGluValIleArgAlaSerMetPhe 185
QY 394 AGTGAAAATGTAGCTCTTCAGCTGGGTATATTCTTTGGAGTGAACGCGTGG 453
Db 186 SerLysGlySerAspValTyrSerTyrGlyValLeuLeuLysValLeuLeuThrGlyGlu 205
QY 454 AAACCTTTGATGAGATGTGGGCCAGCTTCCGAATCATGTGGGCTGTT---CATAT 510
Db 206 ValProPheArgGlyIleAspGly-----LeuArgValAlaTyrGlyValAlaMetAsn 223

QY 511 GGTACTCGACCACTGATATAAAATTTACCTAGCCATTGAGAGCCTGTGACTCGT 570
Db 224 LysLeuAlaLeuProIleProSerThrCysProGluProPheAlaLysLeuMetGluAsp 243
QY 571 TGTGTGCTTAAGATCTTCCAGCGCCCTTCATATGGAGAAATTTGTGAAAATATGACT 630
Db 244 CysTIPAsnProAspProHisSerArgProSerPheThrAsnIleLeuAspGlnLeuThr 263

RESULT 8
T18287
protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C/Accession: T18287
R;Adler, K.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z18856
A:Accession: T18287
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1338 <ADL>
A:Cross-references: EMBL:U64830; NID:g1468982; PID:g1468983; PIDN:AB04999.1
C:Genetics:
A:Introns: 1181/3
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Alignment Scores:
Pred. No.: 3,27e-16 Length: 1338
Score: 362.00 Matches: 80
Percent Similarity: 57.62% Conservative: 41
Best Local Similarity: 38.10% Mismatches: 73
Query Match: 28.91% Indels: 16
DB: 2 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x T18287 (1-1338)
QY 4 GAGCTTCGGAGTTATCCGTTGGTGAACATCTTAATATTGTAAGCTTTATGGAGCTGC 63
Db 1100 GluValSerSerLeuIleLysSerHisProAsnValValThrPheMetGlyAlaArg 1119
QY 64 TTGAATCCAAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGCTG 123
Db 1120 IleAspProCysIlePheThrGluTyrLeuGlnGlyGlySerLeuTyrAspValLeu 1139
QY 124 CAT-----GGTGTGAACCATTCCTCATATTATATCTGCTGCCACCAATGAGT 171
Db 1140 HisIleGlnLysIleLysLeuAsnProLeuMetMetTyrLysMetIleHisAspLeu--- 1158
QY 172 TGGTGTTTACAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTA 231
Db 1159 -----SerLeuGlyMetGluHisLeuHisSerIleGln-----Met 1170
QY 232 ATTCACAGGACCTGAAACCAACCACTTACTGCTGTTGAGGGGGGACAGTCTTAAAA 291
Db 1171 LeuHisArgAspLeuThrSerLysAsnIleLeuLeuAspGluPheLysAsnIle---Lys 1189
QY 292 ATTTGTGATTTTGTACAGCTGTGACATTCACACACATGACC---AATAACAAGGG 348
Db 1190 IleAlaAspPheGlyLeuAlaThrThrLysSerAspMetThrLeuSerGlyIleThr 1209
QY 349 AGTCTGCTGGATGGACCTGAAGTTTTCGAAGTAGTAAATACAGTGAATAATGTGAC 408
Db 1210 AsnProArgTyrArgSerProGluLeuThrLysGlyLeuValTyrAsnGluLysValAsp 1229
QY 409 GTCTTCAGCTGGGTATTTCTTTGGAGTGAATAACGCTCGGAACCCCTTTGATGAG 468
Db 1230 ValTyrSerPheGlyLeuValValTyrGluIleTyrThrGlyLysIleProPheGluGly 1249
QY 469 ATTGGTGGCCAGCTTCCGAATCATGTGGCTGTTTCATATGTTACTCGACCCACTG 528
Db 1250 LeuAspGlyThrAlaSerAlaAlaLysAlaPheGluAsn---TyrArgProAlaIle 1269
QY 529 ATAAAAATTTACCTAAGCCCATTTGAGAGCCTGATGACTCGTTGTTGTTCTTAAAGATCCT 588
```

Db
1269 ProProaspCysProValSerLeuArgLysLeuIleThrLysCysTrpAlaSerAspPro 1288

Qy
589 TCCGAGCGCCCTTCAATCGAGGAANTTCG 618

Dd
1289 SerGlnArgProSerPheThrGluIleLeu 1298

RESULTS

protein kinase 6 (EC 2.7.1.1-) - soybean
S29851
C:Species: Glycine max (soybean)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: S29851; S27760
R:Feng, X.H.; Zhao, Y.; Bottino, P.J.; Kung, S.
Biochim. Biophys. Acta 1172, 200-204, 1993
A:Title: Cloning and characterization of a novel member of protein kinase family from soybean
A:Reference number: S29851; MUID:93176812; PMID:8439562
A:Accession: S29851
A:Molecule type: mRNA
A:Residues: 1-462 <FEN>
A:Cross-references: EMBL:M67449; NID:g170046; PIDN:AAA34002.1; PID:g170047
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:154-419/Domain: protein kinase homology <IN>

Alignment Scores:

Alignment Scores:		
Pred. No.:	1.02e-15	462
Score:	356.00	76
Percent Similarity:	58.88%	Conservative: 50
Best Local Similarity:	35.51%	Mismatches: 74
Query Match:	28.43%	Indels: 14
DB:	2	Gaps: 7

US-09-830-144-1 COPY 408 1091 (1-684) X S29851 (1-462)

QY	4	GAGCTTCGCGACGTTATCCCGTGTGAACCATCTAATATGTAAAGCTTTATGAGGACTGC	63
Db	207	GlulValThrLeuLeuSerArgLeuHisGlnGlnValIleLysPheSerAlaAlaCys	226
QY	64	TTGAATCCA-----GTGTGCTTGTTGATGGAATATATCTGAAAGGGGCTCTTTATATAAT	117
Db	227	ArgLysProProValTyrCysIleIleThrGluTyrLeuAlaGluGlySerLeuArgAla	246
QY	118	GTGCTGCATGGTGTGAACCATTTGCCATATTATTAATCTGCTGCC-----CACGCAATGAGT	171
Db	247	TyrLeuHis-----LysLeuGluHisGlnThrIleSerLeuGlnLysLeuIleAla	263
QY	172	TGGTGTTTACAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGCATGCACCCAAAGCGCTA	231
Db	264	PheAlaLeuAspIleAlaArgGlyMetGluTyrIleHisSer-----GlnGlyVal	280
QY	232	ATTCAACGAGGACCTGAAACACCAACCAATTACTGTGTTGTCACGGGGGACAGTTCCTAAA	291
Db	281	IleHisArgAspLeuLysProGluAsn---IleLeuIleAsnGluAspAsnHisLeuLys	299
QY	292	ATTTGTGATTTTGGTACAGCCTGTGACATTCAGACA-----CACATGACCAATAACAAG	345
Db	300	IleAlaAspPheGlyIleAlaCysGluAlaSerCysAspLeuLeuAlaAspAspPro	319
QY	346	GGGAGTGTCTGTGGATGGGACCTGAAAGTTTGTAAAGGTAGTAAATTCAGTGAATAATGT	405
Db	320	GlyThrTyrArgTyrMetAlaProGluMetIleLysArgLysSerTyrGlyLysLysVal	339
QY	406	GACGTCCTCAGCTGGGGTATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGAT	465
Db	340	AspValIyrSerPheGlyLeuIleLeuTrpGluMetLeuThrGlyThrIleProTyrGlu	359
QY	466	GAGATTGTGTGCCCAGAGCTTTCCGAATCATGTGGGCTGTTTCATAATGCTACTCGACCA	525
Db	360	AspMet---AsnProIleGlnAlaAlaPheAlaValAlaAsnLysAsnSerArgProIle	378
QY	526	CTGATAAAAATTACCTAAGCCCATTTGAGAGCGCTGATGACTCGTTGTGTGTTCTAAAGAT	585

Db IleProSerAsnCysProProAlaMetArgAlaLeuIleGluGlnCysTrpSerIeuGln 398

QY CTTTCCAGCGCCCTCAATGGAGGAATTGTGAAATAATG 627
||| ||| ||| : : : : :
399 ProAspLysArgProGluPheThrGlnValVallyIleLeu 412

Db

RESULT, T 10

protein kinase ATN1-like protein - Arabidopsis thaliana
 N:Alternate names: protein T3A5.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text
 C:Accession: T46150; T08394
 R:Blöcker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.;
 submitted to the Protein Sequence Database, December 1997
 A:Reference number: Z23024
 A:Accession: T46150
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <BLO>
 A:Cross-references: EMBL:AL132979
 A:Experimental source: cultivar Columbia; BAC clone T3A5
 R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.;
 submitted to the Protein Sequence Database, May 1999

A;REFERENCE NUMBER:
A:Accession: T09394

A;Accession: U08394
A;Molecule type: DNA
A;Residues: 1-370 <QUE>
A;Cross-references: ENBL.AL049862; GSPDB:GNC0061; ATSP:Fl8B3.10
A;Experimental source: cultivar Columbia; BAC clone Fl8B3
C;Genetics:
A;Gene: ATSP:Fl8B3.10

A:Map position: 3
A:Introns: 54/3, 98/3, 154/1, 204/3, 255/3

A; ILLIONS: 54/2;
A: Note: T3A5 110

A;NOTE: 13A3.110
 C-Superfamily: basic fibroblast growth factor

c/superramilly: basic fibroblast growth fac

Alignment covered.

Alignment Scores:					
Pred. No.:	1,15e-15	Length:	370		
Score:	355.50	Matches:	79		
Percent Similarity:	56.05%	Conservative:	46		
Best Local Similarity:	35.43%	Mismatches:	81		
Query Match:	28.39%	Indels:	17		
DB:	2	Gave:	9		

U.S.-09-830-144-1 COPY 408 1001 /1 C6A) : E4C1E2 (1 383)

QY	4	GAGCTTCGGCAGCTTATCCCGTGTGAA	63
Db	85	GlulValLeuLeuSerLysMetLysHisAsp	104
QY	64	TGGAATCCA---GTGTGCTTGTGATG	120
Db	105	lleGluProGlnLeuIleIleValThrGlu	124
QY	121	CTGCATGTTGCTGAACATTCCTCCAT	180
Db	125	MetHis---SerArgProGlyPro---Leu	142
QY	181	CAGTGTTCCTCCAAAGGAGTGGCTT	240
Db	143	AspIleSerArgAlaMetGluPheValHis	159
QY	241	GACCTGAAACACCAACTTACTCTGGT	300
Db	160	AspLeuAsnProArgAsnLeuLeuVal	179
QY	301	TTTGGTACAGCCTCT---GACATTCA	357
Db	180	PheGlyIleAlaArgGluGluThrArgGly	199
QY	358	TGAGTGGCACTGAAGTTTTT-----	393

Db 200 TrpMetAlaProGluValTyrSerProGluProLeuArgValGlyGluLysGluTyr 219
 QY 394 AGTGAATAATGTGACGCTTTCAGCTGGGTATTATTCTTTTGGGAAGTGAATAACGCTCGG 453
 Db 220 AspHisLysAlaAspIleTyrSerPheAlaIleValLeuTrpGlnLeuValThrAsnGlu 239
 QY 454 AAACCTTTGATGAGATTGGTGGCCAGCTTTCCGAATCATGTGGCTGTTTCATAATGGT 513
 Db 240 GluProPheProAspValProAsnSerLeuPhe---ValProTyrLeuValSerGlnGly 258
 QY 514 ACTCGACCCACCTGATATAAAATTTACCTTAAGCCCATTCGAGACCTGATGACTCTGTTGT 573
 Db 259 ArgArgProIleLeuThrIysThr---ProAspValPheValProIleValGluSerCys 277
 QY 574 TGGTCTAAAGATCTTCCAGCCGCCCTTCAATCGAGAGAAATTTGAAAATAATGACTCAC 633
 Db 278 TrpAlaGlnAspProAspAlaArgProGluPheLysGluIleSerValMetLeuThrAsn 297
 QY 634 TTGATCGGG 642
 Db 298 LeuLeuArg 300

RESULT 11
 JC2363
 N;Alternate names: leucine-zipper protein kinase
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
 C;Accession: JC2363
 R;Reddy, U.R.; Pleasure, D.
 Biochem. Biophys. Res. Commun. 202, 613-620, 1994
 A;Title: Cloning of a novel putative protein kinase having a leucine zipper domain from
 A;Reference number: JC2363; MUID:94311945; PMID:8037767
 A;Accession: JC2363
 A;Molecule type: mRNA
 A;Residues: 1-668 <RED>
 A;Cross-references: EMBL:U0758
 A;Experimental source: Brain
 A;Note: The nucleotide sequence for this amino acid sequence is inconsistent with that f
 he codon ACC for residue 661 as Pro, the codon GAACACCTCTCCA for residues 664-668 as A
 C;Comment: This protein belongs to the family of non-receptor kinase.
 C;Genetics:
 A;Gene: GDB:ZPK
 A;Cross-references: GDB:383963; OMIM:600447
 A;Map position: 12q13-12q13
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C;Keywords: Atp; leucine zipper; nucleotide binding; P-loop; phosphotransferase
 F;123-371/Domain: protein kinase homology <KIN>
 F;131-139/Region: protein kinase ATP-binding motif
 F;443-471/Region: leucine zipper motif
 F;538-545/Region: nucleotide-binding motif A (P-loop)
 F;152/Active site: Lys #status predicted

Alignment Scores:
 Pred. No.: 1.35e-15 Length: 668
 Score: 353.50 Matches: 75
 Percent Similarity: 54.63% Conservative: 43
 Best Local Similarity: 34.72% Mismatches: 81
 Query Match: 28.23% Indels: 17
 DB: 2 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x JC2363 (1-668)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGACGCTGC 63
 Db 161 AspileLysHisLeuArgLysLeuLysHisProAsnIleIleThrPheLysGlyValCys 180
 QY 64 TTGAATCCA-----GTGTGTTCTGTGATGGAATATGTGAAGGGGCTCTTTATATAT 117
 Db 181 ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlnLeuTyrGlu 200
 QY 118 GTGCTGCATGGTGTGAACCATTCGCATATATATATCTGCTGCCACGCAATGATGTTGGTGT 177

Db 201 ValLeuArgAlaGlyArgProVal-----ThrProSerLeuLeuValAspTrpSer 217
 QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTAC 237
 Db 218 MetGlyIleAlaGlyGlyMetAsnTyrLeuHisLeuHisLys-----IleIleHis 234
 QY 238 AGGACCTCAAAACCCAACTTACTGCTGGTTCAGGGGGGACACAGTCTTCAAAAATTTGT 297
 Db 235 ArgAspLeuLysSerProAsn---MetLeuIleThrTyrAspAspValValLysIleSer 253
 QY 298 GATTTTGGTACGCCGTGACATTCAGACACATGACCAATAACAG-----GGAGT 351
 Db 254 AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr 273
 QY 352 GCTGCTGCATGCACCTGAAGTTTGTGAAGGTAGTAAATTACAGTGAATAATGTGACGTC 411
 Db 274 ValAlaTrpMetAlaProGluValIleArgAsnGluProValSerGluLysValAspIle 293
 QY 412 TTCAGCTGGGGTATTATTCTTTCGGGAAGTGAATACCGTCGGAAACCCCTTTGATGAGATT 471
 Db 294 TrpSerPheGlyValValLeuLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspVal 313
 QY 472 GGTGGCCAGCTTTCGGAATCATGTGGGTGTT---CATTAATGGTACTCCACACCACTG 528
 Db 314 AspSerSerAla-----IleIleTrpGlyValGlySerAsnSerLeuHisLeuProVal 331
 QY 529 ATAAAAATTTACCTTAAGCCCATTCAGAGCTCATGACTCGTTGTTGGTCTTAAAGATCCT 588
 Db 332 ProSerSerCysProAspGlyPheLysIleLeuLeuArgGlnCysTrpAsnSerLysPro 351
 QY 589 TCCACAGCGCCCTTCAATGGAGGAATTTGAAAATATGACTCACTCTG 636
 Db 352 ArgAsnArgProSerPheArgGln-----IleLeuLeuHisLeu 364

RESULT 12
 A55318
 serine/threonine protein kinase (EC 2.7.1.1-) DLK - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Sep-1999
 C;Accession: A55318
 R;Holzman, L.B.; Merritt, S.E.; Fan, G.
 J. Biol. Chem. 269, 30808-30817, 1994
 A;Title: Identification, molecular cloning, and characterization of dual leucine zipper
 S;Reference number: A55318; MUID:95074107; PMID:7983011
 A;Accession: A55318
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-888 <HOL>
 A;Cross-references: GB:U14636; NID:G602677; PIDN:AAA57280.1; PID:G602678
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C;Keywords: Atp; leucine zipper; phosphotransferase
 F;156-404/Domain: protein kinase homology <KIN>
 F;164-172/Region: protein kinase ATP-binding motif

Alignment Scores:
 Pred. No.: 1.26e-15 Length: 888
 Score: 353.50 Matches: 75
 Percent Similarity: 54.63% Conservative: 43
 Best Local Similarity: 34.72% Mismatches: 81
 Query Match: 28.23% Indels: 17
 DB: 2 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x A55318 (1-888)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGACGCTGC 63
 Db 194 AspileLysHisLeuArgLysLeuLysHisProAsnIleIleThrPheLysGlyValCys 213
 QY 64 TTGAATCCA-----GTGTGTTCTGTGATGGAATATGTGAAGGGGCTCTTTATATAT 117
 Db 214 ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlnLeuTyrGlu 233

US-09-830-144-1 COPY 408 1091 (1-684) X D84555 (1-546)

Qy 7 CTTGGCGAGTTATCC-----CGTGTGAACCACTCCATAATTGTA 45
Db 325 LeuArgGluPheSerGlnGluValPheIleMetArgLysValArgHisLysAsnValVal 344
Qy 46 AAGCTTTATGGAGCGCTGCTTGAAT-----CCAGTGTGCTTGTGATGGAAATATGCTCAA 99
Db 345 GlnPheLeuGlyAlaCysThrArgSerProThrLeuCysIleValThrGluPheMetAla 364
Qy 100 GGGGCTCTTTATATAATATGCTGCGATGGCTGAACCACTGCCATATATATGCTGCTGCC 159
Db 365 ArgGlySerIleTyrAspPheLeuHisLysGlnLysCysAla-----PheLysLeuGln 382
Qy 160 CACGCAATGAGTTGGTGGTTTACAGTGTCTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 383 ThrLeuLeuLysValAlaLeuAspValAlaLysGlyMetSerTyrLeuHisGln----- 400
Qy 220 CCCAAGGCGCTAATTCACAGGGACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGG 279
Db 401 ---AsnAsnIleIleHisArgAspLeuLysThrAlaAsnLeuLeuMetAspGluHisGly 419
Qy 280 ACAGTTCTAAATAATTTGTGATTTTGGTACAGCC---TGTGACATTCACACACAC---ATG 333
Db 420 LeuVal---LysValAlaAspPheGlyValAlaArgValGlnIleGluSerGlyValMet 438
Qy 334 ACCAATAACAAGGGGAGTGTGCTTGGATGGCAGCTGAAAGTTTGTGAAGTAGTAATTAC 393
Db 439 ThrAlaGluThrGlyThrTyrArgTTPMetAlaProGluValIleGluHisLysProTyr 458
Qy 394 AGTGAATAATGTGACGCTTCAGCTGGGGGTATATCTTTGGAGAGTGAATACGGCTCGG 453
Db 459 AsnHisLysAlaAspValPheSerTyrAlaIleValLeuTTPGluLeuLeuThrGlyAsp 478
Qy 454 AAACCTTTGATGAGATTTGGTGGCCAGCTTCCGAATCATGTGGCTGTTTCATAATGCT 513
Db 479 IleProTyrAlaPheLeu---ThrProLeuGlnAlaValGlyValValGlnLysGly 497
Qy 514 ACTCGACCACTGATATAAATAATTTACTTAAGACCCATGAGAGCCCTGATGCTGTTGT 573
Db 498 LeuArgProLysIleProLysLysThrHisProLysValLysGlyLeuLeuGluArgCys 517
Qy 574 TGGTCTAAGATCCTTCCAGAGCCCTTCAATGGAGGAATTTGAAATAATGACTACAC 633
Db 518 TrpHisGlnAspProGluGlnArgProLeuPheGluGluIleIleGluMetLeuGlnGln 537
Qy 634 TTGATCGCG 642
Db 538 IleMetLys 540

RESULT 15
T48115
protein kinase ATM1K1 (EC 2.7.1.-) [imported] - Arabidopsis thaliana
N:Alternate names: Protein F16M2.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2001
C:Accession: T48115; T51942
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, R.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T48115
A:Molecule type: DNA
A:Residues: 1-391 <RIE>
A:Cross-references: EMBL:AL138648; NID:g7523397; PIDN:CAB86427.1; PID:g75233408
A:Experimental source: cultivar Columbia, BAC clone F16M2
R:Ichimura, K.; Mizoguchi, T.; Shinozaki, K.
Plant Sci. 130, 171-179, 1997
A:Title: ATM1K1, an Arabidopsis protein kinase related to mammal mixed-lineage kinases
A:Reference number: Z24427
A:Accession: T51942
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-391 <ICH>

A:Cross-references: EMBL:AB006810; NID:G2351096; PIDN:BAA22079.1; PID:G2351097
A:Experimental source: cultivar Columbia
C:Genetics:

C; Genetics:
A; Map position: 3
A; Introns: 109/1; 149/3; 220/2; 278/3; 323/3

A;Locations: 109/1, 149/3, 220/2, 216/3, 323/3
A;Note: F16M2.110
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase

Alignment Scores:	
Pred. No.:	3,44e-15
Score:	348.00
Percent Similarity:	48.15%
Best Local Similarity:	33.74%
Query Match:	27.80%
DB:	2
	DB:
	Gaps:
	Indels:
	Mismatches:
	Conservative:
	Matches:
	Length:
	351

US-09-830-144-1 COPY 408 1091 (1-684) x T48115 (1-391)

Qy	4	GAGCTTCGGCAGTTATCCCGTGTCAACCATCTTAATATTGTAAAGCTTTATGGAGCCCTGC	63
Db	135	GluValAlaValTTPGlnLysLeuAspHisProAsnValThrLysPheIleGlyAlaSer	154
Qy	64	TTG-----	66
Db	155	MetGlyThrSerAspLeuArgIleProLagGlyAspThrGlyGlyArgGlyAsnGly	174
Qy	67	-----AATCCAGTCGTCTTCTTGATGGAATATGCTGAAGGGGGCTCTTTATAT	114
Db	175	AlaHisProAlaArgAlaCysCysValValValGluTyrValAlaGlyGlyThrLeuLys	194
Qy	115	AATGTGTGCATGGTGTGAACCATGTCATATATATCTGCT-----GCCAC	162
Db	195	LysPheLeu-----IleLysLysTyrArgAlaLysLeuProIleLysAsp	209
Qy	163	GCAATGAGTTCGTGTTTACAGTGTGCCAAGAGTGGCTTATCTTCACAGCATGCAACC	222
Db	210	ValIleGlnLeuAlaLeuAspLeuAlaArgGlyLeuSerTyrLeuHisSer-----	226
Qy	223	AAAGCGCTAAATTCACAGGAGCTGAAACACCAACTTACTGCTGGTTGCAGGGGGACA	282
Db	227	LysAlaIleValHisArgAspValLysSerGluAsnMetLeuLeuGlnProAsnLysThr	246
Qy	283	GTTCTAAATAATTGTGATTTTGGTACAGCC-----TGTGACATTGAGCACACATG	333
Db	247	---LeuLysIleAlaAspPheGlyValAlaArgValGluAlaGlnAsnProGlnAspMet	265
Qy	334	ACCAATAACAGGGGAGTGTCTTGGATGGCCACCTGAAGTTTGAAGTAGTAGTAATAC	393
Db	266	ThrGlyGluThrGlyThrLeuGlyTyrMetAlaProGluValLeuGluGlyLysProTyr	285
Qy	394	AGTGAAATAATGACGCTCTCAGCTGGGGGTATATTCTTTGGGAAGTGATAACGGCTCG	453
Db	286	AsnArgLysCysAspValTyr-SerPheGlyValCysLeuTyrGluIleTyrCysCysasp	305
Qy	454	AAACCC-----TTTGATGAGATTGTTGGCCACGCTTCGGAATCATGTGG	498
Db	306	MetProTyrAlaAspCysSerPheAlaGluIleSerHisAla-----	319
Qy	499	GCTGTTTCATAATGGTACTCGACCACTGTATAAAAAATTTTACCTAAGCCCATTTGAGAGC	558
Db	320	ValValHisArgAsnLeuArgProGluIleProLysCysCysProHisAlaValAlaAsn	339
Qy	559	CTGATGACTCGTTGTTGGTCTAAAGACTCTTCCCAGCGCCCTTCATATGGAGAAATTTG	618
Db	340	IleMetLysArgCysTyrAspProAsnProAspArgArgProGluMetGluGluValVal	359
Qy	619	AAATAATG	627
Db	360	LysLeuLeu	362

Search completed: December 4, 2003, 09:08:38

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 07:06:54 ; Search time 16.1757 Seconds
(without alignments)
3977.116 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 1252
Sequence: 1 gtagagcttcggcagttatc.....cattacagtagtcctgttcag 684

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2_1/USPTO_spool/US09830144/runat_03122003_122344_21226/app_query.fasta_1.1230
-DB=SwissProt_41 -QFMT=fastan -SURFIX=rsb -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-LOCALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144 @CGN 1 1 16 @runat_03122003_122344_21226 -NCPU=6 -ICPU=3
-NO MAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	579	1 M3K7 MOUSE	Q62073 mus musculus
2	1252	100.0	606	1 M3K7 HUMAN	O43318 homo sapien
3	435.5	34.8	393	1 M3K7 DROME	P83104 drosophila
4	392.5	31.3	954	1 M3K4 HUMAN	Q02779 homo sapien
5	363.5	29.0	394	1 M3K9 HUMAN	P80192 homo sapien
6	355.5	28.4	888	1 M3K3 RAT	Q63796 rattus norv
7	353.5	28.2	859	1 M3K3 HUMAN	Q12852 homo sapien
8	353.5	28.2	888	1 M3K3 MOUSE	Q60700 mus musculus
9	341	27.2	410	1 KYK2 DICDI	P18161 dictyosteli
10	323	25.8	821	1 CTR1 ARATH	Q05609 arabidopsis
11	307.5	24.6	1115	1 RET MOUSE	P35546 mus musculus
12	304.5	24.3	1114	1 RET HUMAN	P07949 homo sapien
13	301.5	24.1	630	1 TEC MOUSE	P24604 mus musculus
14	301.5	24.1	631	1 TEC HUMAN	P42680 homo sapien
15	299.5	23.9	625	1 ITK MOUSE	Q03526 mus musculus
16	298.5	23.8	620	1 ITK HUMAN	Q08881 homo sapien
17	294.5	23.5	2347	1 KROS HUMAN	P08922 homo sapien
18	292.5	23.4	402	1 KROS_AVISU	P00529 avian sarco

ALIGNMENTS

RESULT 1

M3K7 MOUSE ID M3K7 MOUSE STANDARD; PRT; 579 AA.

AC Q62073;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 7 (EC 2.7.1.-)
DE (Transforming growth factor-beta-activated kinase 1) (TGF-beta-activated kinase 1).
GN MAP3K7 OR TAK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96123277; PubMed=8533096;
RA Yanaguchi K., Shirakabe K., Shibuya H., Irie K., Ohishi I., Ueno N., Taniguchi T., Nishida E., Matsumoto K.;
RT Identification of a member of the MAPKKK family as a potential mediator of TGF-beta signal transduction.;
RL Science 270:2008-2011(1995).
CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS.
CC -!- MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C210RF7.
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CC -----
CC EMBL; D76446; BAA11184.1; -
CC HSSP; P08631; IAD5.
CC MGD; MGI:1346877; Map3k7.
CC InterPro; IPR000719; Prot_kinase.

19 292 23.3 507 1 KROS CHICK
20 290 23.2 1584 1 KYK1 DICDI
21 288.5 23.0 628 1 TESI RAT
22 288 23.0 1307 1 PHYT_CERPU
23 286 22.8 804 1 FPS DROME
24 284.5 22.7 832 1 ANR3 HUMAN
25 283.5 22.6 527 1 TXK MOUSE
26 280 22.4 822 1 FGR1 RAT
27 279 22.3 467 1 MATK RAT
28 278 22.2 822 1 FGR1 HUMAN
29 278 22.2 822 1 FGR1 MOUSE
30 277.5 22.2 786 1 BTKL DROME
31 275 22.0 984 1 EPA3 RAT
32 274.5 21.9 801 1 FGR3 MOUSE
33 271.5 21.7 1062 1 CC7 SCHPO
34 271 21.6 604 1 KRAA MOUSE
35 271 21.6 604 1 KRAA RAT
36 270.5 21.6 503 1 HCK RAT
37 270 21.6 806 1 FGR3 HUMAN
38 269.5 21.5 507 1 MATK HUMAN
39 269.5 21.5 626 1 TESI HUMAN
40 269 21.5 533 1 FPS AVISP
41 269 21.5 819 1 FGR1 CHICK
42 269 21.5 983 1 EPA3 HUMAN
43 268 21.4 830 1 PKN2 MYXXA
44 268 21.4 1052 1 FAK1 HUMAN
45 268 21.4 1055 1 FAK1 RAT

P08941 gallus gall
P18160 dictyosteli
O63572 rattus norv
P25848 ceratodon p
P18106 drosophila
P57078 homo sapien
P42682 mus musculu
O04589 rattus norv
P11243 rattus norv
P11362 homo sapien
P16092 mus musculu
O08630 drosophila
O08680 rattus norv
O61851 mus musculu
P41892 schizosacch
P04627 mus musculu
P14056 rattus norv
P50545 rattus norv
P22607 homo sapien
P42679 homo sapien
O15569 homo sapien
P00541 avian sarco
P21804 gallus gall
P29320 homo sapien
P54736 myxococcus
O05397 homo sapien
O35346 rattus norv

DR InterPro; IPR002290; Ser thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 8 16 POLY-SER.
 FT BIND 36 291 PROTEIN KINASE.
 FT NP BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT SITE 156 156 BY SIMILARITY.
 SQ SEQUENCE 579 AA; 64227 MW; 97C8P6F3C8E283BE CRC64;

Alignment Scores:
 Pred. No.: 2.82e-116 Length: 579
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x M3K7_MOUSE (1-579)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGCAACCATCCTAATATTGTAAGCTTTATGAGCC 60
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnileValLysLeuTyrGlyAla 95
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATGTC 120
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 CTGCATGGTCTGAACCATTCATATATCTGCTGCCACCAATGAGTGTGCTGTTA 180
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 CAGTGTTCACAGAGTGGCTTCTTCACAGATGCACATCCACCCAAAGCGCTAATTCACAGG 240
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuLeuHisArg 155
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 GACCTGAACACCAACTTACTGCTGGTTCAGGGGGACAGCTTCTAAATAATTTGCTGAT 300
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 156 AspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysLleCysAsp 175
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTCTGCTTG 360
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 ATGGCACCTGAAGTCTTTGAAGTACTAATTACAGTGAATAATGTGACGCTTCAGCTGG 420
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 GGTATTATTCTTTGGGAAGTATAGCGCTCGGAACCCCTTTGATCAGATTTGTCGCCCA 480
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 216 GlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyLysPro 235
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 GCTTTCGGAATCATGTGGCTGTTCTAATAGTACTCGACCCACCATGATAAAATTTA 540
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProLeuIleLysAsnLeu 255
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 CTTAAGCCCATTCAGAGCTGTGACTCGTGTGTTGTTGTTAAAGATCTTCCAGCGCCCT 600
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 256 ProLysProIleGluSerLeuMetThrArgCysTyrPserLysAspProSerGlnArgPro 275
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 TCAATCGAGGAATTCGAAATAATGACTCACTTGATCGGTACTTTCACAGAGCAGAT 660
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 GAGCCATTACAGTATCTTGTCTGAC 684
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 296 GluProLeuGlnTyrProCysGln 303
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
 M3K7 HUMAN STANDARD; PRT; 606 AA.
 ID O43318; O43317; O43319;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase kinase 7 (EC 2.7.1.-)
 DE (Transforming growth factor-beta-activated kinase 1) (TGF-beta-activated kinase 1).
 DE MAP3K7 OR TAK1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
 RC TISSUE=Lung;
 RX MEDLINE=98153801; PubMed=9480845;
 RA Sakurai H., Shigemori N., Hasegawa K., Sugita T.;
 RT "TGF-beta-activated kinase 1 stimulates NF-kappa B activation by an NF-kappa B-inducing kinase-independent mechanism";
 RL Biochem. Biophys. Res. Commun. 243:545-549(1998).
 CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS. MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B ACTIVATION.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1B;
 CC IsoId=O43318-1; Sequence=Displayed;
 CC Name=1A;
 CC IsoId=O43318-2; Sequence=VSP_004886;
 CC Name=1C;
 CC IsoId=O43318-3; Sequence=VSP_004887. VSP_004888;
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C21ORF7.
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 CC -----
 CC EMBL; AB0093157; BAA25026.1; -;
 CC EMBL; AB0093156; BAA25025.1; -;
 CC EMBL; AB0093158; BAA25027.2; -;
 CC PIR; JC5955; JC5955.
 CC PIR; JC5956; JC5956.
 CC HSP; P08631; IAD5.
 CC Genew; HGNC:6859; MAP3K7.
 CC MIM; 602614;
 CC GO; GO:0004709; F:MAP kinase kinase kinase activity; TAS.
 CC GO; GO:0007179; P:TGFbeta receptor signaling pathway; TAS.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Alternative splicing.
 FT DOMAIN 8 14 POLY-SER.
 FT BIND 36 291 PROTEIN KINASE.
 FT NP BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 156 156 BY SIMILARITY.

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FT VARSPLIC 404 430 Missing (in isoform 1A).
FT FTID=VSP_004886.
FT VARSPLIC 509 518 PLAPCNSKE -> ARTSRTGPG (in isoform 1C).
FT FTID=VSP_004887.
FT VARSPLIC 519 606 Missing (in isoform 1C).
FT FTID=VSP_004888.
SQ SEQUENCE 606 AA; 67196 MW; 3D8F8147CD174013 CRC64;

Alignment Scores:
Pred. No.: 2,84e-116 Length: 606
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x M3K7_HUMAN (1-606)

QY 1 GTGAGCTTCGGCAGTATCCCTGTCGACCATCTTAATTTCTAAGCTTTATGGAGCC 60
DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 95
QY 61 TGCTTGAATCCAGTGTCTTGTGATGCAATATGCTGAAGGGGCTCTTTATATAATGTG 120
DB 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
QY 121 CTGATGCTGCTGAACCATTTGCCATATTTACTGCTGCCCAACCAATGAGTTGGTTA 180
DB 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTCCCAAGGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAGG 240
DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY 241 GACCTGAACACCAAACTTACTGCTGCTGAGGGGAGCAGTTCTAAAAATTTGTGAT 300
DB 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTGTTGTCACGCTGTGACATTCAGACACACATGACCAATACAGGGAGTGCTGTGG 360
DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGGCACCCTGAAGTTTGTGAAGTGTAGTAAATACAGTGAATAATGTGACGCTCAGTGG 420
DB 196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
QY 421 GGTATTATTCTTGGGAGTGATACCGTCGGAACCCCTTTGATGAGATTGGTGCCCA 480
DB 216 GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
QY 481 GCTTTCGGAATCATGTGGCTGTTTCATATGTTACTCGACCACTGATATAAAATTTA 540
DB 236 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
QY 541 CTTAAGCCCATGTAGAGCTGATACCTGTTGGTCTTAAGATCTCTCCAGCGCCT 600
DB 256 ProlLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCATGAGGAAATTTGMAAATATGACTCATTGATGCGGTACTTTCCAGGAGCAGAT 660
DB 276 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCTCTGTGTCAG 684
DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 3
M3K7 DROME
ID M3K7 DROME STANDARD; PRT; 393 AA.
AC P81104;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

```

DE Putative mitogen-activated protein kinase kinase 7
DE (EC 2.7.1.1.-).
DE TAKL1.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; PubMed=107311132;
RX MEDLINE=20196006; Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celnik S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA Anantides P.G., Scherer S.E., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Beasley E.M.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Borkova D., Butchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fesler C., Gabriell A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RC CONCEPTUAL TRANSLATION.
RP Manning G., Sudarsanam S., Plowman G.;
RA "Prediction of novel protein kinases from the Drosophila genome
RT project and EST sequences.";
RT Unpublished observations (AUG-2001).
CC -!- FUNCTION: Can phosphorylate and activate yet undefined MAPKs.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AE003732; -; NOT ANNOTATED_CDS.
CC FlyBase; FBgn0046689; Tak11.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC Pfam; PF00069; pkinase; 1.

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ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW Tyrosine-protein kinase; ATP-binding.
 FT DOMAIN 11 266 PROTEIN_KINASE.
 FT NP_BIND 17 25 ATP (By similarity).
 FT BINDING 38 38 ATP (By similarity).
 FT ACT_SITE 133 133 BY SIMILARITY.
 SQ SEQUENCE 393 AA; 45238 MW; 43370C98490F0384 CRC64;

Alignment Scores:
 Pred. No.: 3,03e-35 Length: 393
 Score: 435,50 Matches: 91
 Percent Similarity: 60,78% Conservative: 50
 Best Local Similarity: 39,22% Mismatches: 80
 Query Match: 34,78% Indels: 11
 DB: 1 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x M3K7_DROME (1-393)

QY 4 GAGCTTGGGAGTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCGCTGC 63
 Db 54 GluileThrHisLeuSerGluileAspHisGluAsnValileArgValilleGlyArgAla 73
 QY 64 TTGAAT-----CCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTTTTATATAAT 117
 Db 74 SerAsnGlyLysLysAspTyrLeuLeuMetGluTyrLeuGluGlySerLeuHisAsn 93
 QY 118 GTGCTCGATGGTCTGCTGAACCATTTGCCATATATATATATATATATATATATATAT 177
 Db 94 TyrLeuTyrGlyAspAspLysTyrGlu---TyrThrValGluGlnAlaValArgTyrAla 112
 QY 178 TTACAGTGTCTCCAGAGGTGGTGTATCTTCACAGATGCAACCCAAAGCGCTTAATTCAC 237
 Db 113 LeuGlnCysAlaLysAlaLeuAlaTyrLeuHisSerLeuAsp---ArgProIleValHis 131
 QY 238 AGGAGCTCAAAACCAACCACTTACTGCTGTTGTCAGGGGGGACAGTCTTAATAATTTGT 297
 Db 132 ArgAspIleLysProGlnAsnMetLeuLeuTyrAspGlnHisGluAspLeuLysIleCys 151
 QY 298 GATTTGGTACGCTGTGATCATTCAGACACATGACCAATTAACAAAGGGAGTGTCTGCT 357
 Db 152 AspPheGlyLeuAlaThrAspMetSerAsnAsnLysThrAspMetGlnGlyThrLeuArg 171
 QY 358 TGGATGGACCTCAAGTTTGAAGTAGTAATACAGTGAAATATGTCAGCTTCACG 417
 Db 172 TyrMetAlaProGluAlaIleLysHisLeuLysTyrThrAlaLysCysAspValTyrSer 191
 QY 418 TGGGTATTATTCTTTGGGAAGTGATAACGGTCGGAAACCCCTTTGATGAGATTGGTGGC 477
 Db 192 PheGlyIleMetLeuTyrGluLeuMetThrArgGlnLeuProTyrSerHisLeuGluAsn 211
 QY 478 CCA-----GCTTCCGAATCATGTGGGCTGTTCATAATGGTACTCGACCACTG--- 528
 Db 212 ProAsnSerGlnTyrAlaIleMetLysAlaIleSerSerGlyLysLeuProMetGlu 231
 QY 529 -----ATAAAAATTACTAAGCCCATGAGAGCTGATGACGTGTGTGGTCTAAA 582
 Db 232 AlaValArgSerAspCysProGluGlyIleLysGlnLeuMetGluCysCysMetAspIle 251
 QY 583 GATCTCTCCAGCGGCTCAATGAGGAAATTTGTAATATGACTACTACTGATGCGG 642
 Db 252 AsnProGluLysArgProSerMetLysGluIleGluLysPheLeuGlyGlu-----Gln 269
 QY 643 TACTTCCAGGACGATGAGCCATTACAGTATCTCT 678
 Db 270 TyrGluSerGlyThrAspGluAspPheIleLysPro 281

RESULT 4

M3KA_HUMAN

ID M3KA_HUMAN

STANDARD; PRT; 954 AA.

AC Q02779; Q12761; Q14871;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 20-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase kinase 10 (EC 2.7.1.37)
 DE (Mixed lineage kinase 2) (Protein kinase MST).
 GN MAP3K10 OR MLK2 OR MST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96128179; PubMed=8536694;
 RA Dorow D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
 RA Sutherland G.R., Simpson R.J.;
 RT "Complete nucleotide sequence, expression, and chromosomal
 RT localisation of human mixed-lineage kinase 2.";
 RL Eur. J. Biochem. 234:492-500(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95249256; PubMed=7731697;
 RA Katoh M., Hirai M., Sugimura T., Terada M.;
 RT "Cloning and characterization of MSF, a novel (putative)
 RT serine/threonine kinase with SH3 domain.";
 RL Oncogene 10:1447-1451(1995).
 RN [3]
 RP SEQUENCE OF 244-480 FROM N.A.
 RC TISSUE=Colon epithelium;
 RX MEDLINE=9338756; PubMed=8477742;
 RA Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;
 RT "Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains.";
 RL Eur. J. Biochem. 213:701-710(1993).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 DR EMBL; X90846; CAA62351.1; -
 DR EMBL; Z48615; CAA88531.1; -
 DR PIR; S68178; S68178.
 DR HSP; P11362; 1FGK.
 DR Genew; HGNC:6849; MAP3K10.
 DR MIM; 600137; -
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0007254; P:JNK cascade; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000719; Ser_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50002; SH3; 1.
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 FT ATP-binding; SH3 domain.
 FT DOMAIN 2 5
 FT DOMAIN 16 81
 FT DOMAIN 98 360
 FT NP_BIND 104 112
 FT BINDING 125 125
 FT ACT_SITE 222 222
 FT DOMAIN 384 405
 FT DOMAIN 419 440
 FT DOMAIN 449 463
 FT CONFLICT 462 464
 FT CONFLICT 465 480
 FT CONFLICT 471 471
 FT CONFLICT 807 807
 FT CONFLICT 818 818
 SQ SEQUENCE 954 AA; 103623 MW; 538F4AAA559B0ABA CRC64;

Alignment Scores:
 Pred. No.: 6,44e-31 Length: 954
 Score: 392.50 Matches: 88
 Percent Similarity: 56.68% Conservatives: 35
 Best Local Similarity: 40.55% Mismatches: 77
 Query Match: 31.35% Indels: 17
 DB: 1 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x M3KA_HUMAN (1-954)

QY 4 GAGCTTCGGCAGTATATCCCGTGTGCAACCATCTTAATATTGTAAGCTTTATGGAGCTGC 63
 Db 145 GhuAlaArgLeuPheGlyAlaLeuGluHisProAsnIleLeuAlaLeuArgGlyAlaCys 164

QY 64 TTGAATCCA-----GTGTGCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAAT 117
 Db 165 LeuAsnProHisLeuCysLeuValMetGluTyrAlaArgGlyGlyAlaLeuSerArg 184

QY 118 GTGCTCATGTGTGTGAACCATGTCATATATATATCTGCTGCCACCAAGTGTGTGT 177
 Db 185 ValLeuAlaGlyArgValProHisVal-----LeuValAsnTyrAla 200

QY 178 TTACAGTGTTCACAGGAGTGGCTATCTTCACAGCATGCAACCAAGCGCTAATTCAC 237
 Db 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleHis 220

QY 238 AGGACCTGAAACCAACCAACTACTGCTGTT-----GCAGGG 276
 Db 221 ArgAspLeuLysSerIleAsnIleLeuGluAlaIleGluAsnHisAsnLeuAla 240

QY 277 GGGACAGTTCTAAAATTGTGATTTGGTACGCTGTGAC---ATTCAGACACACATG 333
 Db 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGluTyrHisLysThrThrLys 260

QY 334 ACCAATAACAGGGAGTGTGCTGTGATGTCACCTGACCTTGTGAGGTAGTAAATAC 393
 Db 261 MetSerAlaAlaGlyThrTyrAlaTyrMetAlaProGluValIleArgLeuSerLeuPhe 280

QY 394 AGTGAATAATGTACGCTTTCAGCTGGGATATTCTTTGGGAAGTGAATACCGCTCGG 453
 Db 281 SerLysSerSerAspValTyrSerPheGlyValLeuLeuTyrGluLeuLeuThrGlyGlu 300

QY 454 AAACCCCTTTGATGATGTTGGCCCGACGCTTCCGAATCATGTGGCTGTT---CATAA 510
 Db 301 ValProTyrArgGluIle-----AspAlaLeuAlaValAlaTyrGlyValAlaMetAsn 318

QY 511 GGTACTGCACCACTCATATAAAATTTACTAAGCCCATGAGAGCTCATGACTCGT 570
 Db 319 LysLeuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuGluGlu 338

QY 571 TGTGGTCTAAGATCTCTCCAGCGCCCTTCAATGGAGGAAATGTGAAA 621
 Db 339 CysTrpAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355

RESULT 5
 M3K9_HUMAN STANDARD; PRT; 394 AA.
 ID M3K9_HUMAN
 AC P80132;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase kinase 9 (EC 2.7.1.-) (Mixed
 DE lineage kinase 1) (Fragment).
 GN MAP3K9 OR MLK1 OR PRK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon epithelium;
 RX MEDLINE=93238756; PubMed=8477742;
 RA Dorow D.S., Devereux L., Dietzsch E., de Kreseer T.;
 RT "Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains.";
 RL Eur. J. Biochem. 213:701-710(1993).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF
 CC COLONIC, BREAST AND OESOPHAGEAL ORIGIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 DR PIR; S32467; J00229.
 DR HSSP; P12931; IPMK.
 DR Genew; HGNC:6861; MAP3K9.
 DR MIM; 600136; -
 DR GO; GO:0005524; F:ATP binding activity; NAS.
 DR GO; GO:0004708; F:MAP kinase activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR00719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR InterPro; IPR001245; Tyr kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PD00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding.
 FT NON_TER 1 1
 FT DOMAIN 3 271
 FT NP_BIND 9 17
 FT BINDING 30 30
 FT ACT_SITE 127 127
 FT DOMAIN 289 310
 FT DOMAIN 324 345
 FT DOMAIN 354 368
 SQ SEQUENCE 394 AA; 44975 MW; DBE40B7D31047FD8 CRC64;

Alignment Scores:
 Pred. No.: 4.26e-28 Length: 394
 Score: 363.50 Matches: 83
 Percent Similarity: 54.09% Conservatives: 36
 Best Local Similarity: 37.73% Mismatches: 84
 Query Match: 29.03% Indels: 17
 DB: 1 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x M3K9_HUMAN (1-394)

QY 4 GAGCTTCGGCAGTATATCCCGTGTGCAACCATCTTAATATTGTAAGCTTTATGGAGCTGC 63
 Db 50 GhuAlaArgLeuPheAlaMetLeuLysHisProAsnIleLeuAlaLeuArgGlyValCys 69

QY 64 TTGAATCCA-----GTGTGCTTGTGATGAATATGTCGAAGGGGCTCTTTATATAAT 117
 Db 70 LeuLysGluProAsnLeuCysLeuValMetGluPheAlaArgGlyGlyProLeuAsnArg 89

118 GTCTCATGGTCTGACCAATTCATATATATCTGCTGCCACGCAATGAGTGTGT 177
 90 ValLeuSerGlyLysArgIleProProAspIle-----LeuValAsnTrpAla 105
 178 TTACAGTGTTCACAGGAGTGGTATCTTCACAGCATGCAACCAAGCGCTAATTCAC 237
 106 ValGlnIleAlaArgGlyMetAsnTrpLeuHisAspGluAlaIleValProIleHis 125
 238 AGGAGCTGAACACCAACCAATTCATCTGCTGTT-----GCAGGG 276
 126 ArgAspLeuLysSerAsnIleLeuIleGlnLysValGluAsnGlyAspLeuSer 145
 277 GGGACAGTCTAATAATTTGTGATTTTGTGTACGCTGTGC---ATTACAGACACATG 333
 146 AsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTrpHisArgThrThrLys 165
 334 ACCAATAACAGGGAGTGTCTGTGAGCGACCTGAGTGTTCAGGTAGTATATAC 393
 166 MetSerAlaAlaGlyThrTrpAlaTrpMetAlaProGluValIleArgAlaSerMetPhe 185
 394 AGTGAATAATGTGACGTCTTCAGCTGGGTATTATTCTTTGGAGTGTAAACGCTCGG 453
 186 SerLysGlySerAspValTrpSerTrpGlyValLeuLeuTrpGlnLeuLeuThrGlyGlu 205
 454 AAACCCCTTTGATGAGATTTGTGCTGCCAGCTTTCGGAATCATGTGGGTGT---CATAAT 510
 206 ValProPheArgGlyIleAspGly-----LeuArgValAlaTrpGlyValAlaMetAsn 223
 511 GGTACTCGACCACTGATATAAATAATTTACCTAAGCCCATTCAGAGCTGTGATCGT 570
 224 LysLeuAlaLeuProIleProSerThrCysProGluProPheAlaLysLeuMetGluAsp 243
 571 TGTGTCTAAGATCTTCCAGCGCTTCATGAGGAAATTCGAGAAATTCGAAATGACT 630
 244 CysTrpAsnProAspProHisArgProSerPheThrAsnIleLeuAspGlnLeuThr 263

RESULT 6
 M3KC RAT
 ID M3KC RAT STANDARD; PRT; 888 AA.
 AC Q63796;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 12 (BC 2.7.1.37)
 DE (MAPK-upstream kinase) (MUK).
 GN MAP3K12 OR MUK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RN RNP
 RP
 RX MEDLINE=96226099; PubMed=8637721;
 RA Hirai S., Izawa M., Osada S., Spyrou G., Ohno S.;
 RT "Activation of the JNK pathway by distantly related protein kinases,
 RT MEK and MUK";
 RL Oncogene 12:641-650(1996).
 CC -!- FUNCTION: May be an activator of the JNK/SAPK pathway.
 CC Phosphorylates beta-casein, histone 1 and myelin basic protein in
 CC vitro.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
 CC similarity).
 CC -!- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
 CC under basal conditions and dephosphorylated when membrane-
 CC associated (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE KINASE SUBFAMILY.
 CC
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 or send an email to license@isb-sib.ch).

 DR EMBL; D49785; BAA08621.1; -;
 DR HSSP; P12931; LPMK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Magnesium; Membrane.
 FT DOMAIN 158 399 PROTEIN_KINASE.
 FT NP_BIND 164 172 ATP (BY SIMILARITY).
 FT BINDING 185 185 ATP (BY SIMILARITY).
 FT ACT_SITE 269 269 BY SIMILARITY.
 FT DOMAIN 56 62 POLY-GLY.
 FT DOMAIN 668 671 POLY-PRO.
 FT DOMAIN 698 701 POLY-PRO.
 FT DOMAIN 753 758 POLY-GLU.
 FT SEQUENCE 888 AA; 96307 MW; 52AD964006BAE149 CRC64;

 Alignment Scores:
 Pred. No.: 3e-27 Length: 888
 Score: 355.50 Matches: 75
 Percent Similarity: 55.09% Conservative: 44
 Best Local Similarity: 34.72% Mismatches: 80
 Query Match: 28.39% Indels: 17
 DB: 1 Gaps: 8

 US-09-830-144-1_COPY_408_1091 (1-684) x M3KC_RAT (1-888)
 QY 4 GAGCTCGCAGTATCCCGTGTGACCATCTTATATATGTAAGCTTTATGAGCGCTGC 63
 Db 194 AspIleLysHisLeuArgLysHisProAsnIleIleThrPheLysGlyValCys 213
 QY 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGCTTTATATAAT 117
 Db 214 ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlyGlnLeuTrpGlu 233
 QY 118 GTGCTGCATGTGCTGAACCATTTGCCATATATATCTGCTGCCACGCAATGAGTGTGT 177
 Db 234 ValLeuArgAlaGlyArgProVal-----ThrProSerLeuLeuValAspTrpSer 250
 QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCAC 237
 Db 251 MetGlyIleAlaGlyGlyMetAsnTrpLeuHisLeuHisLys-----IleIleHis 267
 QY 238 AGGAGCTGAACACCAACCAATTCATCTGCTGTTCAGGGGGGACAGTCTTAAATTTCT 297
 Db 268 ArgAspLeuLysSerProAsn---MetLeuIleThrTyrAspValValLysIleSer 286
 QY 298 GATTTGTGTACAGCTGTGACATTCAGACACATGACCAATACCAAG-----GGGAGT 351
 Db 287 AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr 306
 QY 352 GCTGCTGTGATGGACCTGAAGTTTGAAGTAGTAAATACAGTGAATAATGTCACGTC 411
 Db 307 ValAlaTrpMetAlaProGluValIleArgAsnGluProValSerGluLysValAspIle 326
 QY 412 TTCAGCTGGGTATTATTCTTTGGGAAGTGAACGCGTGGAAACCCCTTTCATGAGATT 471
 Db 327 TrpSerPheGlyValValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspVal 346
 QY 472 GGTGCCCGCAGCTTCCGATCATGTTGGGCTGT---CATAATGGTACTGACACACCTG 528
 Db 472 GGTGCCCGCAGCTTCCGATCATGTTGGGCTGT---CATAATGGTACTGACACACCTG 528

Db 347 AspSerSerAla-----IleIleTTPGlyValGlySerAsnSerLeuHisLeuProVal 364

QY 529 ATAAAAAATTACTAAGCCCATGAGAGCTGATGACTCGTTGGTGTCTAAGATCCT 588

Db 365 ProSerSerCysProAspGlyPheLeuLeuArgGlnCysTrpAsnArgLysPro 384

QY 589 TCCAGCGCCCTTCAATGGAGGAATGTGAAATATGACTCCTTG 636

Db 385 ArgAsnArgProSerPheArgGln-----IleLeuLeuHisLeu 397

RESULT 7

M3KC_HUMAN

ID M3KC_HUMAN STANDARD; PRT; 859 AA.

AC Q12852; 2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)

DE (leucine-zipper protein kinase) (ZPK).

GN MAP3K12 OR ZPK.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=teratocarcinoma;

RX MEDLINE=94311945; PubMed=8037767;

RA Reddy U.R.; Pleasure D.;

RT "Cloning of a novel putative protein kinase having a leucine zipper

RL domain from human brain.";

RL Biochem. Biophys. Res. Commun. 202:613-620(1994).

CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.

CC Phosphorylates beta-casein, histone 1 and myelin basic protein in

CC vitro.

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.

CC -1- COFACTOR: Magnesium.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By

CC similarity).

CC -1- TISSUE SPECIFICITY: Highly expressed in brain and kidney.

CC -1- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol

CC under basal conditions and dephosphorylated when membrane-

CC associated (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U07358; AAA67343.1; -

DR HSPSP; P12931; 1PMK.

DR Genew; HGNC:6851; MAP3K12.

DR MTM; 600447; -

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0007254; P:JNK cascade; TAS.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR01245; Tyr_kinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Phosphorylation; Magnesium; Membrane.

FT DOMAIN 125 366 PROTEIN KINASE.

FT NP_BIND 131 139 ATP (BY SIMILARITY).

FT BINDING 152 152 ATP (BY SIMILARITY).

FT ACT_SITE 236 236 BY SIMILARITY.

FT DOMAIN 665 668 POLY-PRO.

FT DOMAIN 720 725 POLY-GLU.

SQ SEQUENCE 859 AA; 93188 MW; 0E5209792C5C6F05 CRC64;

Alignment Scores:

Pred. No.: 4.72e-27 Length: 859

Score: 353.50 Matches: 75

Percent Similarity: 54.63% Conservative: 43

Best Local Similarity: 34.72% Mismatches: 81

Query Match: 28.23% Indels: 17

DB: 1 Gaps: 8

US-09-830-144-1_COPY_408_1091 (1-684) x M3KC_HUMAN (1-859)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTTATGAGCCTGC 63

Db 161 AspileyHisLeuArgLysLeuLysHisProAsnIleIleThrPheLysGlyValCys 180

QY 64 TTGAATCCA-----GTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTATATAT 117

Db 181 ThrGlnAlaProCysTyrCysIleLeuMetGluPheCysAlaGlnGlyGlnLeuTyrGlu 200

QY 118 GTGCTGCATGGTCTGNAACCATTCATTTATCTGCTGCCACCGCAATGAGTGGTGT 177

Db 201 ValLeuArgAlaGlyArgProVal-----ThrProSerLeuLeuValAspTrpSer 217

QY 178 TTACAGTGTTCCTCAAGGAGTGGCTTATCTTCACAGATGCAACCCAAAGCGCTAATTCAC 237

Db 218 MetGlyIleAlaGlyGlyMetAsnTyrLeuHisLeuHisLys-----IleIleHis 234

QY 238 AGGAGCTGAAACACCACTTACTGCTGGTTCAGGGGGGAGCTTCTAAATTTGT 297

Db 235 ArgAspLeuLysSerProAsn---MetLeuIleThrTyrAspAspValValLysIleSer 253

QY 298 GATTTGGTACAGCTGTGACATTCAGACACATGACCAATACAAAG-----GGGAGT 351

Db 254 AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr 273

QY 352 GCTGCTTGGATGCGCCTGAACTTTTGAAGGTAGTAGTAATACAGTGAATAATGTGAGTGC 411

Db 274 ValAlaTrpMetAlaProGluValIleArgAsnGluProValSerGluLysValAspIle 293

QY 412 TTCAGCTGGGGTATTATTTTCGGAAGTAGTAACCGCTCGGAACCTTTGATGAGATT 471

Db 294 TrpSerPheGlyValValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspVal 313

QY 472 GGTGGCCAGCTTCCGAATCATGTGGGCTGTT---CATTAATGGTACTCGACCACTG 528

Db 314 AspSerSerAla-----IleIleTrpGlyValGlySerAsnSerLeuHisLeuProVal 331

QY 529 ATAAAAAATTACCTAAGCCCATGAGCTGATGACTCGTTGTTGGTCTAAAGATCCT 588

Db 332 ProSerSerCysProAspGlyPheLysIleLeuLeuArgGlnCysTrpAsnSerLysPro 351

QY 589 TCCAGCGCCCTTCAATGGAGGAATTTGTAAGGTAGTAGTAATGAGTCTCCTTG 636

Db 352 ArgAsnArgProSerPheArgGln-----IleLeuLeuHisLeu 364

RESULT 8

M3KC_MOUSE

ID M3KC_MOUSE STANDARD; PRT; 888 AA.

AC Q60700; P70286;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)

DE (leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing

DE kinase) (DLK).

GN MAP3K12 OR ZPK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Brain;
 RX MEDLINE=95074107; PubMed=7983011;
 RA Holzman L.B., Merritt S.E., Fan G.;
 RT "Identification, molecular cloning, and characterization of dual
 RT leucine zipper bearing kinase. A novel serine/threonine protein kinase
 RT that defines a second subfamily of mixed lineage kinases.";
 RT J. Biol. Chem. 269:30808-30817(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR X Swiss Webster; TISSUE=Brain;
 RX MEDLINE=96365388; PubMed=8769565;
 RA Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;
 RT "Cell-specific expression of the ZPK gene in adult mouse tissues.";
 RT DNA Cell Biol. 15:631-642(1996).
 RN [3]
 RP PHOSPHORYLATION, AND MUTAGENESIS OF LYS-185 AND GLU-192.
 RX MEDLINE=96279269; PubMed=8663324;
 RA Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;
 RT "Characterization of dual leucine zipper-bearing kinase, a mixed
 RT lineage kinase present in synaptic terminals whose phosphorylation
 RT state is regulated by membrane depolarization via calcineurin.";
 RT J. Biol. Chem. 271:16888-16896(1996).
 RL J. Biol. Chem. 271:16888-16896(1996).
 CC -!- FUNCTION: May be an activator of the JNK/SAPK pathway.
 CC Phosphorylates beta-casein, histone 1 and myelin basic protein in
 CC vitro.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
 CC -!- TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart,
 CC testis, gastrointestinal tract, stomach, liver and pancreas.
 CC Within the nervous system, predominantly expressed in neurons and
 CC enriched in synaptic terminals.
 CC -!- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
 CC under basal conditions and dephosphorylated when membrane-
 CC associated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC
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 CC
 CC EMBL; U14636; AA57280.1; --
 CC EMBL; U23789; AB17123.1; --
 CC PIR; A55318; A55318.
 CC HSP; P12931; LPMK.
 CC MGD; MGI:1346881; Map3k12.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00069; pkinase; 1
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 CC TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Magnesium; Membrane.
 FT DOMAIN 158 399 PROTEIN KINASE.
 FT NP_BIND 164 172 ATP (BY SIMILARITY).
 FT BINDING 185 185 ATP.
 FT ACT_SITE 269 269 BY SIMILARITY.
 FT DOMAIN 56 62 POLY-GLY.
 FT DOMAIN 668 671 POLY-PRO.

FT DOMAIN 698 701 POLY-PRO.
 FT DOMAIN 753 758 POLY-GLU.
 FT MUTAGEN 185 K->A: NO CATALYTIC ACTIVITY.
 FT MUTAGEN 192 E->A: NO CHANGE.
 FT CONFLICT 18 V -> A (IN REF. 2).
 FT CONFLICT 18 KL -> NV (IN REF. 2).
 FT CONFLICT 28 S -> T (IN REF. 2).
 FT CONFLICT 382 EQ -> DE (IN REF. 2).
 FT CONFLICT 494 N -> D (IN REF. 2).
 FT CONFLICT 517 E -> G (IN REF. 2).
 FT CONFLICT 794 E -> G (IN REF. 2).
 SQ SEQUENCE 888 AA; 96083 MW; CFECD1D34F899ABB CRC64;
 Alignment Scores:
 Pred. No.: 4,74e-27 Length: 888
 Score: 353.50 Matches: 75
 Percent Similarity: 54.63% Conservative: 43
 Best Local Similarity: 34.72% Mismatches: 81
 Query Match: 28.23% Indels: 17
 DB: 1 Gaps: 8
 US-09-830-144-1_COPY_408_1091 (1-684) x M3KC_MOUSE (1-888)
 QY 4 GAGCTTCGCGAGTTATCCCGTGTGAACCATCTCTAATATATGTAAGCTTTATGAGCGCTGC 63
 Db 194 AspilleYshHisLeuArgLysHisProAsnilleileThrPhelysGlyValCys 213
 QY 64 TTGAATCCA-----GTGTGTCTGTGATGGAATATGCTGAAGGGGGCTCTTATATAAT 117
 Db 214 ThrGlnAlaProCysTyrCysileuMetGluPheCysAlaGlnGlyGlnLeuTyrGlu 233
 QY 118 GTGCTGCATGTGCTGAACCATTCATGCTGCTGCCACCAATAGCTTGCTGT 177
 Db 234 ValLeuArgAlaGlyArgProVal-----ThrProSerLeuLeuValAspTpsr 250
 QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGTAAATCAC 237
 Db 251 MetGlyileAlaGlyMetAsnTyrLeuHisLeuHisLys-----llelleHis 267
 QY 238 AGGGACCTGAAACCAACCACTTCTGCTGTTGTCAGGGGGGACACTTCTAAAAATTTGT 297
 Db 268 ArgAspLeuLysSerProAsn--MetLeulleThrTyrAspValValLysileSer 286
 QY 298 GATTTTGTGTACGCTGTGCATTCAGACACATGACCAATAACAAG-----GGGAGT 351
 Db 287 AspPheGlyThrSerLysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThr 306
 QY 352 GCTGCTGTGATGCGCCTGAAAGTGTGAGGTAGTAAATACAGTGAATAATGTGACGTC 411
 Db 307 ValAlaTTrpMetAlaProGluValilleArgAsnGluProValSerGluLysValAspIle 326
 QY 412 TTCAGTGGGGTATTATCTTTGGGAAGTGATAACGCGTCGGAAACCCCTTGATGAGATT 471
 Db 327 TrpSerPheGlyValValLeuTrpGluLeuLeuThrGlyGluilleProTyrLysAspVal 346
 QY 472 GGTGGCCAGCTTTCGATCATGTGGGCTGTT---CATATGCTACTCGACCCACCTG 528
 Db 347 AspSerSerAla-----llelleTrpGlyValGlySerAsnSerLeuHisLeuProVal 364
 QY 529 ATAAAAAATTACCTTAAGCCCATGAGCCTGATGACTCGTTGTTGTTGCTAAAGATCCT 588
 Db 365 ProSerSerCysProAspGlyPheLysilleLeuLeuArgGlnCysTrpAsnSerLysPro 384
 QY 589 TCCAGCGCCCTTCAATGAGGAATTTGAAATAATGACCTCCTG 636
 Db 385 ArgAsnArgProSerPheArgGln-----lleLeuLeuHisLeu 397
 RESULT 9
 KYK2_DICDI
 ID KYK2_DICDI STANDARD; PRT; 410 AA.
 AC P18161;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

Tyrosine-protein kinase 2 (EC 2.7.1.112) (Fragment).
 GN PYKB OR DPYK2.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 ON NCBI_TaxID=44689;
 RX SEQUENCE FROM N.A.
 RY MEDLINE=90287147; PubMed=1972546;
 RA Tan J.L., Spudich J.A.;
 RT "Developmentally regulated protein-tyrosine kinase genes in
 Dictyostelium discoideum";
 RL Mol. Cell. Biol. 10:3578-3583(1990).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M33784; AAA33203.1; --
 DR PIR; B35670; B35670.
 DR HSPSP; P08631; 1AD5.
 DR DictyDb; D003011; PykB.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
 KW NON_TPR 1 1
 FT DOMAIN 108 381 PROTEIN_KINASE.
 FT NP_BIND 114 122 ATP (BY SIMILARITY).
 FT BINDING 135 135 ATP (BY SIMILARITY).
 FT ACT_SITE 232 232 BY SIMILARITY.
 SQ SEQUENCE 410 AA; 46386 MW; E93918B605B9AEC1 CRC64;

Alignment Scores:
 Pred. No.: 7,34e-26 Length: 410
 Score: 341.00 Matches: 74
 Percent Similarity: 54.21% Conservative: 42
 Best Local Similarity: 34.58% Mismatches: 84
 Query Match: 27.24% Indels: 14
 DB: 1 Gaps: 7

US-09-830-144-1_COPY_408_1091 (1-684) x KYK2_DICDI (1-410)

QY 4 GAGCTCGGAGTTCATCCCTGTGAACCATCTAATATTGTAAGCTTTATGAGCCTGC 63
 Db 153 GluValGlnAsnLeuLysGlyAsnHisGlnAsnLeuValMetPheIleGlyAlaCys 172
 QY 64 TTGAATCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGCTG 123
 Db 173 TyrLysProAlaCysIleIleThrGluTyrMetAlaGlyGlySerLeuTyrAsnIleLeu 192
 QY 124 CAT-----GGTGTGACCATTCGCATATTATCTACTGCTGCCAGCAATGAGTGG 174
 Db 193 HisAsnProAsnSerThrProLysValLysTyrSerPheProLeuValLeuLysMet 212
 QY 175 TGTTTACAGTCTTCCCAAGGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATT 234
 Db 213 AlaThrAspMetAlaLeuGlyLeuLeuHisHisSerIle-----ThrIleVal 229
 QY 235 CACAGGACCTGAACACCAACTTACTGCTGGTTCAGGGGGGACAGCTTTCTAAAAATT 294
 Db 230 HisArgAspLeuThrSerGlnAsnIleLeuLeuAspGluLeuGlyAsnIle---LysIle 248

QY 295 TGTGATTTCGTACAGCTGTGAC-----ATTGACACACATGACCAATAACAAGGGG 348
 Db 249 SerAspPheGlyLeuSerAlaGluLysSerArgGluGlySerMetThrMetThrAsnGly 268
 QY 349 -----AGTGTGCTGTGGATGGCACCTGCAAGTTTGAAGGT---AGTAATTACAGT 396
 Db 269 GlyIleCysAsnProAspTyrArgProProGluLeuThrLysAsnLeuGlyHisTyrSer 288
 QY 397 GAAAAATGTGACGCTCTCAGCTGGGTATTATCTTTGGGAAGTGAATACCGCTCGGAA 456
 Db 289 GluLysValAspValTyrCysPheSerLeuValTyrGluIleLeuThrGlyGluIle 308
 QY 457 CCCTTTCATGAGATTGGTGGCCAGCTTCGGAATCATGTGGGCTGTTCATAATGGTACT 516
 Db 309 ProPheSerAspLeuAspGly---SerGlnArgSerAlaGlnValAlaTyrAlaGlyLeu 327
 QY 517 CGACCCACCTGATAAAATTTTACCTAAGCCATGAGAGCCCTGATGACTCGTTGTGG 576
 Db 328 ArgProIleProGluTyrCysAspProGluLeuLysLeuLeuLeuThrGlnCysTrp 347
 QY 577 TCTAAGATCTTCCAGCGCCCTTCAATGAGGAGAAATTGTG 618
 Db 348 GluAlaAspProAsnAspArgProPheThrTyrIleVal 361

RESULT 10
 CTRL_ARATH
 ID_CTRL_ARATH STANDARD; PRT; 821 AA.
 AC Q05609;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase CTRL (EC 2.7.1.37).
 DE CTRL OR AT5G03730 OR FL7C15150.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia; TISSUE=Seedling;
 RC MEDLINE=93161417; PubMed=8431946;
 RA Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.;
 RT "CTRL, a negative regulator of the ethylene response pathway in
 Arabidopsis, encodes a member of the raf family of protein kinases.";
 RL Cell 72:427-441(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 EX MEDLINE=21016721; PubMed=11130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno A., Murai A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
 RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
 RA Wagner-McPherson C., Wollam A., Yokum M., Bell M., Dedhia N.,
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckaert G., Mambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Entian K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
 RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirks W., Mooijman P., Klein Lankhorst R.,
 RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,

RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RL thaliana";
 CC Nature 408:823-826 (2000).
 CC -1- FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
 CC PATHWAY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULT PLANTS.
 CC -1- MISCELLANEOUS: CTRL MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES,
 CC RESULTING IN PLANTS WITH SMALL, UNEXPANDED LEAVES AND WHOSE SEED
 CC COTYLEDON GROWTH IS IMPAIRED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC
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 CC
 CC EMBL; L08789; AAA32779.1; -;
 CC EMBL; L08790; AAA32780.1; -;
 CC EMBL; AL162506; CAB82938.1; -;
 CC F1R; T48400; T48400.
 CC InterPro; IPR000719; prot kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00669; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot kinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE; PS00107; "PROTEIN KINASE ATP; 1."
 CC PROSITE; PS00108; "PROTEIN KINASE ST; 1."
 CC PROSITE; PS00111; "PROTEIN KINASE DOM; 1."
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding.
 CC
 CC FT DOMAIN 65 69 POLY-GLY.
 CC FT DOMAIN 135 141 POLY-GLY.
 CC FT DOMAIN 551 809 PROTEIN KINASE.
 CC FT NP_BIND 557 565 ATP (BY SIMILARITY).
 CC FT BINDING 578 578 ATP (BY SIMILARITY).
 CC FT ACT_SITE 676 676 BY SIMILARITY.
 CC FT MUTAGEN 596 596 E->K: IN CTRL-4; EXHIBITS ETHYLENE-
 CC TREATED PHENOTYPE.
 CC FT MUTAGEN 694 694 D->E: IN CTRL-1; EXHIBITS ETHYLENE-
 CC TREATED PHENOTYPE.
 CC SQ SEQUENCE 821 AA; 90306 MW; 2922D3DCD0CC15BC CRC64;
 Alignment Scores:
 Pred. No.: 5e-24 Length: 821
 Score: 323.00 Matches: 74
 Percent Similarity: 54.59% Conservative: 45
 Best Local Similarity: 33.94% Mismatches: 91
 Query Match: 25.80% Indels: 8
 DB: 1 Gaps: 6
 US-09-830-144-1_COPY_408_1091 (1-684) x CTRL_1PATH (1-821)
 QY 4 GAGCTTCGGCAGTATCCCGTGTGAACCACTCTAATATTGTAAGCTTTATGAGCGCTGC 63
 Db 596 GiuValAlaLeuMetIysArgLeuArgHisProAsnIleValLeuPheMetGlyAlaVal 615
 QY 64 TTGAATCCCA-----GTGGTCTGTGGATCGATATGCTGAAGGGGCTCTTATATAT 117
 Db 616 ThrGlnProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArg 635
 QY 118 GTGCTGCATGCTGCTGAACCACTTGCATATATATCTGCTGCCACCAATGAGTTGGTGT 177
 Db 636 LeuLeuHisLysSerGlyAlaArgGluGlnLeuAspGluArgArgLeuSerMetAla 655
 QY 178 TTACAGTGTCCAGGAGTGGCTTATCTTTCACAGATGCAACCCAAAGCGCTAATTCAC 237

Db 656 TyrAspValAlaLysGlyMetAsnTyrLeuHisAsnArgAsnPro----ProIleValHis 674
 QY 238 AGGAGCTGAACCAACCACTTACTGCTGTTGCAGGGGGGACAGTCTTAAATAATTGT 297
 Db 675 ArgAspLeuLysSerProAsnLeuValAspLysTyrThrVal---LysValCys 693
 QY 298 GATTTTGGT---ACAGCTGTGACATTCAGACACATGACCAATACAAAG-----GGG 348
 Db 694 AspPheGlyLeuSerArgLeuLysAlaSerThrPheLeuSerSerLysSerAlaAlaGly 713
 QY 349 AGTGCTGTGGATGGCAGCTGAAGTTTGTGAAGTAGTAATACAGTGAATAATGTGAC 408
 Db 714 ThrProGluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAsp 733
 QY 409 GCTTTCAGCTGGGTATTCTTTCGGAAGTCATAACGCTCGGAACCCCTTTGATGAG 468
 Db 734 ValTyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnProTrpGlyAsn 753
 QY 469 ATTGCTGGGCCAGCTTTCGGAATCATGTGGCTGTTCATAATGCTACTCGACCCACTG 528
 Db 754 Leu---AsnProAlaGlnValValAlaAlaValGlyPheLysCysLysArgLeuGluIle 772
 QY 529 ATFAAAATTTACCTAAGCCCTAGAGCCTGATGACCTGTTGGTGTCTAAAGATCCT 588
 Db 773 ProArgAsnLeuAsnProGlnValAlaAlaIleIleGluGlyCysTrpThrAsnGluPro 792
 QY 589 TCCACAGCGCCTCAATGAGGAAATGTGAAATAATGACTCCTACTGATGCGG 642
 Db 793 TrpLysArgProSerPheAlaThrIleMetAspLeuLeuArgProLeuIleLys 810
 RESULT 11
 RET_MOUSE STANDARD; PRT; 1115 AA.
 AC P35546;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase receptor ret precursor
 DE (EC 2.7.1.112) (C-ret).
 GN RET.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN (1)_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93205390; PubMed=8455936;
 RA Iwamoto T., Taniguchi M., Asai N., Ohkusu K., Nakashima I.,
 RA Takahashi M.;
 RT "cDNA cloning of mouse ret proto-oncogene and its sequence similarity
 RT to the cadherin superfamily";
 RL Oncogene 8:1087-1091 (1993).
 [2]
 RP INTERACTION WITH DOK2; DOK4 AND DOK5, PHOSPHORYLATION, AND MUTAGENESIS
 OF TYR-1063.
 RX MEDLINE=21363571; PubMed=11470823;
 RA Grimm J., Sachs M., Britsch S., Di Cesare S., Schwarz-Romond T.,
 RA Alitalo K., Birchmeier W.;
 RT "Novel p62dok family members, dok-4 and dok-5, are substrates of the
 RT c-ret receptor tyrosine kinase and mediate neuronal
 RT differentiation";
 RL J. Cell Biol. 154:345-354 (2001).
 CC -1- FUNCTION: Probable receptor with tyrosine-protein kinase activity;
 CC important for development.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Phosphorylated form interacts with the PBT domain of
 CC DOK2, DOK4 and DOK5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in peripheral nerve cells and
 CC hematopoietic cells.
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.

RT kinase with two potential transmembrane domains.";
 RL Oncogene 3:571-578(1988).
 RN [3]
 RP SEQUENCE OF 588-1063 FROM N.A.
 RX MEDLINE=97257826; PubMed=3037315;
 RA Takahashi M., Cooper G.M.;
 RA "ret transforming gene encodes a fusion protein homologous to
 RT tyrosine kinases.";
 RL Mol. Cell. Biol. 7:1378-1385(1987).
 RN [4]
 RP TYROSINE AUTOPOHOSPHORYLATION, AND MUTAGENESIS OF TYR-1015 AND
 RP TYR-1062.
 RX MEDLINE=20513733; PubMed=11061555;
 RA Salvatore D., Barone M.V., Salvatore G., Melillo R.M., Chiappetta G.,
 RA Mineo A., Penzi G., Vecchio G., Fusco A., Santoro M.;
 RA "Tyrosines 1015 and 1062 are in vivo autophosphorylation sites in ret
 RT and ret-derived oncoproteins.";
 RL J. Clin. Endocrinol. Metab. 85:3898-3907(2000).
 RN [5]
 RP REVIEW ON HSCR VARIANTS.
 RX MEDLINE=98023959; PubMed=9359036;
 RA Hofstra R.M.W., Osinga J., Buys C.H.C.M.;
 RA "Mutations in Hirschsprung disease: when does a mutation contribute to
 RT the phenotype.";
 RL Eur. J. Hum. Genet. 5:180-185(1997).
 RN [6]
 RP REVIEW ON VARIANTS
 RX MEDLINE=97220587; PubMed=9067749;
 RA Eng C., Mulligan L.M.;
 RA "Mutations of the RET proto-oncogene in the multiple endocrine
 RT neoplasia type 2 syndromes, related sporadic tumours, and
 RT Hirschsprung disease.";
 RL Hum. Mutat. 9:97-109(1997).
 RN [7]
 RP VARIANTS MEN2A/FMTC TRP-611; SER-618; ARG-620; TYR-620 AND ARG-634.
 RX MEDLINE=93372843; PubMed=8103403;
 RA Donis-Keller H., Dou S., Chi D., Carlson K.M., Toshima K.,
 RA Laitmore T.C., Howe J.R., Moley J.F., Goodfellow P., Wells S.A. Jr.;
 RA "Mutations in the RET proto-oncogene are associated with MEN 2A and
 RT FMTC.";
 RL Hum. Mol. Genet. 2:851-856(1993).
 RN [8]
 RP VARIANTS MEN2A GLY-618; 632-ASP-VAL-ARG-634; GLX-634; PHE-634; TYR-634
 RP AND SER-634.
 RX MEDLINE=93275414; PubMed=8099202;
 RA Mulligan L.M., Kwok J.B.J., Healey C.S., Elsdon M.J., Eng C.,
 RA Gardner E., Love D.R., Mole S.E., Moore J.K., Papi L., Ponder M.A.,
 RA Telenius H., Tunncliffe A., Ponder B.A.J.;
 RA "Germ-line mutations of the RET proto-oncogene in multiple endocrine
 RT neoplasia type 2A.";
 RL Nature 363:458-460(1993).
 RN [9]
 RP VARIANTS HSCR PRO-40; LEU-399; GLN-762; PRO-765; GLN-897; GLY-972 AND
 RP LEU-973.
 RX MEDLINE=95219414; PubMed=7704557;
 RA Yin L., Barone V., Seri M., Bolino A., Bocciaardi R., Ceccherini I.,
 RA Pasini B., Tocco T., Lerone M., Cywes S., Moore S.,
 RA Vanderwinden J.-M., Abramowicz M.J., Kristofferson U., Larsson L.T.,
 RA Hamel B.C.J., Silengo M., Martucciello G., Romeo G.;
 RA "Heterogeneity and low detection rate of RET mutations in Hirschsprung
 RT disease.";
 RL Eur. J. Hum. Genet. 2:272-280(1994).
 RN [10]
 RP VARIANT MEN2B THR-918.
 RX MEDLINE=94272459; PubMed=7911697;
 RA Eng C., Smith D.P., Mulligan L.M., Nagai M.A., Healey C.S.,
 RA Ponder M.A., Gardner E., Scheumann G.F., Jackson C.E., Tunncliffe A.,
 RA Ponder B.A.J.;
 RA "Point mutation within the tyrosine kinase domain of the RET
 RT proto-oncogene in multiple endocrine neoplasia type 2B and related
 RT sporadic tumours.";
 RL Hum. Mol. Genet. 3:237-241(1994).
 RN [11]

RP VARIANTS MEN2A/FMTC ARG-618; SER-618; PHE-620; ARG-620; PHE-634;
 RP GLY-634 AND TYR-634.
 RX MEDLINE=94348513; PubMed=79151565;
 RA Xue F., Yu H., Maurer L.H., Memoli V.A., Nutile-Mcmenemy N.,
 RA Schuster M.K., Browden D.W., Mao J.-I., Noll W.W.;
 RA "Germline RET mutations in MEN 2A and FMTC and their detection by
 RT simple DNA diagnostic tests.";
 RL Hum. Mol. Genet. 3:635-638(1994).
 RN [12]
 RP VARIANTS FMTC/MEN2A TYR-609; ARG-618; SER-618 AND SER-620.
 RX MEDLINE=95152521; PubMed=7849720;
 RA Blaugrund J.E., Johns M.M. Jr., Eby Y.J., Ball D.W., Baylin S.B.,
 RA Hruban R.H., Sidransky D.;
 RA "RET proto-oncogene mutations in inherited and sporadic medullary
 RT thyroid cancer.";
 RL Hum. Mol. Genet. 3:1895-1897(1994).
 RN [13]
 RP VARIANTS FMTC, AND VARIANTS MEN2A.
 RX MEDLINE=95179108; PubMed=7874109;
 RA Schuffenecker I., Billaud M., Calender A., Chambe B., Ginot N.,
 RA Calmettes C., Modigliani E., Lenoir G.M.;
 RA "RET proto-oncogene mutations in French MEN 2A and FMTC families.";
 RL Hum. Mol. Genet. 3:1939-1943(1994).
 RN [14]
 RP VARIANT HSCR TRP-609, VARIANT HSCR/MEN2A ARG-618, AND VARIANT
 RP HSCR/FMTC ARG-620.
 RX MEDLINE=95181155; PubMed=7881414;
 RA Mulligan L.M., Eng C., Attie T., Lyonnet S., Marsh D.J., Hyland V.J.,
 RA Robinson B.G., Frilling A., Verellen-Dumoulin C., Safar A.,
 RA Venter D.J., Munnich A., Ponder B.A.J.;
 RA "Diverse phenotypes associated with exon 10 mutations of the RET
 RT proto-oncogene.";
 RL Hum. Mol. Genet. 3:2163-2167(1994).
 RN [15]
 RP VARIANT MEN2B THR-918.
 RX MEDLINE=94159102; PubMed=7906866;
 RA Hofstra R.M.W., Landsvater R.M., Ceccherini I., Stulp R.P.,
 RA Stelwagen T., Luo Y., Pasini B., Hoepfner J.W.M., van Amstel H.K.F.,
 RA Romeo G., Lips C.J.M., Buys C.H.C.M.;
 RA "A mutation in the RET proto-oncogene associated with multiple
 RT endocrine neoplasia type 2B and sporadic medullary thyroid
 RT carcinoma.";
 RL Nature 367:375-376(1994).
 RN [16]
 RP VARIANTS HSCR PRO-765; GLN-897 AND GLY-972.
 RX MEDLINE=94159103; PubMed=8114938;
 RA Romeo G., Ronchetto P., Luo Y., Barone V., Seri M., Ceccherini I.,
 RA Pasini B., Bocciaardi R., Lerone M., Kaarlainen H., Martucciello G.;
 RA "Point mutations affecting the tyrosine kinase domain of the RET
 RT proto-oncogene in Hirschsprung's disease.";
 RL Nature 367:377-378(1994).
 RN [17]
 RP VARIANTS HSCR LEU-32; LEU-64; GLN-330 AND LEU-393.
 RX MEDLINE=94159104; PubMed=8114939;
 RA Edery P., Lyonnet S., Mulligan L.M., Pelet A., Dow E., Abel L.,
 RA Holder S., Nihoul-Fkete C., Ponder B.A.J., Munnich A.;
 RA "Mutations of the RET proto-oncogene in Hirschsprung's disease.";
 RL Nature 367:378-380(1994).
 RN [18]
 RP VARIANT MEN2B THR-918.
 RX MEDLINE=94151373; PubMed=7906417;
 RA Carlson K.M., Dou S., Chi D., Scavarda N., Toshima K., Jackson C.E.,
 RA Wells S.A. Jr., Goodfellow P.J., Donis-Keller H.;
 RA "Single missense mutation in the tyrosine kinase catalytic domain of
 RT the RET protooncogene is associated with multiple endocrine neoplasia
 RT type 2B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1579-1583(1994).
 RN [19]
 RP VARIANTS MTC, FMTC, MEN2A AND MEN2B.
 RX MEDLINE=96223053; PubMed=8625130;
 RA Kommeth P., Kunz E.K., Matias-Guiu X., Hiort O., Christiansen G.,
 RA Colomer A., Roth J., Heitz P.U.;
 RA "Analysis of RET protooncogene point mutations distinguishes heritable


```

Pred. No.: 6,54e-22 Length: 630
Score: 301.50 Matches: 71
Percent Similarity: 52.51% Conservative: 44
Best Local Similarity: 32.42% Mismatches: 89
Query Match: 24.08% Indels: 15
DB: 1 Gaps: 7

US-09-830-144-1_COPY_408_1091 (1-684) x TEC_MOUSE (1-630)

QY 4 GAGCTTCGGAGCTATCCCGTGAACCATCTCTAATATGTTAAAGCTTTTGGAGCCTGC 63
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 412 GluAlaLysValMetMetLysLeuThrHisProLysLeuValGlnLeuTyrGlyValCys 431
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 64 TTG-----AATCCAGTGTCTCTGTCATGGAATATCTGAAGGGGCTCTTATATAAT 117
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 432 ThrGlnGlnLysProIleTyrIleValThrGluPheMetGluArgGlyCysLeuAsn 451
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 118 GTGCTGTCATGCTGTGAACCATTCGCCATATATATCTGTCGCCACGCAATGAGTTGGTGT 177
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 452 PheLeuArgGlnArgGln-----GlyHisPheSerArgAspMetLeuLeuSerMetCys 469
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 178 TTACAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTTAATTCAC 237
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 470 GlnAspValCysGluGlyMetGluTyrLeu-----GluArgAsnSerPheIleHis 486
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 238 AGGACCTGAAACACCAACTTACTGCTGCTGCAGGGGGACAGTCTTAAAAATTGT 297
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 487 ArgAspLeuAlaAlaArgAsnCysLeuValAsnGluAlaGly----ValValLysValSer 505
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 298 GATTTTGGTACAGCC-----TGTGACATTCAGACACACATGACCAATAACAAG 345
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 506 AspPheGlyMetAlaArgTyrValLeuAspAspGlnTyrThrSerSerGlyValAlaLys 525
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 346 GGGAGTCTGCTGGAGTGGACCTGGAAGTTTTCAGAGTAGTAATACAGTGAATAATGT 405
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 526 PheProValLysTrpCysProGluValPheAsnTyrSerArgPheSerSerLysSer 545
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 406 GAGCTCTTCAGTGGGTATATCTTTGGAGTGAAGTAAAGCGT---CGAAGACCCCTTT 462
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 546 AspValTrpSerPheGlyValLeuMetTrpGluIlePheThrGluGlyArgMetProPhe 565
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 463 GATGAGATTGTGGCCCGAGCTTTCGGAATCATGTGGGTGTTTCATATGGTACTCGACCA 522
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 566 GluLys-----AsnThrAsnTyrGluValValThrMetValThrArgGlyHisArgLeu 583
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 523 CCACTGATAAAAAATTTACCTAAGCCCATTCAGAGCCTGATGACTCGTTGTTGCTCTAAA 582
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 584 HisArgProLysLeuAlaThrLysTyrLeuTyrGluValMetLeuArgCysTrpGlnGlu 603
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 583 GATCCTTCCAGCGCCCTTCATGAGGAGAAATTTGTGAATAATATGACTCACTTGATG 639
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 604 ArgProGluGlyArgProSerLeuGluAspLeuLeuThrIleAspGluLeuVal 622
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 14
TEC_HUMAN
ID TEC_HUMAN STANDARD; PRT; 631 AA.
AC P42680;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase Tec (EC 2.7.1.112).
GN TEC OR PSTK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95019807; PubMed=7934162;
RA Sato K., Mano H., Ariyama T., Inazawa J., Yazaki Y., Hirai H.;
RT "Molecular cloning and analysis of the human Tec protein-tyrosine
kinase."

```

Alignment Scores:

Pred. No.: 6,54e-22 Length: 631
 Score: 301.50 Matches: 73
 Percent Similarity: 51.80% Conservative: 42
 Best Local Similarity: 32.88% Mismatches: 86
 Query Match: 24.08% Indels: 21
 DB: 1 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x TEC_HUMAN (1-631)
 QY 4 GAGCTTCGGCAGTATCCCGTGTGAACCATCCCTAATATGTAAGCTTTATGAGCGCTGC 63
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 413 GluAlaLysValMetMetLysLeuThrHisProLysLeuValGlnLeuTyrGlyValCys 432
 QY 64 TTG-----AATCCAGTGTCTTGTGATGAATATGTCGAAGGGGCTCTTTATATAAT 117
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 433 ThrGlnGlnLysProIleTyrIleValThrGluPheMetGluArgGlyCysLeuLeuAsn 452
 QY 118 GTGCTGATGGTCTGACCATTCGCAATTCATATATGCTGCTCCACGCAATGATGGTGT 177
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 453 PheLeuArgGlnArgGln-----GlyHisPheSerArgAspValLeuLeuSerMetCys 470
 QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCACCCAAAGCGCTAATTCAC 237
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 471 GlnAspValCysGluGlyMetGluTyrLeu-----GluArgAsnSerPheIleHis 487
 QY 238 AGGCACTGAAACACCAACCTTACTGCTGTTGCAGGGGGGACAGTTCTTAAATAATTGT 297
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 488 ArgAspLeuAlaAlaArgAsnCysLeuValSerGluAlaGly--ValValLysValSer 506
 QY 298 GATTTGGTACAGCC-----TGTGACATTCAGACACACATGACCAATAACAAG 345
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 507 AspPheGlyMetAlaArgTyrPheLeuAspGlnTyrThrSerSerSerGlyAlaLys 526
 QY 346 GGGAGTGTCTGGATGGCAGCTGAGTTTGAAGTAGTAAATTACAGTGAATAATGT 405
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 527 PheProValLysTrpCysProProGluValPheAsnTyrSerArgPheSerLysSer 546
 QY 406 GAGCTCTCAGCTGGGGTATTATCTTTGGGAAGTGATAACGGCT---CGGAACACCTTT 462
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 547 AspValTrpSerPheGlyValLeuMetTrpGluValPheThrGluGlyArgMetProPhe 566
 QY 463 GATGAGATTGTGGCCAGCTTTCCGAATCATGTGGGTGTTTCAATGATGATCTCA--- 519
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 567 GluLysTyrThrAsn-----TyrGluValValThrMetValThrArgGlyHisArgLeu 584
 QY 520 -----CCACCACTGATAAAATTTACCTTAACCCATTGAGACCTGATGCTGCTGT 573
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 585 TyrGlnProLysLeuAlaSerAsnTyr-----ValTyrGluValMetLeuArgCys 601
 QY 574 TGGTCTAAAGATCTTTCCAGCGCCCTTCAATGGAGAAATTTGTAATAATATGACTCAC 633
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 602 TrpGlnGluLysProGluGlyArgProSerPheGluAspLeuLeuArgThrIleAspGlu 621
 QY 634 TTGATG 639
 ||||| : : : : :
 Db 622 LeuVal 623

RESULT 15

ID ITK_MOUSE STANDARD; PRT; 625 AA.
 AC Q03526;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase ITK/TSK (EC 2.7.1.112) (T-cell-specific
 DE kinase) (Il-2-inducible T-cell kinase) (Kinase EMT) (Kinase ITK).
 GN ITK OR TSK OR EMT OR TLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.

TISSUE=Thymocytes;
 MEDLINE=93087493; PubMed=1280821;
 RA Siliciano J.D., Morrow T.A., Desiderio S.V.;
 RT "Itk, a T-cell-specific tyrosine kinase gene inducible by interleukin
 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11194-11198(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=93133848; PubMed=8421704;
 RA Heyeck S.D., Berg L.J.;
 RT "Developmental regulation of a murine T-cell-specific tyrosine kinase
 gene, Tsk.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:669-673(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB4/J; TISSUE=Mast cells;
 RX MEDLINE=93236578; PubMed=8476425;
 RA Yamada N., Kawakami Y., Kimura H., Fukumachi H., Baier G.,
 Altman A., Kato T., Inagaki Y., Kawakami T.;
 RT "Structure and expression of novel protein-tyrosine kinases, Emb and
 Bmt, in hematopoietic cells.";
 RL Biochem. Biophys. Res. Commun. 192:231-240(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ogata M., Sawada M., Fujiwara H., Hamaoka T.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP STRUCTURE BY NMR OF 160-236.
 RX MEDLINE=97138229; PubMed=8985255;
 RA Andreotti A.H., Bunnell S.C., Feng S., Berg L.J., Schreiber S.L.;
 RT "Regulatory intramolecular association in a tyrosine kinase of the
 Tec family.";
 RL Nature 385:93-97(1997).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=95023908; PubMed=7524075;
 RA August A., Gibson S., Kawakami Y., Kawakami T., Mills G.B., Dupont B.;
 RT "CD28 is associated with and induces the immediate tyrosine
 phosphorylation and activation of the Tec family kinase ITK/EMT in
 the human Jurkat leukemic T-cell line.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9347-9351(1994).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=97098950; PubMed=8943565;
 RA King P.D., Sadra A., Han A., Liu X.-R., Sunder-Plassmann R.,
 Reinherz E.L., Dupont B.;
 RT "CD2 signaling in T cells involves tyrosine phosphorylation and
 activation of the Tec family kinase, EMT/ITK/TSK.";
 RL Int. Immunol. 8:1707-1714(1996).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=20040393; PubMed=10570288;
 RA Ching K.A., Kawakami Y., Kawakami T., Tsoukas C.D.;
 RT "Emt/Itk associates with activated TCR complexes: role of the
 pleckstrin homology domain.";
 RL J. Immunol. 163:6006-6013(1999).
 CC -!- FUNCTION: MAY PLAY A ROLE IN T-CELL DEVELOPMENT, POTENTIALLY IN
 CC THYMIC SELECTION.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: LIGATION OF CD2, TCR OR CD28 INDUCES ACTIVATION AND
 CC TYROSINE PHOSPHORYLATION OF ITK.
 CC -!- SUBCELLULAR LOCATION: LOCALIZES TO CELL SURFACE RECEPTORS IN THE
 CC PLASMA MEMBRANE AFTER STIMULATION WITH RESPECTIVE RECEPTORS (TCR,
 CC CD28, CD2) IN T-CELLS.
 CC -!- TISSUE SPECIFICITY: IS DETECTED IN THE THYMUS, LYMPH NODE AND VPERY
 CC FAINTLY IN THE SPLEEN, BUT IS NOT DETECTED IN THE LIVER, LUNG,
 CC KIDNEY, HEART, BRAIN, INTESTINE OR TESTIS. EXPRESSED IN T-
 CC LYMPHOCYTES AND MAST CELLS. IT MAY ALSO BE EXPRESSED IN NATURAL
 CC KILLER CELLS.
 CC -!- DEVELOPMENTAL STAGE: IS PRESENT IN THE FETAL THYMUS AS EARLY AS
 CC DAY 14 OF GESTATION. THE LEVELS ARE 5- TO 10-FOLD HIGHER IN

THYMOCYTES THAN IN PERIPHERAL T CELLS, AND INCREASE IN THE THYMUS DURING DEVELOPMENT FROM NEONATE TO ADULT.

-1- INDUCTION: By interleukin-2.

-1- DOMAIN: THE PH DOMAIN MEDIATES TARGETING OF ITK/TSK AND IS INDISPENSIBLE FOR THE ACTIVATION THROUGH TCR/CD3.

-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TEC SUBFAMILY.

-1- SIMILARITY: Contains 1 SH2 domain.

-1- SIMILARITY: Contains 1 SH3 domain.

-1- SIMILARITY: Contains 1 PH domain.

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EMBL; L00619; AAA39337.1; -;
 EMBL; L05631; AAA40518.1; -;
 EMBL; L10628; -; NOT_ANNOTATED_CDS.
 EMBL; D14042; BAA03129.1; -;
 PIR; A43030; A43030.
 PDB; 1AWJ; 14-JAN-98.
 PDB; 1LUK; 27-NOV-02.
 PDB; 1LUM; 27-NOV-02.
 PDB; 1LUN; 27-NOV-02.
 MGD; MGI:96621; Itk.
 InterPro; IPR001562; BTK.
 InterPro; IPR001849; PH.
 InterPro; IPR000719; Prot_kinase.
 InterPro; IPR000980; SH2.
 InterPro; IPR001452; SH3.
 InterPro; IPR001245; Tyr_pkinase.
 Pfam; PF00779; BTK; 1.
 Pfam; PF00169; PH; 1.
 Pfam; PF00069; pkinase; 1.
 Pfam; PF00017; SH2; 1.
 Pfam; PF00018; SH3; 1.
 PRINTS; PR00401; SH2DOMAIN.
 PRINTS; PR00402; TBCBTDOMAIN.
 PRINTS; PR00109; TYRKINASE.
 ProDom; PD000001; Prot_kinase; 1.
 ProDom; PD000093; SH2; 1.
 ProDom; PD000066; SH3; 1.
 SMART; SM00107; BTK; 1.
 SMART; SM00233; PH; 1.
 SMART; SM00252; SH2; 1.
 SMART; SM00326; SH3; 1.
 SMART; SM00219; TyzKc; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PROSITE; PS50001; SH2; 1.
 PROSITE; PS50002; SH3; 1.
 PROSITE; PS50003; PH_DOMAIN; 1.
 Transferrase; Tyrosine-protein kinase; Phosphorylation;
 ATP-binding; SH2 domain; SH3 domain; 3D-structure.
 DOMAIN 4 117
 PH.
 DOMAIN 177 237
 SH3.
 DOMAIN 245 343
 SH2.
 DOMAIN 368 620
 PROTEIN_KINASE.
 NP_BIND 374 382
 ATP (BY SIMILARITY).
 BINDING 396 396
 ATP (BY SIMILARITY).
 ACT_SITE 487 487
 BY SIMILARITY.
 MOD_RES 517 517
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CONFLICT 82 87
 MISSING (IN REF. 2, 3 AND 4).
 CONFLICT 535 535
 F -> S (IN REF. 3).
 Y -> C (IN REF. 3).
 CONFLICT 540 540
 STRAND 188 188
 TURN 193 194
 STRAND 198 198

FT TURN 209 210
 FT STRAND 214 214
 FT STRAND 228 230
 FT TURN 230 231
 SQ SEQUENCE 625 AA; 72291 MW; F7A4A18A8A1AADDCC CRC64;

Alignment Scores:

Pred. No.: 1.03e-21 Length: 625
 Score: 299.50 Matches: 72
 Percent Similarity: 48.66% Conservative: 37
 Best Local Similarity: 32.14% Mismatches: 88
 Query Match: 23.92% Indels: 27
 DB: 1 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x ITK_MOUSE (1-625)

Qy 4 GAGCTTCGGCAGTGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCCCTGC 63
 Db 411 GluAlaGluValMetMetLysLeuSerHisProLysLeuValGlnLeuTyrGlyValCys 430
 Qy 64 TTGAAT-----CCAGTGTCTTGTGATGAATATGCTGAAGGGGGCTCTTTATATAAT 117
 Db 431 LeuGluGlnAlaProLleCysLeuValPheGluPheMetGluHisGlyCysLeuSerAsp 450
 Qy 118 GTGCTGCATGGTCTGAACCATTCCTATATATATCTGCTGCCACGCAATGAGTTGGTGT 177
 Db 451 TyrLeuArgSerGlnArgGlyLeu-----PheAlaAlaGluThrLeuLeuGlyMetCys 468
 Qy 178 TTACAGTGTTCCTCCCAAGGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTAATTCAC 237
 Db 469 LeuAspValCysGluGlyMetAlaTyrLeu-----GluLysAlaCysValIleHis 485
 Qy 238 AGGACCTGAAACCAACCAACTTACTCTGTTTCAGGGGGGAGCAGTTCTAAAAATTGT 297
 Db 486 ArgAspLeuAlaAlaArgAsn---CysLeuValGlyGluAsnGlnValIleLysValSer 504
 Qy 298 GATTTTGGT-----ACAGCCTGTGCACATTGACACACACATGACCAATAACAG 345
 Db 505 AspPheGlyMetThrArgPheValLeuAspGlnTyrThrSerSerThrGlyThrLys 524
 Qy 346 GGGAGTCTGCTTGGATGGCAGCTGAAGTTTTCAGGTAGTAAATTTACAGTGAATAATGT 405
 Db 525 PheProValLysTyrAlaSerProGluValPheSerPheSerArgTyrSerSerLysSer 544
 Qy 406 GAGCTCTTCAGCTGGGCTATTATTCTTTGGGAAGTGAACGCGTCGGA---CCCTTT 462
 Db 545 AspValTyrSerPheGlyValLeuMetTyrGluValPheSerGluGlyLysIleProTyr 564
 Qy 463 GATCAGATTGGTGGCCCGCTTCCGCAATCATGTGGGCTGTTCAATATGGTACTCGACCA 522
 Db 565 GluAsnArgSerAsnSer-----GluValValGluAspIleSerThrGlyPheArg--- 581
 Qy 523 CCAGTGATAAAAAATTACCTTAAGCC-----ATTGAGAGCTGTGATG 564
 Db 582 -----LeuTyrLysProArgLeuAlaSerCysHisValTyrGlnIleMet 596
 Qy 565 ACTGTTGTTGGTCTAAAGATCTCTCCAGCGCCCTTCAATGGAGGAAATGTGAAATA 624
 Db 597 AsnHisCysTyrLysGluLysProGluAspArgProPheSerGlnLeuLeuSerGln 616
 Qy 625 ATGACTCACTTG 636
 Db 617 LeuAlaGluIle 620

Search completed: December 4, 2003, 09:03:39

Job time : 25.1757 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 08:22:54 ; Search time 77.7973 Seconds
(without alignments)
4537.638 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 1252

Sequence: 1 gtgagcttcggcagttatc.....cattacagtatcctgttcag 684

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09830144/runat_03122003_122344_21277/app_query.fasta_1.1230
-DB=SPTRMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144 -CGEN_1_100 @runat_03122003_122344_21277 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL_23:.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rviro.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	100.0	478	4 Q9NTR4	Q9ntr4 homo sapien

2	1252	100.0	491	4 Q9NZ70	Q9nz70 homo sapien
3	1252	100.0	539	4 Q9NTR1	Q9ntr1 homo sapien
4	1252	100.0	566	4 Q9NTR2	Q9ntr2 homo sapien
5	1252	100.0	606	11 Q923A8	Q923a8 mus musculus
6	1221	97.5	616	13 Q73613	Q73613 xenopus lae
7	700	55.9	678	5 Q9V3Q6	Q9v3q6 drosophila
8	414	33.1	258	5 Q9VCV0	Q9vcv0 drosophila
9	379	30.3	422	10 Q8GV29	Q8gv29 oryza sativ
10	376	30.0	371	13 Q90ZY8	Q90zy8 brachydanio
11	375.5	30.0	2631	5 Q8MYR1	Q8myr1 dictyosteli
12	374.5	29.9	2964	5 Q8I7W7	Q8i7w7 dictyosteli
13	374	29.9	411	10 Q9ZQ31	Q9zq31 arabidopsis
14	373	29.8	412	10 Q9M085	Q9m085 arabidopsis
15	373	29.8	417	10 Q8GV30	Q8gv30 oryza sativ
16	372	29.7	289	11 Q8BR73	Q8br73 mus musculus
17	372	29.7	454	11 Q9ESL3	Q9esl3 mus musculus
18	372	29.7	802	11 Q9ESL4	Q9esl4 mus musculus
19	371	29.6	455	4 Q9HCC4	Q9hcc4 homo sapien
20	371	29.6	800	4 Q9NVE9	Q9nyv9 homo sapien
21	371	29.6	800	4 Q9NYL2	Q9nyl2 homo sapien
22	371	29.6	800	4 Q9HCC5	Q9hcc5 homo sapien
23	371	29.6	800	4 Q9HDD2	Q9hdd2 homo sapien
24	368	29.4	416	10 Q94C42	Q94c42 triticum ae
25	366	29.2	637	10 Q94V41	Q94v41 oryza sativ
26	363.5	29.0	1148	5 Q95VF6	Q95vf6 drosophila
27	363.5	29.0	1161	5 Q9SUN8	Q9sun8 drosophila
28	362	28.9	422	5 Q23846	Q23846 dictyosteli
29	362	28.9	1338	5 Q23927	Q23927 dictyosteli
30	360.5	28.8	608	11 Q8BIG8	Q8big8 mus musculus
31	360.5	28.8	1066	4 Q9H2N5	Q9h2n5 homo sapien
32	356.5	28.5	888	11 Q8CBX3	Q8cbx3 mus musculus
33	356	28.4	462	10 Q39886	Q39886 glycine max
34	355.5	28.4	370	10 Q9S7D5	Q9s7d5 arabidopsis
35	355	28.4	421	10 Q8GV28	Q8gv28 oryza sativ
36	355	28.4	564	4 Q9H1Y7	Q9h1y7 homo sapien
37	354.5	28.3	1161	5 Q8MRK7	Q8mrk7 drosophila
38	353.5	28.2	859	4 Q8WY25	Q8wy25 homo sapien
39	353.5	28.2	888	11 Q8CDL6	Q8cdl6 mus musculus
40	351.5	28.1	977	5 Q9VMW24	Q9vmw24 drosophila
41	351	28.0	570	4 Q8WNW2	Q8wnw2 homo sapien
42	351	28.0	1036	4 Q8WNW1	Q8wnw1 homo sapien
43	350	28.0	546	10 Q22558	Q22558 arabidopsis
44	349	27.9	1001	11 Q8VDG6	Q8vdg6 mus musculus
45	348	27.8	391	10 Q8LCP3	Q8lcp3 arabidopsis

ALIGNMENTS

RESULT 1

Q9NTR4	ID	Q9NTR4	PRELIMINARY;	PRT;	478 AA.
AC	Q9NTR4;				
DT	01-OCT-2000	(TrEMBLrel. 15, Created)			
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
DE	D154G14.1.3	(Mitogen-activated protein kinase kinase kinase 7 (TGF-beta activated kinase 1c (TAK1))) (Fragment)			
GN	MAP3K7.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RA	Tracey A.;				
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
DR	EMBL; AL121964; CAB87604.1; -				
DR	HSSP; P12931; 1PMK.				
DR	InterPro; IPR000719; Prot kinase.				
DR	InterPro; IPR002290; Ser thr kinase.				
DR	InterPro; IPR001245; Tyr_kinase.				
DR	Pfam; PF00069; pkinase; 1.				

DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 478 AA; 52482 MW; 177CC8CFA9D8DBF8 CRC64;

Alignment Scores:
Pred. No.: 5,79e-134 Length: 478
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x Q9NZ70 (1-478)

QY 1 GTAGAGCTTCGGCAGTATCCGCTGTGAACCTCTTAATATTCTAAAGCTTTATGAGCC 60
Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 55
QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 75
QY 121 CTGCATGGTGTGAACCATTCGATGCAATATATCTGCTGCCACGCAATAGTGGTGTAA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 95
QY 181 CAGTGTTCACAGGAGTGTCTATCTTCACAGCATCAACCAAGCGCTAAATTCACAG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 115
QY 241 GACCTGAACCCAACTTACTGCTGTTCAGGGGGGACAGTCTCTAAATTTTGTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 135
QY 301 TTGGTACAGCTGTGACATTCACACATGACCAATACCAAGGGAGTGTGCTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 155
QY 361 ATGGCAGCTGAAGTGTTCAGGTAGTAAATTCAGTGAAGTGTGACCTCTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 175
QY 421 GGTATTATCTTTGGGAAGTATACGCTGCGAAACCCCTTTGATGAGATTTGTCGCCCA 480
Db GlyIleLeuLeuTrpGluValIleThrArgGlySerProPheAspGluIleGlyGlyPro 195
QY 481 GCTTCCGAAATCATGTCGCTGTTCATATGTTACTCGACCACTCATATAAAATTTA 540
Db AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 215
QY 541 CCTAACCCATTGAGAGCTGATGCTGTGCTGTAAAGATCCTTCCAGAGCCCTT 600
Db ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 235
QY 601 TCAATGAGGAAATTTGAAATATATGACTCATCTGCGGTACCTTCAGAGAGAGAT 660
Db SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 255
QY 661 GAGCAATTACAGTATCTTGTGTCAG 684
Db GluProLeuGlnTyrProCysGln 263

RESULT 2
Q9NZ70 PRELIMINARY; PRT; 491 AA.
AC Q9NZ70; Q9NZ70;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE TGF beta-activated kinase splice variant d (DJ154G14.1.4) (Mitogen-
DE activated protein kinase kinase kinase 7 (TGF-beta activated kinase 1d
DE (TAK1)))
GN TAK1 OR MAP3K7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20568765; PubMed=11118615;
RA Dempsey C.E., Sakurai H., Sugita T., Guesdon F.;
RT "Alternative splicing and gene structure of the transforming growth
RT factor beta-activated kinase 1."; (2000).
RL Biochim. Biophys. Acta 1517:46-52 (2000).
RN [2]
RP SEQUENCE OF 41-491 FROM N.A.
RA Tracey A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF218074; AAF27652.1; -.
DR EMBL; AL121964; CAB87605.1; -.
DR HSSP; P08631; IAD5.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR001245; Ty_r_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 491 AA; 53739 MW; B7D832E286A99C5 CRC64;

Alignment Scores:
Pred. No.: 5,83e-134 Length: 491
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x Q9NZ70 (1-491)

QY 1 GTAGAGCTTCGGCAGTATCCGCTGTGAACCTCTTAATATTCTAAAGCTTTATGAGCC 60
Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 115
QY 121 CTGCATGGTGTGAACCATTCGATGCAATATATCTGCTGCCACCAATAGTGGTGTAA 180
Db LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCACAGGAGTGTCTTATCTTCACAGCATCAACCAAGCGCTAAATTCACAG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
QY 241 GACCTGAACCCAACTTACTGCTGTTCAGGGGGGACAGTCTCTAAATTTTGTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY 301 TTGGTACAGCTGTGACATTCACACATGACCAATACCAAGGGAGTGTGCTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
QY 361 ATGGCAGCTGAAGTGTTCAGGTAGTAAATTCAGTGAAGTGTGACCTCTCAGCTGG 420
Db MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 215

QY 421 GGTATTATTCTTTGGGAAGTATACCGCTCGAAACCTTTTGATGAGATTGGTGCCCA 480
 DB 216 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
 QY 481 GCTTTCCGAATCATGTGGCTGTTTCATATGCTACTCGACACCACTGATATAAAATTTA 540
 DB 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCCCATGAGAGCTGATGACTCTGTTGGTCTTAAGATCCTTCCAGCGCCCT 600
 DB 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
 QY 601 TCAATGAGAGAAATGTGAAATAATGACTCACTTGTGCTGCTTCCAGGAGCAGAT 660
 DB 276 SerMetGluGluIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCATTACAGTATCTCTGTCAG 684
 DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 3

Q9NTR1 ID Q9NTR1 PRELIMINARY; PRT; 539 AA.
 AC Q9NTR1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE D154G14.1.1 (Mitogen-activated protein kinase kinase 7 (TGF-
 beta activated kinase 1a (TAK1))) (Fragment).
 GN MAP3K7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; ALI21964; CAB87607.1; -.
 DR HSSP; P12931; 1FMK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 539 AA; 60006 MW; E6183F553CC7F324 CRC64;

Alignment Scores:

Pred. No.: 5,97e-134 Length: 539
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x Q9NTR1 (1-539)

QY 1 GTAGCTTCGGCAGTATCCCGTGTGAACCATCTATATGTAAAGCTTTATGAGCC 60
 DB 36 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 55
 QY 61 TGCTTGAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 DB 56 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 75

QY 121 CTGCATGTGTCTGACCACTTGCATATTATCTGCTGCCCGCAATGAGTTGGTGTTA 180
 DB 76 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 95
 QY 181 CAGTGTTCCTCCAGGAGTGGCTTACTTCCACAGCATGCAACCAAGCCGCTAATTCACAGG 240
 DB 96 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 115
 QY 241 GACCTGAAACCAACCAACTTACTGCTGCTGCAGGGGACAGTTCTAAAAATTTGTGAT 300
 DB 116 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 135
 QY 301 TTTGGTACAGCTGTGACCTTCAGACACACATGACCATTAACAAGGGAGTGCTGCTGG 360
 DB 136 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 155
 QY 361 ATGCACCTGAAAGTATTTTGAAGGTAGTAATPACAGTGAATAATGTGACGCTCTTCAGCTGG 420
 DB 156 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 175
 QY 421 GGTATTATTCTTTGGGAAGTATACCGCTCGAAACCTTTTGATGAGATTGGTGCCCA 480
 DB 176 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 195
 QY 481 GCTTTCCGAATCATGTGGCTGTTTCATATGCTACTCGACACCACTGATATAAAATTTA 540
 DB 196 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 215
 QY 541 CCTAAGCCCATGAGAGCTGATGACTCTGTTGGTCTTAAGATCCTTCCAGCGCCCT 600
 DB 216 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 235
 QY 601 TCAATGAGAGAAATGTGAAATAATGACTCACTTGTGCTGCTTCCAGGAGCAGAT 660
 DB 236 SerMetGluGluIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 255
 QY 661 GAGCATTACAGTATCTCTGTCAG 684
 DB 256 GluProLeuGlnTyrProCysGln 263

RESULT 4

Q9NTR2 ID Q9NTR2 PRELIMINARY; PRT; 566 AA.
 AC Q9NTR2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE D154G14.1.2 (Mitogen-activated protein kinase kinase 7 (TGF-
 beta activated kinase 1b (TAK1))) (Fragment).
 GN MAP3K7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; ALI21964; CAB87606.1; -.
 DR HSSP; P12931; 1FMK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 566 AA; 62972 MW; 32CDAC1211B200CF CRC64;

Alignment Scores:
 Pred. No.: 6,04e-134 Length: 566
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x Q9NTR2 (1-566)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCACTCTTAATATCTAAAGCTTTATGAGCC 60
 Db 36 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 55
 QY 61 TGTCTGAATCCAGTGTCTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATG 120
 Db 56 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 75
 QY 121 CTGCTAGTGTGCTGAACCACTTACTGCTGCTGCCCGCACTGAGTTCGTTGTTA 180
 Db 76 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 95
 QY 181 CAGTGTTCCTCAAGGAGTGTCTATCTTCACAGCATGCAACCCCAAGCGCTTAATTCACAG 240
 Db 96 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 115
 QY 241 GACCTGAAACCCACCAACTTACTGCTGTTGCGGGGGACAGTCTCTAAATAATTTGTGAT 300
 Db 116 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 135
 QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATCAACCAAGGGAGTGTGCTGG 360
 Db 136 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 155
 QY 361 ATGCGACCTCAAGTCTTTTGAAGTGTAGTATTAACAGTGAAATAATGTGACGCTTCAGCTGG 420
 Db 156 MetAlaProGluValPheGluGlySerAsnTyrSerGulysCysaspValPheSerTrp 175
 QY 421 GGTATTATCTTTGGGAAGTGTAAACGCGTCGGAACCCCTTTGATGAGATGTGGGCCCA 480
 Db 176 GlyIleIleLeuTrpGluValIleThrArgLysProPheAspGluIleGlyGlyPro 195
 QY 481 GCTTTCCGATCATGTGGCTGTCTATATGTTACTGCTACACCATGACCATGATAAATAATTA 540
 Db 196 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProLeuIleLysAsnLeu 215
 QY 541 CCTAAGCGAAATGTGAAATAATGACTCATCTGATGCGGTACTTTCCAGGAGCAGAT 600
 Db 216 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysaspProSerGlnArgPro 235
 QY 601 TCAATGGAGAAATGTGAAATAATGACTCATCTGATGCGGTACTTTCCAGGAGCAGAT 660
 Db 236 SerMetGluGluIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 255
 QY 661 GAGCCATTACAGTATCTTGTCTAG 684
 Db 256 GluProLeuGlnTyrProCysGln 263

RESULT 5
 Q923A8 PRELIMINARY; PRT; 606 AA.
 AC Q923A8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Unknown (Protein for MGC:5989).
 GN MAP3K7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; BC006665; AA06665.1; -.
 DR MBL; MGI:1346877; Map3k7.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00669; pkinase; 1.
 DR PRINTS; PRO109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 606 AA; 67194 MW; AB8664F389272102 CRC64;

Alignment Scores:
 Pred. No.: 6.15e-134 Length: 606
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x Q923A8 (1-606)

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCACTCTTAATATCTAAAGCTTTATGAGCC 60
 Db 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 95
 QY 61 TGTCTGAATCCAGTGTCTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATG 120
 Db 96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
 QY 121 CTGCTAGTGTGCTGAACCACTTACTGCTGCTGCCCGCACTGAGTTCGTTGTTA 180
 Db 116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 135
 QY 181 CAGTGTTCCTCAAGGAGTGTCTATCTTCACAGCATGCAACCCCAAGCGCTTAATTCACAG 240
 Db 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
 QY 241 GACCTGAAACCCACCAACTTACTGCTGTTGCGGGGGACAGTCTCTAAATAATTTGTGAT 300
 Db 156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
 QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATCAACCAAGGGAGTGTGCTTGG 360
 Db 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
 QY 361 ATGCGACCTGAAGTCTTTTGAAGTGTAGTATTAACAGTGAAATAATGTGACGCTTCAGCTGG 420
 Db 196 MetAlaProGluValPheGluGlySerAsnTyrSerGulysCysaspValPheSerTrp 215
 QY 421 GGTATTATCTTTGGGAAGTGTAAACGCGTCGGAACCCCTTTGATGAGATGTGGGCCCA 480
 Db 216 GlyIleIleLeuTrpGluValIleThrArgLysProPheAspGluIleGlyGlyPro 235
 QY 481 GCTTTCCGATCATGTGGCTGTCTATATGTTACTGCTACACCATGACCATGATAAATAATTA 540
 Db 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProLeuIleLysAsnLeu 255
 QY 541 CCTAAGCGAAATGTGAAATAATGACTCATCTGATGCGGTACTTTCCAGGAGCAGAT 600
 Db 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysaspProSerGlnArgPro 275
 QY 601 TCAATGGAGAAATGTGAAATAATGACTCATCTGATGCGGTACTTTCCAGGAGCAGAT 660
 Db 276 SerMetGluGluIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
 QY 661 GAGCCATTACAGTATCTTGTCTAG 684


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Db      296 GluProLeuGlnTyrProCysGln 303
RESULT 6
073613 PRELIMINARY; PRT; 616 AA.
ID O73613
AC O73613;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE TAK1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=98130593; PubMed=9463380;
RA Shibuya H., Iwata H., Masuyama N., Gotoh Y., Yamaguchi K., Irie K.,
RA Matsumoto K., Nishida E., Ueno N.;
RT "Role of TAK1 and TAB1 in BMP signaling in early Xenopus
RT development.";
RL EMO J. 17:1019-1028 (1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U92030; AAC14008.1; --
DR HSP; P12931; IFMK.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 616 AA; 68464 MW; 493AD2A05ADC38B6 CRC64;

Alignment Scores:
Pred. No.: 2,16e-130 Length: 616
Score: 1221.00 Matches: 222
Percent Similarity: 98.68% Conservative: 3
Best Local Similarity: 97.37% Mismatches: 3
Query Match: 97.52% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x O73613 (1-616)
QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCCTTAATTTGTAAGCTTTATGGAGCC 60
Db 65 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnLeuValLeuTyrGlyAla 84
QY 61 TGGTGAATCCAGTGTCTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 85 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 104
QY 121 CTGCATGCTGCTGAACCATGCTCAATATATCTGCTGCCACCAATGAGTTGGTGTTA 180
Db 105 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 124
QY 181 CAGTGTTCACCAAGAGTGGCTTATCTTCAGCATGCAACCAAGCGCTTAATTCACAGG 240
Db 125 GlnCysAlaGlnGlyValAlaTyrLeuHisSerMetCysProLysAlaLeuHisArg 144
QY 241 GACCTGAACCAACCAACTTACTGCTGGTTGCGAGGGGACAGTCTTAAATAATTCGTAT 300
Db 145 AspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysLeuCysAsp 164
QY 301 TTGGTACAGCTGTGACATTCAGACACATGACCAATACCAAGGGAGTGTGCTGTGG 360
Db 165 PheGlyThrAlaCysAspLeuGlnThrHisMetAsnAsnLysGlySerAlaAlaTyr 184

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QY 361 ATGGCAGCTGAGCTTTTGAAGGTAGTAAATACAGTGAATAATGAGCTTTCAGCTGG 420
Db 185 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 204
QY 421 GGTATTATTCTTTGGGAAGTGATAACGCGTCGGAAACCCCTTTGATGAGATTGGTGGCCCA 480
Db 205 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 224
QY 481 GCTTTCGGAATCATGTGGGTGTTCATAATGTTACTCGACACCACTGATATAAAATTTA 540
Db 225 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 244
QY 541 CCTAAGCCCATTCGAGAGCCTGATGACCTGTTGGTCTAAGATCCTTCCACGCGCCT 600
Db 245 ProLysProIleLeuSerLeuMetThrArgCysTrpSerLysAspProProGlnArgPro 264
QY 601 TCAATGAGGAGAAATTTGTAATAATACACTCACTTGTATGCGGTACTTTCAGGAGCAGAT 660
Db 265 SerMetGluGluIleValIleMetThrHisLeuMetGlnTyrPheProGlyAlaAsp 284
QY 661 GAGCCATTACAGTATCTTCTCTCAG 684
Db 285 ValSerLeuGlnTyrProCysGln 292

RESULT 7
QY9V3Q6 PRELIMINARY; PRT; 678 AA.
ID QY9V3Q6
AC QY9V3Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative TAK1 protein (CG1386 protein) (L042274P).
GN TAK1 OR CG1386 OR CG18492.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RX George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RX Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RX Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RX Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RX Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RX Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RX Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RX Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RX Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RX Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RX Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
RX Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RX Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RX Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RX Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RX Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RX Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Takatsu Y., Nakamura M., Stapleton M., Danos M., Matsumoto M.,
RA O'Connor M.B., Shibuya H., Ueno N.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF003571; AAF50895.1; -;
DR EMBL; AF199466; AAF06815.1; -;
DR EMBL; AY051953; AAK93377.1; -;
DR HSP; P08631; IAD5;
DR Flybase; FBgn0262323; Tak1.
DR InterPro; IPR001990; Granin.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR001245; Tyr pkinase.
DR Pfam; PF00669; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot kinase; 1.
DR PROSITE; PS00422; GRANINS 1; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 678 AA; 75674 MW; 87EBA80CDB8CDE45 CRC64;

Alignment Scores:
Pred. No.: 8, 2e-71
Score: 700.00
Percent Similarity: 73.01%
Best Local Similarity: 57.52%
Query Match: 55.91%
Indels: 4
Gaps: 3
DB: 5

US-09-830-144-1_COPY_408_1091 (1-684) x Q9V3Q6 (1-678)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGA----- 57
Db 60 GluVallysglnLeuSerArgVallyshisProAsnleileAlaLeuHisGlyIleSer 79
QY 58 GCTGCTTGATCCAGTGTCTTGTGATGATATGCTCAAGGGGCTTTATATAT 117
Db 80 SerTyrGlnGlnAlaThrTyrLeuileMetGluPheAlaGluGlySerLeuHisAsn 99
QY 118 GTGCTGCATGCTGTGTAACCATTCCTCCATATTAATCTGCTCCACGCAATGAGTTGTGT 177
Db 100 PheLeuHisGly---LysVallyshisProAlaTyrSerLeuAlaHisAlaMetSerTrpAla 118
QY 178 TTAAGTGTTCACAGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTTAATTCAC 237
Db 119 ArgGlnCysAlaGluGlyLeuAlaTyrLeuHisAlaMetThrProLysProLeuileHis 138
QY 238 AGGACCTGAACACCAACCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
Db 139 ArgaspVallyshisProLeuAsnLeuLeuThrAsnLysGlyArgAsnLeuLysIleCys 158
QY 298 GATTTTGTGACAGCTGTGACATTCAGACACACATGACCAATACAAAGGGAGTGTGCT 357

Db 159 AspPheGlyThrValAlaAspLysSerThrMetMetThrAsnAsnArgGlySerAlaAla 178
QY 358 TCGATGGCAGCTGAAGTGTGTTGAAGCTAGTAAATACAGTGAATAATGTGACCTCTTCAGC 417
Db 179 TrpMetAlaProGluValPheGluGlySerLysTyrThrGluLysCysAspIlePheSer 198
QY 418 TGGGCTATTATTCTTTGGGAAGTGATACGCGTCGGAACCCCTTTGATGAGATTGCTGCGC 477
Db 199 TrpAlaIleValLeuTrpGluValLeuSerArgLysGlnProPheLysGlyIleAspAsn 218
QY 478 CGAGCTTTCGGAATCATGTGGCTGTTCAATATGTTACTCGACCACTGATAAAAT 537
Db 219 ---AlaTyrThrIleGlnTrpLysIleTyrLysGlyGluArgProLeuLeuThrThr 237
QY 538 TTACCTTAAGCCCATTTGAGAGCGCTGATGACTCGTGTGCTGCTTAAAGATCCTTCCAGCGC 597
Db 238 CysProLysArgIleGluAspLeuMetThrAlaCysTrpLysThrValProGluAspArg 257
QY 598 CTTTCAATGGAGGAAATTTGTGAAATAATGACTCACTGATCGGTGTTTCCAGGAGCA 657
Db 258 ProSerMetGlnTyrIleValGlyValMetHisGluIleValLysAspTyrThrGlyAla 277
QY 658 GATGAGCCATTACAGTAT 675
Db 278 AspLysAlaLeuGluTyr 283

RESULT 8
Q9V3Q6
ID Q9V3Q6 PRELIMINARY; PRT; 258 AA.
AC Q9V3Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG4803-PA.
GN TAKL2.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7221;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.H., Plazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hattis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Massarman D.A., Weinscock G.M., Weissbach J.,
RA Williams S.M., Woodgett, Korley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Chape M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Hock J., Kruse D., Li P., Mattei B., Moshrefi A.,
RA Ibegwam C., Jaijali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Carlson B., Carlson J.W., Celnik S.E.,
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RA FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003740; AAF56055.2; -
DR FlyBase; Fg90039015; Tak12.
SQ SEQUENCE 258 AA; 29480 MW; D117DA8922BFABE1E CRC64;

Alignment Scores:
Pred. No.: 3-23e-38 Length: 258
Score: 414.00 Matches: 82
Percent Similarity: 59.69% Conservative: 35
Best Local Similarity: 41.84% Mismatches: 53
Query Match: 33.07% Indels: 26
DB: 5 Gaps: 4

US-09-830-144-1_COPY_408_1091 (1-684) x Q9VCV0 (1-258)

QY 4 GAGCTTCGGCAGTATCCCGTGTGAACCACTCTTAATTTGTAAGCTTTATGAGCCTGC 63
Db 54 GluileTyr-GlnLeuThrLysAlaSerHisValAsnIleValGluLeuTyrGlyThrSer 73
QY 64 TTGAATCCAGTGTG-----CTTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 74 ArgHisGluGlyCysAlaLeuLeuLeuMetGluPheValAspGlyGlySerLeuSerSer 93
QY 118 GTGCTCATGGTCTGAACCAATGCTCATATTTACTGCTGCCCAACCAATGATGCTGT 177
Db 94 PheLeuHis---AlaLysSerLysProSerTyrSerHisAlaHisAlaPheAsnTrpAla 112
QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCCAAGCGCTAATTCAC 237
Db 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCCAAGCGCTAATTCAC 237

Db 113 HisGlnIleAlaGlnGlnIleAlaTyrLeuHisGlyMetGlnProLysAlaValIleHis 132
QY 238 AGGACTCTGAACACCAACTTACTCTGCTGAGGGGGGACAGTTCTAAAAATTGT 297
Db 133 ArgAspileLysProLeuAsnThrLeuLeuCysGlnLysGlyLeuLysLysCys 152
QY 298 GATTTGGTACAGCCTGTGACATTCACACATGACACATTAACAGGGAGTGTGCT 357
Db 153 AspPheGlyThrValValAspLeuSerGlnSerIleSerCysAsnAlaGlyThrCysArg 172
QY 358 TGGATGGCAGCTGAA----- 372
Db 173 TyrLysAlaProGluValArgGluLeuPheAspPheLysSerAsnArgIleIleAsn 192
QY 373 -----GTTTTGAAGGTAGTAATTACAGTGAAAAATGTGAGTGC 411
Db 193 GlnProThrGlyPheGlnLysValLeuGlnGlyAsnLysProAspGluLysCysAspVal 212
QY 412 TTCAGCTGGGGTATTATCTTTCGGAGTATACACGGCTCGGAACCCCTTGTAGAT 471
Db 213 TyrSerTrpAlaIleThrPheTrpGluIleLeuSerArgLysGluProPheGluGlnTyr 232
QY 472 GGTGGCCAGCTTTCGGAATCATGTGGCTGTTCATAATGCTACTCGA 519
Db 233 ---AsnThrLeuPheGluLeuTyrMetAlaIleAsnGluGlyLysArg 247

RESULT 9
Q8GV29 PRELIMINARY; PRT; 422 AA.
AC Q8GV29;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
GN DPX2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z.M., Zhang H.S., Huang J.;
RT "Molecular Cloning And Characterization Of A Novel Serine/Threonine
RT Protein Kinase Gene Family From Rice";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY156511; AAN84503.1; -
KW Kinase.
SQ SEQUENCE 422 AA; 46587 MW; BCC22F1FC6CFF62C CRC64;

Alignment Scores:
Pred. No.: 3-66e-34 Length: 422
Score: 379.00 Matches: 85
Percent Similarity: 58.18% Conservative: 43
Best Local Similarity: 38.64% Mismatches: 70
Query Match: 30.27% Indels: 22
DB: 10 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x Q8GV29 (1-422)

QY 4 GAGCTTCGGCAGTATCCCGTGTGAACCACTCTTAATTTGTAAGCTTTATGAGCCTGC 63
Db 190 GluValMetMetLeuAlaThrLeuArgHisProAsnIleValLysPheIleGlyAlaCys 209
QY 64 TTGAATCCAGTGTG-----TGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 210 ArgLysProMetValTrpCysIleValThrGluTyrAlaLysGlyGlySerValArgGln 229
QY 118 GTGCTG-----CATGGCTGAACCAATGCTCATATTTACTGCTGCCCAACCAAGCGCTAATTCAC 165
Db 230 PheLeuMetLysArgGluAsnArgSerValProLeuLysLeu-----Ala 244
QY 166 ATGAGTGTGTTTACAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCCAAG 225

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Db 245 VailLysGlnAlaLeuAspValAlaArgGlyMetAlaTyrValHisAlaLeu----- 261
QY 226 GCGCTAAATTCACAGGAGCTGAACACCAACTTACTGCTGGTTCAGGGGGGACAGTT 285
Db 262 GlyPheIleHisArgAspLeuLysSerAspAsn---LeuLeuIleSerGlyAspLysSer 280
QY 286 CTAAAAATTTGATTTGGTACAGCC---TGTGACATTCACACACAC---ATGACCAAT 339
Db 281 IleLysIleAlaAspPheGlyValAlaArgIleGluValLysThrGluGlyMetThrPro 300
QY 340 AACAGGGGAGGCTGCTGGATGCGACCTGAAGTTTTCAGAGGTAGTAAATACAGTGAA 399
Db 301 GluThrGlyTyrArgTirPheAlaProGluMetIleGlnHisArgProTyrAspGln 320
QY 400 AAATGTGAGCTCTCAGCTGGGGTATTAATCTTTGGGAAGTCAATACCGCTCGGAACCC 459
Db 321 LysValAspValTyrSerPheGlyIleValLeuTyrPheGluIleThrGlyMetLeuPro 340
QY 460 TTTGATGAGATTGGTGGC-----CCAGCTTCCGAAATCATGTGGCTGTTCAATAGGT 513
Db 341 PheAlaAsnMetThrAlaValGlnAlaAlaPheAlaVal-----ValAsnLysGly 357
QY 514 ACTGACCAACCACTGATAAAATTTACCTAAGCCCATTCAGAGCCTGATGACTCTTGT 573
Db 358 ValArgProAlaIleProGlnAspCysLeuProValLeuSerGluIleMetThrArgCys 377
QY 574 TGGTCTAAAGATCTTCCAGCGCCCTTCAATGGAGGAATTTGGAATAATAGTACTAC 633
Db 378 TrpAspProAsnProAspValArgProProPheThrGluValValArgMetLeuGluHis 397

RESULT 10
Q90ZY8 PRELIMINARY; PRT; 371 AA.
AC Q90ZY8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF265343; AAK52416.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 371 AA; 42456 MW; 9B918B8A8B20D296 CRC64;

Alignment Scores:
Pred. No.: 7,82e-34 Length: 371
Score: 376.00 Matches: 82
Percent Similarity: 56.67% Conservative: 37
Best Local Similarity: 39.05% Mismatches: 81
Query Match: 30.03% Indels: 10
DB: 13 Gaps: 7

US-09-830-144-1_COPY_408_1091 (1-684) x Q90ZY8 (1-371)

QY 4 GAGTTCGGCAGTATCCCGTGAACCACTCTAATATTAATGTAAGCTTTATGAGCGTGC 63
Db 84 GluAlaGluIleLeuSerValLeuSerHisLysAsnIleIleGlnPheTyrGlyAlaIle 103

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QY 64 TTGAATCCAGTG-----TGCTTCTGATGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 104 LeuGluAlaProAsnAspGlyIleValThrGluTyrAlaSerArgGlySerLeuTyrGlu 123
QY 118 GTGCTGATGCTGGTGAACCACTTCCATTAATGCTGCTGCCACCAATGATGGTGT 177
Db 124 TyrLeuSerSerAlaAspSer---GluGluMetAspMetAspGlnValMetThrTrpAla 142
QY 178 TTACAGTGTTCACAGGAGTGGCTTATCTTCACACATGCACCAACCAACGCGTAAATTCAC 237
Db 143 MetGluIleAlaLysGlyMetHisTyrLeuHisAlaGluAlaProLeuLysValIleHis 162
QY 238 AGGACCTCGAACCACCACTTACTGCTGCTGGTTCAGGGGGGACAGTCTTAAAAATTTGT 297
Db 163 ArgAspLeuLysSerArgAsnValValLeuThrAla---AspAsnValLeuLysIleCys 181
QY 298 GATTTTGTGACAGCTGTGACATTCAGACACATGCACCAATACCAAG-----GGAGT 351
Db 182 AspPheGly---AlaSerLysMetValSerHisThrThrHisMetSerLeuValGlyThr 200
QY 352 GCTGCTTGGATGCGACCTGAAGTTTTCAGAGGTAGTAAATACAGTGAATAATGTGACGTC 411
Db 201 PheProTirPheMetAlaProGluValIleGlnSerLeuProValSerGluThrCysAspThr 220
QY 412 TTCAGTGGGGTATTAATCTTTGGGAAGTGAATAACGCGTCGGAAACCCCTTTGATGAGATT 471
Db 221 TyrSerTyrGlyValValLeuTyrPheGluMetLeuThrArgGluValProPheLys----- 238
QY 472 GGTGCGCCAGCTTCGGAATCANGTG---GCTGTTCATAATGTTACTGACACCACTG 528
Db 239 GlyPheGluGlyLeuGlnValAlaTrpLeuValValGluLysHisGluArgProThrIle 258
QY 529 ATAAAAAATTTACCTAAGCCCATTCAGAGCCTGATGACTGCTGTTGGTGTAAAGATCCT 588
Db 259 ProSerSerCysProAlaSerPheAlaAspLeuMetArgCysTrpAsnAlaGluPro 278
QY 589 TCCAGCGCCCTTCAATGGAGGAATTTGTG 618
Db 279 LysGluArgProGlnPheLysGlnIleLeu 288

RESULT 11
Q8MVR1 PRELIMINARY; PRT; 2631 AA.
AC Q8MVR1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cyclic GMP-binding protein C.
GN GBPC.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Bosgraaf L., Russcher H., Smith J.L., Wessels D., Solls D.R.,
RA Van Haastert P.J.M.;
RT "A novel cGMP signalling pathway mediating myosin phosphorylation and
RT chemotaxis in Dictyostelium.";
RL EMBO J. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22008080; PubMed=12011437;
RA Goldberg J.M., Bosgraaf L., Van Haastert P.J., Smith J.L.;
RT "Identification of four candidate cGMP targets in Dictyostelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:6749-6754(2002).
DR EMBL; AF481923; AAM34041.1; -.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000591; DEP_.
DR InterPro; IPR004182; GRAM dom.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000651; RasGEFN.

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DR	InterPro; IPR001895; RasGRF_CDC25.
DR	InterPro; IPR001806; Ras trnsfrmg.
DR	InterPro; IPR002290; Ser thr pkinese.
DR	InterPro; IPR001245; Tyf_pkinase.
DR	Pfam; PF00027; cNMP binding; 2.
DR	Pfam; PF00610; DEP; 1.
DR	Pfam; PF02893; GRAM; 1.
DR	Pfam; PF00069; pkinase; 1.
DR	Pfam; PF00617; RasGEF; 1.
DR	Pfam; PF00618; RasGEFN; 1.
DR	PRINTS; PR00449; RASTRNSFRMNG.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD000001; Prot kinase; 1.
DR	SMART; SM00049; DEP; 1.
DR	SMART; SM00568; GRAM; 1.
DR	SMART; SM00369; LRR_TYP; 2.
DR	SMART; SM00147; RasGEF; 1.
DR	SMART; SM00220; S_TKc; 1.
DR	SMART; SM00219; TyrKc; 1.
DR	PROSITE; PS00042; CNMP_BINDING_3; 2.
DR	PROSITE; PS00186; DEP; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ATP-binding; GTP-binding; Transference.
SQ	SEQUENCE 2631 AA; 294124 MW; 5BB7AABD0A637701 CRC64;

Alignment Scores:

Pred. No.:	1.45e-33	Length:	2631
Score:	375.50	Matches:	88
Percent Similarity:	53.66%	Conservative:	44
Best Local Similarity:	35.77%	Mismatches:	75
Query Match:	29.9%	Indels:	39
DB:	5	Gaps:	9

US-09-830-144-1_COPY_408_1091 (1-684) x Q8MVRI (1-2631)

QY	4	GAGCTTCGGCAGTTATCCGCTGTGAACCATCCTTAATTATGTAAAGCTTATGGAGCGTCG	63
Dd	947	GlUValTyrrMetSerGlyLeuAsnHisProAsnValMetLysIleSerGlyPheCys	966
QY	64	TGGAATCCAGTGCTCTGTGCATGGATATCTCTGAAGGGGCTTTATATAATGTGCTG	123
Dd	967	IleGlnProLeuCysMetAlaLeuGluTyrrValArgTyrrGlySerLeuTyrrSerLeuLeu	986
QY	124	CATGGTGCTGAACCATATGCCATATTACTGCTGCCACCAATAGTAGTGTGTTA---	180
Dd	987	Ser-----AsnSerSerIleGluIleSerTrpGlyLeuArg	998
QY	181	-----CAGTGTCACAGGAGTGCTTATCTTACAGCATGCAACCCAAA	225
Dd	999	LeuGlnIleAlaSerGluIleAlaLysGlyMetGlnHisLeuHisSerHisAsnPro---	1017
QY	226	GCCTAATTCACAGGACCTGAAACCACCAACTTACTGCTG-----GTTCAGGGGGG	279
Dd	1018	ProValIleHisArgAspLeuLysSerProAsnIleLeuLeuAsnGlyIleThrGluGly	1037
QY	280	-----ACAGTTCCTAAAAATTGCTGATTTGGTACGCTGTGACATTCACACACACATG	333
Dd	1038	GlnAsnSerValAlaThrIleIleAspPheGlyThrSer-----	1050
QY	334	ACCAATAACAGGGAGTGTGCT-----TGGATGGCA	366
Dd	1051	ThrAlaLeuTyrrGlyGlyAlaAlaLeuIleArgCysValAspGlnProLeuTrpLeuGly	1070
QY	367	CCTGAAGTTTTCAAGGTAGTAAATACAGTGAANAATGTGACGCTTTCAGCTGGGTATT	426
Dd	1071	ProGluValLeuAlaGlyThrAlaTyrrSerGluProSerAspValTyrrSerPheGlyIle	1090
QY	427	ATTCTTTGGGAAGTGATACCGCTCGGAACCCCTTTGATGAG-----ATTGTTGGCCCCA	480
Dd	1091	IleLeuTrpGluLeuTyrrThrArgAlaHisProPheAspGluPheGlnPheGlnTrp	1110

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Db 2263 TrpLeuAlaProGluLeuLeuAsnLysThrLysGluAlaSerThrGlnThrAspValTyr 2282
QY 415 AGCTGGGGTATTATCTTTGGGAAGTATAAGCGCTCGAAACCCCTTTGATGAGATTGGT 474
Db 2283 AlaPheGlyValLeuLeuTipGluLeuValThrArgLysAspTyrPheGlyGluLeuGly 2302
QY 475 GGCCAGCTTCCGAATCATGTGGCTGTTCTATATGTTACTCGACCACTGATAAAA 534
Db 2303 PheMetThrLeu---IleGluGluLysValIleAsnGlyGluArgProLysIleProGlu 2321
QY 535 AATTACCTAAGCCCATTCAGAGCTGATGACTGCTGTTGTTGTTCTAAAGATCTCCAG 594
Db 2322 AspCysProGluMetTyrSerLysLeuIleValGluCysTrpGlnThrAspAlaSerGln 2341
QY 595 CGCCCTTCAATGGAGAAATT 615
Db 2342 ArgProLysPheSerGluIle 2348
QY 595 CGCCCTTCAATGGAGAAATT 615
Db 2342 ArgProLysPheSerGluIle 2348
RESULT 13
Q9ZQ31 PRELIMINARY; PRT; 411 AA.
AC Q9ZQ31: Q94A10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN AT2G24360.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yu G., Yu S., Bowser L., Carninci P., Chen H.,
RA Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RA "Full Length cDNA of gene T28124.9/At2g24360 (GI:4337195).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan H.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,
RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yu G., Yuan S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RL "Arabidopsis Open Reading Frame (ORF) Clones.";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL; AC006403; AAD18109.2; -
DR EMBL; AY046026; AAK76700.1; -
DR EMBL; AY133876; AAM91810.1; -
DR HSSP; P12931; 1FMK.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinae.
DR InterPro; IPR001245; Tyr pkinae.
DR Pfam; PF00069; pkinase; 1.

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DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 411 AA; 46001 MW; 3B7001CFBB411BAA CRC64;

Alignment Scores:
Pred. No.: 1-36e-33 Length: 411
Score: 374.00 Matches: 86
Percent Similarity: 57.80% Conservative: 40
Best Local Similarity: 39.45% Mismatches: 70
Query Match: 29.87% Indels: 22
DB: 10 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x Q9ZQ31 (1-411)
QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTATATTTGTAAGCTTTTATGGAGCTGC 63
Db 179 GluValSerMetLeuAlaAsnLeuLysHisProAsnIleValArgPheIleGlyAlaCys 198
QY 64 TTGAATCCAGTC-----TGCTTTGTGATGAATATGCTGAAGGGGCTCTTTATATAAT 117
Db 199 ArgLysProMetValTrpCysIleValThrGluTyrAlaLysGlySerValArgGln 218
QY 118 GTGCTG-----CATGCTGCTGAACCATTCGCCATATTTATATCTGCTGCCACGCA 165
Db 219 PheLeuThrArgArgGlnAsnArgAlaValProLeuLysLeu-----Ala 233
QY 166 ATGAGTTGGTGTTCACAGTGTTCCTCCAGAGGTGGCTTATCTTCACAGCATGCACCCAAA 225
Db 234 ValLysGlnAlaLeuAspValAlaArgGlyMetAlaTyrValHisGly-----Arg 250
QY 226 GCCTTAATTCACAGGACCTGAACCCACCACTTACTGCTGCTGCAGGGGGACAGTT 285
Db 251 AsnPheIleHisArgAspLeuLysSerAspAsnLeuIleSerAlaAspLysSerIle 270
QY 286 CTAAAAAATTTGTGATTTTGTGTACAGCC--TGTGACATTCAGACACAC---ATGACCAAT 339
Db 271 ---LysIleAlaAspPheGlyValAlaArgGluValGlnThrGluGlyMetThrPro 289
QY 340 AACACGGGAGTCTGCTGTCGATGGCACCTGAAGTCTTTTCAAGGTAGTAGTATTACAGTAA 399
Db 290 GluThrGlyThrTyrArgTrpMetAlaProGluMetIleGlnHisArgAlaTyrAsnGln 309
QY 400 AATGTGACGCTCTTCAGCTGGGTATTTCTTTGGAGCTGATGAACCGCTCGAAACCC 459
Db 310 LysValAspValTyrSerPheGlyIleValLeuTrpGluLeuIleThrGlyLeuLeuPro 329
QY 460 TTTGATGAGATTGCTGGC-----CCAGCTTTCCGAATCATGTGGGCTGTTCATAATGGT 513
Db 330 PheGlnAsnMetThrAlaValAlaGlnAlaPheAlaVal-----ValAsnArgGly 346
QY 514 ACTCGACCACTGATATAAAAAATTTACCTAAGCCCATTCAGAGCTGTGAGCTGATGCTGTGT 573
Db 347 ValArgProThrValProAsnAspCysLeuProValLeuSerAspIleMetThrArgCys 366
QY 574 TGGTCTAAAGATCTTCCAGCGCCCTTCAATGGAGGAAATTTGAAAAAATG 627
Db 367 TrpAspAlaAsnProGluValArgProCysPheValGluValValLysLeuLeu 384

RESULT 14
Q9M085 PRELIMINARY; PRT; 412 AA.
ID Q9M085
AC Q9M085;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE protein kinase-like protein (AT4G31170/P6E21_90).
GN AT4G31170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Thu Dec 4 17:00:21 2003

Percent Similarity: 57.34% Conservative: 41
 Best Local Similarity: 38.53% Mismatches: 71
 Query Match: 29.79% Indels: 22
 DB: 10 Gaps: 9

US-09-830-144-1_COPY_408_1091 (1-684) x Q8GV30 (1-417)

```

QY 4 GAGCTTCGGCAGTTATCCGGTGTGACCATCTCTATATGTAAAGCTTTATGGAGCTGC 63
DB 185 GluValMetMetLeuAlaThrLeuArgHisSerAsnIleValLysPheValGlyAlaCys 204
QY 64 TTGAATCCAGTG-----TGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAAT 117
DB 205 ArgLysProMetCysIleValThrGluTyrAlaLysGlyGlySerValArgAsn 224
QY 118 GTGCTGCATGGTCTGAA-----CCATTGCCATATTACTCTGCTGCCACGCA 165
DB 225 PheLeuAsnArgArgGlnAsnArgSerValProLeuLysLeu-----Ala 239
QY 166 ATGAGTTGGTGTTCAGTGTTCCTCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAA 225
DB 240 ValLysGlnAlaLeuAspValAlaArgGlyMetAlaTyrValHisGlyLeu----- 256
QY 226 GCGCTAATTACAGGACCTGAACACCAAACTTACTGTCTGTTCAGGGGGACAGTT 285
DB 257 GlyPheIleHisArgAspLeuLysSerAspAsn---LeuLeuIleSerGlyAspLysSer 275
QY 286 CTAATAATTGTGATTTGTACAGCC---TGTGACATTCAGACACAC---ATGACCAAT 339
DB 276 IleLysIleAlaAspPheGlyValAlaArgIleGluValLysThrGluGlyMetThrPro 295
QY 340 AACAGGGAGTCTGCTGGATGGCAGCTGAGTCTTTTGAAGGTAGTATTACAGTGAA 399
DB 296 GluThrGlyThrTyrArgTyrMetAlaProGluValIleGlnHisArgProTyrAspGln 315
QY 400 AATGTGACCTCTTCAGCTGGGTATTATTCTTTGGGAAGTATAGCGCTCGGAAACCC 459
DB 316 LysValAspValTyrSerPheGlyIleValLeuTyrGluLeuValThrGlyAsnLeuPro 335
QY 460 TTTGATGAGATTGGTGGC-----CCAGCTTTCGAATCATGTGGGCTGTTCAATGGT 513
DB 336 PheAlaAsnMetThrAlaValGlnAlaPheAlaVal-----ValAsnLysGly 352
QY 514 ACTGACACCACTGATAAATAATTTACCTAAGCCCATTTGAGAGCCTGATGACTCTGTGT 573
DB 353 ValArgProAlaIleProHisAspCysLeuProAlaLeuAlaGluIleMetThrArgCys 372
QY 574 TGGTCTAAAGATCCTCCAGCGCCCTTCAATGGAGGAATTTGAAAAAATG 627
DB 373 TrpAspAlaAsnProAspAlaArgProPheThrGluValValArgMetLeu 390

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Search completed: December 4, 2003, 09:07:12
 Job time : 86.7973 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 00:43:57 ; Search time 352.013 Seconds
(without alignments)
5245.298 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 684

Sequence: 1 gtagagcttcggcagttatc.....cattacagatcctgtgtcag 684

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	100.0	1704	20 AAX99698	Human TGF-beta act
2	684	100.0	1788	20 AAX56285	Human TAK1-6xHis e
3	684	100.0	1959	18 AAT85095	Human transforming
4	684	100.0	2656	20 AAX56279	Human TAK1 encoding
5	684	100.0	2856	21 AAX39105	Human TAK-1 nucleo
6	684	100.0	2769	24 ABL88437	Pain regulated cDN
7	684	100.0	2785	20 AAX99696	Human TGF-beta act
8	684	100.0	2866	20 AAX99697	Human TGF-beta act

9	586.4	85.7	2443	18	AAT85094
10	175.6	25.7	3367	23	ABL02489
11	108	15.8	10997	23	ABL02488
12	72.2	10.6	759	23	ABL08337
13	65.4	9.6	1428	24	ABZ13077
14	56.6	8.3	1398	24	ABZ12828
15	56.6	8.3	1401	21	AAC45777
16	56.6	8.3	1809	21	AAC45239
17	56.6	8.3	1820	21	AAC44893
18	56	8.2	1591	21	AAC40839
19	55.2	8.1	2283	21	AAC48526
20	54.6	8.0	426	21	AAC03589
21	54.6	8.0	1063	22	AAC34976
22	54.6	8.0	1365	21	AAC299727
23	54.6	8.0	1706	21	AAZ5674
24	54.6	8.0	2069	21	AAZ99737
25	54.6	8.0	2120	21	AAZ99726
26	54.6	8.0	2191	22	AAH99263
27	54.6	8.0	2194	21	AAZ99734
28	54.6	8.0	2220	21	AAZ93783
29	54.6	8.0	2254	21	AAZ99735
30	54.6	8.0	2272	21	AAZ99736
31	54.6	8.0	2403	22	AAZ44701
32	54.6	8.0	2592	24	AB060980
33	54.6	8.0	2622	22	AAZ75336
34	54.6	8.0	3967	22	AAH73366
35	54.4	8.0	1419	21	AAC44653
36	53.8	7.9	1631	21	AAC39537
37	52.6	7.7	3072	23	ABL04365
38	52	7.6	1251	20	AAH81855
39	52	7.6	1251	21	AAH80002
40	52	7.6	1353	20	AAH81858
41	52	7.6	1353	21	AAA08005
42	52	7.6	1737	22	AAZ29901
43	52	7.6	3020	22	AAK94468
44	52	7.6	3160	25	ACC50232
45	52	7.6	3179	22	AAK94508

ALIGNMENTS

RESULT 1
AAX99698
ID AAX99698 standard; cDNA to mRNA; 1704 BP.
AC AAX99698;
AC

DT 18-OCT-1999 (first entry)

DE Human TGF-beta activated kinase (TAK) 1c encoding nucleotide sequence.

XX Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
KW endotoxin shock; septicemia; human; hTAK1c; ss.

XX Homo sapiens.

OS
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1704
FT /*tag= a
FT /product= "hTAK1c"

XX WO9940202-A1.

XX 12-AUG-1999.

XX 02-FEB-1999; 99WO-JP00422.

XX 30-OCT-1998; 98JP-0309316.

XX 06-FEB-1998; 98JP-0026003.

PA (TANA) TANABE SEIYAKU CO.
 XX Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 XX WPI: 1999-494298/41.
 DR P-PSDB; AAY28998.
 XX
 PT Nuclear factor kappa B activation inhibitors, useful as preventives
 for, e.g. autoimmune diseases
 XX
 PS Examples; Page 43-46; 49pp; Japanese.
 XX
 CC The invention provides a method for identifying or screening a nuclear
 factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 test substance on modulating the functions of TGF-beta activated kinase
 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the nucleotide sequence of human TAK1C
 CC (hTAK1C) protein.
 XX
 SQ Sequence 1704 BP; 511 A; 381 C; 401 G; 411 T; 0 other;
 Query Match 100.0%; Score 684; DB 20; Length 1704;
 Best Local Similarity 100.0%; Pred. No. 2.3e-214; Indels 0; Gaps 0;
 Matches 684; Conservative 0; Mismatches 0;
 QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTTATGAGCC 60
 DB 226 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTTATGAGCC 285
 QY 61 TGCTTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGGCTTTTATATAATGTG 120
 DB 286 TGCTTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGGCTTTTATATAATGTG 345
 QY 121 CTGCATGTGCTGAACATGTCATATTAATCTGCTGCCACGCAATGATGCTGCTTTA 180
 DB 346 CTGCATGTGCTGAACATGTCATATTAATCTGCTGCCACGCAATGATGCTGCTTTA 405
 QY 181 CAGTGTTCACAGAGTGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCACAGG 240
 DB 406 CAGTGTTCACAGAGTGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCACAGG 465
 QY 241 GACCTGAACCCACCAACTTACTGCTGTGTCAGGGGGGACAGTCTTAAATAATGTGAT 300
 DB 466 GACCTGAACCCACCAACTTACTGCTGTGTCAGGGGGGACAGTCTTAAATAATGTGAT 525
 QY 301 TTTGGTACAGCTGTGACATTCACACATGACCAATACCAAGGGAGTGTGCTTGG 360
 DB 526 TTTGGTACAGCTGTGACATTCACACATGACCAATACCAAGGGAGTGTGCTTGG 585
 QY 361 ATGGCCACTGAAGTTTTTGAAGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 420
 DB 586 ATGGCCACTGAAGTTTTTGAAGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 645
 QY 421 GGTATATTTCTTGGGAAGTGAATACCGCTGCGAACCCTTGTATGATGATGTTGGCCCA 480
 DB 646 GGTATATTTCTTGGGAAGTGAATACCGCTGCGAACCCTTGTATGATGATGTTGGCCCA 705
 QY 481 GCTTTCGGAATCATGTGGCTGTTCAATATGTTACTCGACACCACTGATAAAAAATTTA 540
 DB 706 GCTTTCGGAATCATGTGGCTGTTCAATATGTTACTCGACACCACTGATAAAAAATTTA 765
 QY 541 CCTAAGCCCATTTGAGAGCTTGATGACCTGTTGTTGGTCTAAAGATCCTTCCAGCGCCCT 600
 DB 766 CCTAAGCCCATTTGAGAGCTTGATGACCTGTTGTTGGTCTAAAGATCCTTCCAGCGCCCT 825
 QY 601 TCAATGAGGAATTTGTAATAATGATCCTGATGATGATGATGATGATGATGATGATGAT 660
 DB 826 TCAATGAGGAATTTGTAATAATGATCCTGATGATGATGATGATGATGATGATGATGAT 885
 QY 561 GAGCCATTACAGTATCTTGTGCAG 684

DB 886 GAGCCATTACAGTATCTTGTGCAG 909
 RESULT 2
 AAX56285
 ID AAX56285 standard, DNA; 1788 BP.
 XX AAX56285;
 AC AAX56285;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TAK1-6xHis encoding DNA.
 XX
 KW Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 CDS 7..1779
 /*tag= a
 FT
 FT
 XX WO9921010-A1.
 EN
 XX 29-APR-1999.
 PD
 XX 22-OCT-1998; 98WO-JP04796.
 PF
 XX 22-OCT-1997; 97JP-0290188.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Ohtomo T, Ono K, Tsuchiya M;
 PI
 XX WPI: 1999-312645/26.
 DR
 DR P-PSDB; AAY09547.
 XX
 PT Screening for TGF- beta inhibitory substances, which are useful as
 drugs for treatment of diseases relating to its disorder
 XX
 XX Example 1; Page 167-171; 195pp; Japanese.
 XX
 CC A method has been developed for screening for substances which inhibit
 the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence encodes TAK1-6xHis from an example of
 CC the present invention.
 XX
 SQ Sequence 1788 BP; 551 A; 394 C; 413 G; 430 T; 0 other;
 Query Match 100.0%; Score 684; DB 20; Length 1788;
 Best Local Similarity 100.0%; Pred. No. 2.3e-214; Indels 0; Gaps 0;
 Matches 684; Conservative 0; Mismatches 0;
 QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTTATGAGCC 60
 DB 232 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTTATGAGCC 291
 QY 61 TGCTTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGGCTTTTATATAATGTG 120

Db 292 TGCTTGAATCCAGTGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 351
Qy 121 CTGATGTGTGTGAACCAATTCGCATATTATATCTGCGCCACGCAATGAGTTGGTGTTA 180
Db 352 CTGATGTGTGTGAACCAATTCGCATATTATATCTGCGCCACGCAATGAGTTGGTGTTA 411
Qy 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 240
Db 412 CAGTGTTCCTCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 471
Qy 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGAAGTCTTAAATAATTTGTAT 300
Db 472 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGAAGTCTTAAATAATTTGTAT 531
Qy 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATACAGGGGAGTGTCTTGG 360
Db 532 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATACAGGGGAGTGTCTTGG 591
Qy 361 ATGCACCTGAAGTTTGTGAAGGTAGTAATACAGTGAATAATGTGACGTCTTCAGCTGG 420
Db 592 ATGCACCTGAAGTTTGTGAAGGTAGTAATACAGTGAATAATGTGACGTCTTCAGCTGG 651
Qy 421 GGTATTATCTTTGGAGTGAATACCGTGTGCGAAACCTTTGATGAGATTGGTGGCCCA 480
Db 652 GGTATTATCTTTGGAGTGAATACCGTGTGCGAAACCTTTGATGAGATTGGTGGCCCA 711
Qy 481 GCTTTCCGAATCATGTGGCTGTTCATAATGTGATCTGACACACACATGATAAAAAATTA 540
Db 712 GCTTTCCGAATCATGTGGCTGTTCATAATGTGATCTGACACACACATGATAAAAAATTA 771
Qy 541 CCTAAGCCCATTTGAGCCCTGATGACTCGTTTGTGGTCTAAAGATCCTTCCAGCGCCT 600
Db 772 CCTAAGCCCATTTGAGCCCTGATGACTCGTTTGTGGTCTAAAGATCCTTCCAGCGCCT 831
Qy 601 TCAATGAGAAATTTGAAATAATGACTCATCTGTATGCGGTACTTCCAGGAGCAGAT 660
Db 832 TCAATGAGAAATTTGAAATAATGACTCATCTGTATGCGGTACTTCCAGGAGCAGAT 891
Qy 661 GAGCCATTACAGTATCCTTGTTCAG 684
Db 892 GAGCCATTACAGTATCCTTGTTCAG 915

RESULT 3

AA8785095

ID AA8785095 standard; cDNA; 1959 BP.

XX AC AA8785095;

XX DT 19-NOV-1997 (first entry)

XX DE Human transforming growth factor-beta activated kinase TAK-1 cDNA.

XX DX TGF-beta; signal transduction; TGF-beta activated kinase;

XX KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;

XX KW protein kinase; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 183..1922

XX FT /*tag= a

XX FT /product= TAK-1

XX PN JP09163990-A.

XX PD 24-JUN-1997.

XX PF 27-SEP-1996; 96JP-0256747.

XX PR 24-JUL-1996; 96US-0685625.

XX PR 29-SEP-1995; 95JP-0253549.

XX XX

(CHUS.) CHUGAI PHARM CO LTD.

(UENO/) UENO N.

WPI; 1997-380171/35.

P-PSDB; AAW27093.

DNA encoding transforming growth factor-beta-activated kinase, TAK-1

- useful for studying the TGF-beta signal transduction system

Claim 9; Page 13-15; 20pp; Japanese.

The present sequence encodes human transforming growth factor-beta

TAK-1 protein which is involved in the TGF-beta family signal

transduction system. TAK-1, also known as activator of MAPK Kinase

(AMK-1), is an enzyme which is activated by TGF-beta and bone

morphogenetic protein (BMP) and activates MAPK kinase by

phosphorylation.

Sequence 1959 BP; 571 A; 447 C; 481 G; 460 T; 0 other;

Query Match 100.0%; Score 684; DB 18; Length 1959;

Best Local Similarity 100.0%; Pred. No. 2.4e-214;

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCACTTAATTTGTAAGCTTTATGAGGCC 60

Db 408 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCACTTAATTTGTAAGCTTTATGAGGCC 467

Qy 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120

Db 468 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527

Qy 121 CTGATGTGTCTGAACCAATTCGCATATTATCTGCTCCACGCAATGAGTTGGTGTTA 180

Db 528 CTGATGTGTCTGAACCAATTCGCATATTATCTGCTCCACGCAATGAGTTGGTGTTA 587

Qy 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGCTTAATTCACAGG 240

Db 588 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGCTTAATTCACAGG 647

Qy 241 GACCTGAACCAACCAACTTACTGCTGTGAGGGGGGACAGTTCTTAAAAATTTGTGAT 300

Db 648 GACCTGAACCAACCAACTTACTGCTGTGAGGGGGGACAGTTCTTAAAAATTTGTGAT 707

Qy 301 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAGGGAGTGTCTTGG 360

Db 708 TTTGGTACAGCTGTGACATTCAGACACACATGACCAATAACAGGGAGTGTCTTGG 767

Qy 361 ATGGCACCTGAAGTTTGAAGGTAGTAATTCAGTCAAAAAATGTGACGTCTTCAGCTGG 420

Db 768 ATGGCACCTGAAGTTTGAAGGTAGTAATTCAGTCAAAAAATGTGACGTCTTCAGCTGG 827

Qy 421 GGTATTATCTTTGGAGAGTGAACCGTGTGAAACCCCTTTCATGATGAGTTGGTGGCCCA 480

Db 828 GGTATTATCTTTGGAGAGTGAACCGTGTGAAACCCCTTTCATGATGAGTTGGTGGCCCA 887

Qy 481 GCTTTCCGAATCATGTGGCTGTTCATAATGTGATCTGACACACACATGATAAAAAATTA 540

Db 888 GCTTTCCGAATCATGTGGCTGTTCATAATGTGATCTGACACACACATGATAAAAAATTA 947

Qy 541 CCTAAGCCCATTTGAGCCCTGATGACTCGTTTGTGGTCTTAAAGATCCTTCCAGCGCCT 600

Db 948 CCTAAGCCCATTTGAGCCCTGATGACTCGTTTGTGGTCTTAAAGATCCTTCCAGCGCCT 1007

Qy 601 TCAATGAGAAATTTGTAATAATGACTCATCTGATGCGGTACTTCCAGGAGCAGAT 660

Db 1008 TCAATGAGAAATTTGTAATAATGACTCATCTGATGCGGTACTTCCAGGAGCAGAT 1067

Qy 661 GAGCCATTACAGTATCCTTGTTCAG 684

Db 1068 GAGCCATTACAGTATCCTTGTTCAG 1091

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RESULT 4
AAX56279
ID AAX56279 standard; DNA; 2656 BP.
XX
AC AAX56279;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human TAK1 encoding DNA.
XX
KW Human; TAK1; screening; inhibition; TGF-beta;
transforming growth factor beta; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 183..1922
FT CDS /tag= a
XX
PN WO9921010-A1.
XX
PD 29-APR-1999.
XX
PF 22-OCT-1998; 98WO-JP04796.
XX
PR 22-OCT-1997; 97JP-0290188.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Ono K, Tsuchiya M;
XX
DR WPI; 1999-312645/26.
XX
DR P-PSDB; AAY09542.
XX
PT Screening for TGF- beta inhibitory substances, which are useful as
drugs for treatment of diseases relating to its disorder
XX
PS Example 1; Page 150-154; 195pp; Japanese.
XX
CC A method has been developed for screening for substances which inhibit
CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
CC comprises: (a) contacting the polypeptide in the presence of a sample;
CC and (b) detecting the amount of bound polypeptide, in which the sample
CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
CC indications e.g. as TGF-beta signal transduction inhibitors or
CC activators, or extracellular matrix protein production enhancement
CC inhibitors or activators, or cell proliferation prevention inhibitors or
CC activators, or monocyte migration inhibitors or activators, or
CC physiological activity induction inhibitors or activators, or
CC immunosuppression inhibitors or activators, or amyloid beta protein
CC precipitation inhibitors or activators, and such substances can also be
CC inhibitors of the TAK1 polypeptide function, particularly kinase
CC activity. The present sequence encodes human TAK1.
XX
SQ Sequence 2656 BP; 778 A; 557 C; 620 G; 701 T; 0 other;

Query Match 100.0%; Score 684; DB 20; Length 2656;
Best Local Similarity 100.0%; Pred. No. 2.8e-214;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCACTTAATATGTAAAGCTTTATGGAGCC 60
Db 408 GTAGAGCTTCGGCAGTATCCCGTGTGAACCACTTAATATGTAAAGCTTTATGGAGCC 467
QY 61 TCGTTGAATCCAGTGTCTTGTGTGAATATCTCAAGGGGCTCTTTATATAATGTG 120
Db 468 TCGTTGAATCCAGTGTCTTGTGTGAATATCTCAAGGGGCTCTTTATATAATGTG 527
QY 121 CTGCATGCTGTGAACCACTTGCCTATATATCTCTGCCACGCAATGAGTGTGTTTA 180
Db 528 CTGCATGCTGTGAACCACTTGCCTATATATCTCTGCCACGCAATGAGTGTGTTTA 587

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RESULT 5

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AAX39105
ID AAA39105 standard; DNA; 2656 BP.
XX
AC AAA39105;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human TAK-1 nucleotide sequence SEQ ID NO:1.
XX
KW Human; TAK-1; TAB-1; mitogen activated protein kinase; MAPK;
KW screening; signal transduction; inhibition; inflammatory cytokine;
KW IL-1; interleukin 1; TNF; tumour necrosis factor; inflammation;
KW antiinflammatory; suppression; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 183..1922
FT CDS /tag= a
FT /product= "TAK-1"
XX
PN WO200023610-A1.
XX
PD 27-APR-2000.
XX
PF 21-OCT-1999; 99WO-JP05817.
XX
PR 21-OCT-1998; 98JP-0299962.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Ohtomo T, Sugamata Y, Matsumoto K;
XX
DR WPI; 2000-339707/29.

```

DR P-PSDB; AAY91000.
 XX Method for screening inhibitors of TAK1 signal transduction for
 PT suppression of inflammatory cytokine production and use as
 PT antiinflammatory agents -
 XX
 PS Example 1; Page 73-80; 100pp; Japanese.
 XX
 CC The present invention describes a method for screening compounds for
 CC inhibition of inflammatory cytokine signal transduction by contacting
 CC the sample with TAK1 and its receptor TAB1 and selecting for inhibition
 CC of TAK1/TAB1 binding. Also described is a method for screening compounds
 CC for inhibition of inflammatory cytokine signal transduction in which the
 CC inhibition of TAK1 phosphorylation is selected for; and drug
 CC compositions for the treatment of inflammatory disorders containing as
 CC active component an inflammatory cytokine signal transduction inhibitor.
 CC TAK1 is an essential component of the signalling process which results
 CC in release of inflammatory cytokines such as interleukin-1 (IL-1),
 CC IL-10, tumour necrosis factor (TNF) and IL-6. The methods can be used
 CC for the selection of effective antiinflammatory agents. The present
 CC sequence encodes human TAK-1, which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 2656 BP; 778 A; 557 C; 620 G; 701 T; 0 other;
 Query Match 100.0%; Score 684; DB 21; Length 2656;
 Best Local Similarity 100.0%; Pred. No. 2.8e-214;
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GTAGAGCTTCGGCAGTGTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60
 408 GTAGAGCTTCGGCAGTGTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 467
 61 TCGTTGAATCCAGGTGCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 468 TCGTTGAATCCAGGTGCTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527
 121 CTGCATGGTGTGAACCATTCGCCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA 180
 528 CTGCATGGTGTGAACCATTCGCCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA 587
 181 CAGTGTTCGAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTTAATTCACAGG 240
 588 CAGTGTTCGAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTTAATTCACAGG 647
 241 GACCTGAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCGAAAATTTGTGAT 300
 648 GACCTGAACCCACCAACTTACTGCTGGTTCAGGGGGGACAGTTCGAAAATTTGTGAT 707
 301 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATACCAAGGGGAGTGGCTTGG 360
 708 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATACCAAGGGGAGTGGCTTGG 767
 361 ATGGCAGCTGAAGTTTGTGAAGTAGTAAATTCAGATGAAAAATGTGACGCTTTCAGCTGG 420
 768 ATGGCAGCTGAAGTTTGTGAAGTAGTAAATTCAGATGAAAAATGTGACGCTTTCAGCTGG 827
 421 GGTATTATCTTTGGGAGTAAACCGCTGCGAAACCTTTGATGAGATTGGTGGCCCA 480
 828 GGTATTATCTTTGGGAGTAAACCGCTGCGAAACCTTTGATGAGATTGGTGGCCCA 887
 481 GCTTTCGGAATCATGTGGGCTGTTTCAATATGTTGCTGACACACCTGATAAAAAATTTA 540
 888 GCTTTCGGAATCATGTGGGCTGTTTCAATATGTTGCTGACACACCTGATAAAAAATTTA 947
 541 CCTAAGCCCATTTGAGAGCCTGATGACTCGTGTGTGTTCTAAAGATCCTTCCAGCGCCCT 600
 948 CCTAAGCCCATTTGAGAGCCTGATGACTCGTGTGTGTTCTAAAGATCCTTCCAGCGCCCT 1007
 601 TCAATGAGGAATCTGGAATTAATGACTCACTTGTATGCGGTAATTTCCAGAGCAGAT 660
 1008 TCAATGAGGAATCTGGAATTAATGACTCACTTGTATGCGGTAATTTCCAGAGCAGAT 1067

QY 661 GAGCCATTACAGTATCCTTGTGTCAG 684
 Db 1068 GAGCCATTACAGTATCCTTGTGTCAG 1091
 RESULT 6
 ABL88437
 ID ABL88437 standard; cDNA; 2769 BP.
 AC ABL88437;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Pain regulated cDNA sequence 80.
 XX
 KW Pain; analgesic; gene therapy; neurological disorder;
 KW neurodegenerative disease; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200212338-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 03-AUG-2001; 2001WO-EP09011.
 XX
 PR 03-AUG-2000; 2000DE-1037759.
 XX
 PA (CHEF) GRUENENTHAL GMBH.
 XX
 PI Gillen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;
 XX
 DR WPI; 2002-257469/30.
 DR P-PSDB; ABB85033.
 XX
 PT Identifying pain-regulating compounds, useful for treating chronic pain
 PT and for diagnosis, by measuring binding of compounds to specific
 PT peptides and proteins -
 PS Claim 1; Fig 44; 213pp; German.
 XX
 CC The invention relates to identifying pain-regulating substances (A)
 CC comprises (i) incubating a test substance with a cell (or preparation
 CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
 CC either binding of the test substance to (B) or some functional parameter
 CC that is altered by this binding. The method is useful for identifying
 CC pain-regulating substances (A) with analgesic activity. (A) along with
 CC nucleic acid (ABL88411-ABL88441) that encode proteins (B,
 CC ABB85006-ABB85037) that interact with (A); (B); vectors containing the
 CC nucleic acid; antibodies against (B); cells that express (B) and agents
 CC that bind to (B), are all useful for treating pain, particularly chronic
 CC pain, including use in gene therapy. The same materials can also be used
 CC for diagnosis, e.g. of neurological and neurodegenerative diseases. The
 CC present sequence is that of a polynucleotide of the invention.
 XX
 SQ Sequence 2769 BP; 811 A; 565 C; 640 G; 753 T; 0 other;
 Query Match 100.0%; Score 684; DB 24; Length 2769;
 Best Local Similarity 100.0%; Pred. No. 2.9e-214;
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GTAGAGCTTCGGCAGTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 60
 388 GTAGAGCTTCGGCAGTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGGAGCC 447
 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
 448 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 507
 121 CTGCATGGTGTGAACCATTCGCCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA 180
 508 CTGCATGGTGTGAACCATTCGCCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA 567

QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 240
 PT |||||
 Db 568 CAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 627
 QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTGAGGGGGGACAGTCTTAAAAATTTGTGAT 300
 Db 628 GACCTGAAACCAACCAACTTACTGCTGTGTGAGGGGGGACAGTCTTAAAAATTTGTGAT 687
 QY 301 TTGTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTCTGCTGG 360
 Db 688 TTGTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTCTGCTGG 747
 QY 361 ATGCGACCTGAAGTTTTCGAAGTACTAATTCAGTGAATAATGACGCTCTTCAGCTGG 420
 Db 748 ATGCGACCTGAAGTTTTCGAAGTACTAATTCAGTGAATAATGACGCTCTTCAGCTGG 807
 QY 421 GGTATTATCTTTGGGAAGTGATAACGCGTFCGGAACCCCTTGAATGAGATTGGTGGCCCA 480
 Db 808 GGTATTATCTTTGGGAAGTGATAACGCGTFCGGAACCCCTTGAATGAGATTGGTGGCCCA 867
 QY 481 GCTTTCGGAATCATGTGGCTGTTCATATGTTACTCGACCCACTGATAAAAAATTAA 540
 Db 868 GCTTTCGGAATCATGTGGCTGTTCATATGTTACTCGACCCACTGATAAAAAATTAA 927
 QY 541 CCTAAGCCCATTCGAGAGCCTGATGACTCGTGTGTGTGCTAAGATCCTTCCAGCGCCCT 600
 Db 928 CCTAAGCCCATTCGAGAGCCTGATGACTCGTGTGTGTGCTAAGATCCTTCCAGCGCCCT 987
 QY 601 TCAATGAGGAAATTTGTAATAATGACTCACTGATGCGGTAATTCAGAGGAGAT 660
 Db 988 TCAATGAGGAAATTTGTAATAATGACTCACTGATGCGGTAATTCAGAGGAGAT 1047
 QY 661 GAGCCATTACAGTATCCTTGTGAG 684
 Db 1048 GAGCCATTACAGTATCCTTGTGAG 1071

RESULT 7

AAX99696
 ID AAX99696 standard; cDNA to mRNA; 2785 BP.

AC AAX99696;

XX 18-OCT-1999 (first entry)

DT Human TGF-beta activated kinase (TAK) 1a encoding nucleotide sequence.

XX Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
 KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
 KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
 KW endotoxin shock; septicemia; human; hTAK1a; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 163..1902

FT /*tag= a

FT /product= "hTAK1a"

XX WO9940202-A1.

PD 12-AUG-1999.

XX 02-FEB-1999; 99WO-JP00422.

XX 30-OCT-1998; 98JP-0309316.

PR 06-FEB-1998; 98JP-0026003.

XX (TANA) TANABE SEIYAKU CO.

XX Hasegawa K, Kageyama N, Sakurai H, Sugita T;

XX WPI; 1999-494298/41.

RESULT 8

DR P-PSDB; AAY28996.

XX Nuclear factor kappa B activation inhibitors, useful as preventives
 PT for, e.g. autoimmune diseases

XX Examples; Page 35-39; 49pp; Japanese.

CC The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the nucleotide sequence of human TAK1a
 CC (hTAK1a) protein.

XX Sequence 2785 BP; 827 A; 565 C; 640 G; 753 T; 0 other;

SQ Query Match 100.0%; Score 694; DB 20; Length 2785;

Best Local Similarity 100.0%; Pred. No. 2.9e-214;

Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCCTAATATTGTAAGCTTTATGAGCC 60
 Db 388 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCCTAATATTGTAAGCTTTATGAGCC 447
 QY 61 TGCTTGAATCCAGTGTCTGTGTGATGGAATATGCTGAAGGGGGCTCTTATATAATGTG 120
 Db 448 TGCTTGAATCCAGTGTCTGTGTGATGGAATATGCTGAAGGGGGCTCTTATATAATGTG 507
 QY 121 CTGCATGGTGTGAACCATTCGATATTAATCTGTGCGCCACGCAATGAGTGTGTTA 180
 Db 508 CTGCATGGTGTGAACCATTCGATATTAATCTGTGCGCCACGCAATGAGTGTGTTA 567
 QY 181 CAGTGTTCGACAGGAGTGTCTTCTCAGCATGCAACCCAAAGCGCTTAATTCACAGG 240
 Db 568 CAGTGTTCGACAGGAGTGTCTTCTCAGCATGCAACCCAAAGCGCTTAATTCACAGG 627
 QY 241 GACCTGAACCCACCAACTTACTGTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGAT 300
 Db 628 GACCTGAACCCACCAACTTACTGTGTTGTCAGGGGGGACAGTCTTAAAAATTTGTGAT 687
 QY 301 TTGTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTGCTGG 360
 Db 688 TTGTGTACAGCTGTGACATTCAGACACACATGACCAATAACAAGGGGAGTGTGCTGG 747
 QY 361 ATGCGACCTGAAGTTTTCGAAGTACTAATTCAGTGAATAATGTCAGCTCTTCAGCTGG 420
 Db 748 ATGCGACCTGAAGTTTTCGAAGTACTAATTCAGTGAATAATGTCAGCTCTTCAGCTGG 807
 QY 421 GGTATTATCTTTGGGAAGTGATAACGCGTFCGGAACCCCTTGAATGAGATTGGTGGCCCA 480
 Db 808 GGTATTATCTTTGGGAAGTGATAACGCGTFCGGAACCCCTTGAATGAGATTGGTGGCCCA 867
 QY 481 GCTTTCGGAATCATGTGGCTGTTCATPAATGTTACTCGACCAACCATGATAAAAAATTAA 540
 Db 868 GCTTTCGGAATCATGTGGCTGTTCATPAATGTTACTCGACCAACCATGATAAAAAATTAA 927
 QY 541 CCTAAGCCCATTCGAGAGCCTGATGACTCGTGTGTGCTAAGATCCTTCCAGCGCCCT 600
 Db 928 CCTAAGCCCATTCGAGAGCCTGATGACTCGTGTGTGCTAAGATCCTTCCAGCGCCCT 987
 QY 601 TCAATGAGGAAATTTGTAATAATGACTCACTTGAATGCGGTAATTCAGAGGAGCAGAT 660
 Db 988 TCAATGAGGAAATTTGTAATAATGACTCACTTGAATGCGGTAATTCAGAGGAGCAGAT 1047
 QY 661 GAGCCATTACAGTATCCTTGTGAG 684
 Db 1048 GAGCCATTACAGTATCCTTGTGAG 1071

AAX99697
 ID AAX99697 standard; cDNA to mRNA; 2866 BP.
 AC AAX99697;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Human TGF-beta activated kinase (TAK) 1b encoding nucleotide sequence.
 XX
 KW Nuclear factor kappa B; NF-kB; inhibitor; TGF-beta activated kinase 1;
 KW TAK1; autoimmune disease; chronic rheumatoid arthritis; inflammation;
 KW intractable disease; atrophic dermatitis; psoriasis; viral infection;
 KW endotoxin shock; septicemia; human; hTAK1b; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 163..11983
 FT /*tag= a
 FT /product= "hTAK1b"
 XX
 XX WO9940202-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 02-FEB-1999; 99WO-JP00422.
 XX
 PR 30-OCT-1998; 98JP-0309316.
 PR 06-FEB-1998; 98JP-0026003.
 XX
 XX (TANA) TANABE SEIYAKU CO.
 PA
 XX
 PI Hasegawa K, Kageyama N, Sakurai H, Sugita T;
 XX
 DR WPI; 1999-494298/41.
 DR P-PSDB; AAY28997.
 XX
 XX Nuclear factor kappa B activation inhibitors, useful as preventives
 PT for, e.g. autoimmune diseases
 XX
 PS Examples; Page 39-43; 49pp; Japanese.
 CC
 CC The invention provides a method for identifying or screening a nuclear
 CC factor kappa B (NF-kB) activation inhibitor by examining the effect of a
 CC test substance on modulating the function(s) of TGF-beta activated kinase
 CC 1 (TAK1). The NFkB activation inhibitors targeting on TAK1 can be used to
 CC treat or prevent autoimmune diseases (e.g. chronic rheumatoid arthritis),
 CC intractable diseases with inflammation (such as atrophic dermatitis and
 CC psoriasis), viral infection, endotoxin shock, septicemia and others. The
 CC present sequence represents the nucleotide sequence of human TAK1b
 CC (hTAK1b) protein.
 CC
 XX
 SQ Sequence 2866 BP; 848 A; 588 C; 656 G; 774 T; 0 other;
 XX
 Query Match 100.0%; Score 684; DB 20; Length 2866;
 Best Local Similarity 100.0%; Pred. No. 2.9e-214;
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 GTAGAGCTTCGGCAGTATCCCGTGTGACCACTCTTAATTTCTAAAGCTTTATGAGCC 60
 DB 388 GTAGAGCTTCGGCAGTATCCCGTGTGACCACTCTTAATTTCTAAAGCTTTATGAGCC 447
 QY 61 TGTCTGAATCCAGTGTCTTTGTGAGGAATATCTGCTGCCCGCCCAATGAGTGGTCTTTA 180
 DB 448 TGTCTGAATCCAGTGTCTTTGTGAGGAATATCTGCTGCCCGCCCAATGAGTGGTCTTTA 567
 QY 121 CTGCATGGTCTGAACCAATTCGCAATATTAATCTGCTGCCCGCCCAATGAGTGGTCTTTA 180
 DB 508 CTGCATGGTCTGAACCAATTCGCAATATTAATCTGCTGCCCGCCCAATGAGTGGTCTTTA 567
 QY 181 CAGTGTTCACAGGAGTGGCTTATCTTCACAGCAATGCCAATGCCAATGCCAATGCCAATGCCA 240
 DB 568 CAGTGTTCACAGGAGTGGCTTATCTTCACAGCAATGCCAATGCCAATGCCAATGCCAATGCCA 240

QY 241 GACCTGAACACCAAACTTACTGCTGTGTCAGGGGGACAGTTCCTAAAAATTTTGAT 300
 DB 628 GACCTGAACACCAAACTTACTGCTGTGTCAGGGGGACAGTTCCTAAAAATTTTGAT 587
 QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAGGGGAGTCTGCTTGG 360
 DB 688 TTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAGGGGAGTCTGCTTGG 747
 QY 361 ATGGCACCTGAAGTTTTTGAAGGTAGTAATTACAGTGAATAATGTGACGTCTTCAGCTGG 420
 DB 748 ATGGCACCTGAAGTTTTTGAAGGTAGTAATTACAGTGAATAATGTGACGTCTTCAGCTGG 807
 QY 421 GGTATTATCTTTGGGAAGTGATAACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 480
 DB 808 GGTATTATCTTTGGGAAGTGATAACCGCTCGGAACCCCTTTGATGAGATTGGTGGCCCA 867
 QY 481 GCTTTCGAATCATGTGGGCTGTTCAATAATGTTACTGACCACTGATAAAAATTTTA 540
 DB 868 GCTTTCGAATCATGTGGGCTGTTCAATAATGTTACTGACCACTGATAAAAATTTTA 927
 QY 541 CCTAAGCCCATTTGAGAGCTGATGACTCGTGTGTTGTTCTTAAGATCCCTCCAGGCGCCT 600
 DB 928 CCTAAGCCCATTTGAGAGCTGATGACTCGTGTGTTGTTCTTAAGATCCCTCCAGGCGCCT 987
 QY 601 TCAATGGAGGAATTTGAAATAATGACTCACTGATGCGGTACTTTCCAGGAGCAGAT 660
 DB 988 TCAATGGAGGAATTTGAAATAATGACTCACTGATGCGGTACTTTCCAGGAGCAGAT 1047
 QY 661 GAGCCATTACAGTATCCTTGTCTCAG 684
 DB 1048 GAGCCATTACAGTATCCTTGTCTCAG 1071

RESULT 9
 AAT85094
 ID AAT85094 standard; cDNA; 2443 BP.
 XX
 AC AAT85094;
 XX
 DT 19-NOV-1997 (first entry)
 XX
 DE Mouse transforming growth factor-beta activated kinase TAK-1 cDNA.
 XX
 KW TGF-beta; signal transduction; TGF-beta activated kinase;
 KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;
 KW protein kinase; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 CDS 157..1896
 FT /*tag= a
 FT /product= TAK-1
 XX
 XX JP09163990-A.
 XX
 PD 24-JUN-1997.
 XX
 PF 27-SEP-1996; 96JP-0256747.
 XX
 PR 24-JUL-1996; 96US-0685625.
 PR 29-SEP-1995; 95JP-0253549.
 XX
 XX (CHUS) CHUGAI PHARM CO LTD.
 PA (UENO/) UENO N.
 XX
 DR WPI; 1997-380171/35.
 DR P-PSDB; AAW27092.
 XX
 XX DNA encoding transforming growth factor-beta-activated kinase, TAK-1
 PT - useful for studying the TGF-beta signal transduction system
 XX

PS Claim 2; Page 10-12; 20pp; Japanese.

XX The present sequence encodes mouse transforming growth factor-beta (TGF-beta) activated kinase, TAK-1. The DNA is used to produce the TAK-1 protein which is involved in the TGF-beta family signal transduction system. TAK-1, also known as activator of MAPK Kinase (AMK-1), is an enzyme which is activated by TGF-beta and bone morphogenetic protein (BMP) and activates MAPK kinase by phosphorylation.

XX Sequence 2443 BP; 669 A; 567 C; 647 G; 559 T; 1 other;

Query Match 85.7%; Score 586.4; DB 18; Length 2443;
Best Local Similarity 91.1%; Pred. No. 3.7e-182;
Matches 623; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GTAGAGCTCGGACGTTATCCGCTGGAACCATCTTAATTTGTAAGCTTTATGAGCC 60
Db |||||
QY 61 TCGTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTTTTATATATGTG 120
Db |||||
QY 442 TGCCTGAATCCAGTATGCTTGTGATGGAATATGCAAGGGGGCTCAATGTATATGTG 501
Db |||||
QY 121 CTGCAATGCTGAACCATGTCATATTAATCTGCTGCCACGCAATGATGTTGTTTA 180
Db |||||
QY 502 CTGCATGCTGTAACCATTTGCCCTTACTACTGCTGCTCATGCCATGAGCTGTTTA 561
Db |||||
QY 181 CAGTGTTCACAGGAGTGTCTTCTTACAGCATGCAACCCAAAGCGCTTAATTCACAG 240
Db |||||
QY 562 CAGTGTTCACAGGAGTGTCTTCTTACAGCATGCAACCCAAAGCGCTTAATTCACAG 621
Db |||||
QY 241 GACCTGAACACCAAACTTACTGCTGTTGCAAGGGGACAGTCTTAAATTTGTGAT 300
Db |||||
QY 622 GACCTGAACCTTCAAACTTGTCTGTTGTCAGGAGGACAGTCTTAAATTTGTGAT 691
Db |||||
QY 301 TTTGGTACAGCTGTGACATTCAGACATGACCAATTAACAGGGAGTGTCTTGG 360
Db |||||
QY 682 TTTGGTACAGCTGTGACATTCACCAACACATGACCAATTAACAGGGAGTGTCTTGG 741
Db |||||
QY 361 ATGCACTGCAAGTCTTTTGAAGTAGTAAATACAGTGAATAATGTGACGCTTTCAGCTG 420
Db |||||
QY 742 ATGCGGCTGAAGTCTTTGAAGTAGTAAATACAGTGAATAATGTGACGCTTTCAGCTG 801
Db |||||
QY 421 GGTATTAATCTTTGGGAAGTGATAACCGCTCGAAACCTTTGATGAGATTTGTGGCCCA 480
Db |||||
QY 802 GGTATTAATCTTTGGGAAGTGATAACACGCGGGAACCTTTGATGAGATCGGTGGCCCA 861
Db |||||
QY 481 GCTTTCCGAATCATGTTGGCTGTTCATTAATGTTACTGACACACATGATAAAATTTA 540
Db |||||
QY 862 GCTTTCCGAATCATGTTGGCTGTTCATTAATGTTACTGACACACATGATAAAATTTA 921
Db |||||
QY 541 CCTAAGCCCATGAGACCTGATGACATCGTTGTTGGTCTAAAGATCTTCCAGCGCCCT 600
Db |||||
QY 922 CCTAAGCCCATGAGACCTGATGACACGCTGTTGGTCTAAGACCCATCTCAGCGCCCT 981
Db |||||
QY 601 TCAATGAGGAAATTTGAAATTAATGACTCATCTTGTATGCGGTACTTTTCAGAGGAGAT 660
Db |||||
QY 982 TCAATGAGGAAATTTGAAATTAATGACTCATCTTGTATGCGGTACTTTCCAGAGGAGAT 1041
Db |||||
QY 661 GAGCCATTACAGTATCTTTGTCAG 684
Db |||||
QY 1042 GAGCCATTACAGTATCTTTGTCAG 1065
Db |||||

RESULT 10
ABLO2489 standard; cDNA; 3367 BP.
XX ABLO2489;
AC ABLO2489;
XX 26-MAR-2002 (first entry)
DT
XX

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1949.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS WO200171042-A2.
PN 27-SEP-2001.
PD 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI: 2001-656860/75.
XX P-PSDB; ABB58386.
DR New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 1949; 21pp + Sequence Listing; English.
PS The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 3367 BP; 938 A; 898 C; 856 G; 675 T; 0 other;
QY Query Match 25.7%; Score 175.6; DB 23; Length 3367;
Db Best Local Similarity 56.7%; Pred. No. 8.2e-47;
Matches 388; Conservative 0; Mismatches 284; Indels 12; Gaps 3;
QY 4 GAGCTTCGGCAGTTATCCCGTGTGAACCATCTCTTAATATTGTAAGCTTTATGAGCCTGC 63
Db |||||
QY 64 TTGAATC-----CAGTGTGCTTGTGATGAAATATCTGAAGGGGCTCTTTATATAAT 117
Db |||||
QY 1172 TCGTACAGCAGGCGCCCTACCTGATATGAGATTCGCCGAGGTGATCGCTGCACAC 1231
Db |||||
QY 118 GTGCTCATGCTGTGTAACCATTTGCCATATTATCTGCTGCCACGCAATGAGTGTGT 177
Db |||||
QY 1232 TTCTTTCACGCAAGGTGAAGCGGCATATT---CTCTGCCACCGCATGAGCTGGCG 1288
Db |||||
QY 178 TTACAGTGTTCAGAGGAGTGGCTTATCTTCAAGCATGCAACCAAGCGCTAATTCAC 237
Db |||||
QY 1289 CGCCATATGTGCAGAGGCTTGGCATATTTCATGCCATGACGCCAAACCACTAATCAT 1348
Db |||||
QY 238 AGGACCTGAAACCAACCACTTACTGCTGTGTTGAGGGGGGACAGTTCTTAAATTTGT 297
Db |||||
QY 1349 GCGACGTTGAAGCGCTGAACTCTCTTGTGACCAACAGGACCGCATCTGAAGATATGC 1408
Db |||||
QY 298 GATTTTGTGTACAGCTGTGACATTTACAGACACATGACCAATACAGGGAGTGTCTCT 357
Db |||||
QY 1409 GACTTCGGCACGGTGGCGGACAGTGCACCATGATGACCAACAATCGCGGAGTCCGCT 1468
Db |||||
QY 358 TGGATGCCACCTGAGTTTTTGAAGGTAGTAAATACAGTGAATAATGTGACGCTCTTCAGC 417
Db |||||

PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.

PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
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 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
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 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 8.3%; Score 56.6; DB 21; Length 1401;
 Best Local Similarity 52.3%; Pred. No. 8.3e-08;
 Matches 150; Conservative 0; Mismatches 134; Indels 3; Gaps 1;
 Qy 186 TTCCCAAGAGTGGCTTATCTTCACAGCATGGAACCCAAAGCGCTAATTCACAGGACCT 245
 Db 714 TGCAGAAATCGTCTCTGCAGTTTTCCCATCTCCATGAGAAAGGCAATATGACAGAGATCT 773
 Qy 246 GARACCAACCAAACTTACTGCTGTGCGAGGGGACAG---TTCTAAAAATTTTGATTTT 302
 Db 774 GAAACCCGAAACATCTCTATGATACAGATGCCACGTGATGCTAACAGATTTTGTTT 833
 Qy 303 TGGTACAGCCTGTGCATTCAGACATCAGACACATGACCAATAACAGGGGAGTCTGCTTGGAT 362
 Db 834 AGCAAGGAATTTGAGAAACACAGATCAAACTCCATGTGCGGAACCTACGAGATAT 893
 Qy 363 GGCACCTGAAGTTTTTGAAGGTAGTATTACAGTGAATAATGTACCTTTCACGTGGG 422
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 Db 954 GATTCCTCTGTATGATGATCTCAGGAAAGCCACCGTTTCTCGGA 1000

Search completed: December 4, 2003, 05:02:26
 Job time : 357.013 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 00:51:52 ; Search time 3168.12 Seconds
(without alignments)
8832.421 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 684

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*

2: gb_htg:*

3: gb_in:*

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6: gb_pat:*

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8: gb_pl:*

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10: gb_ro:*

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12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pi:*

26: em_ro:*

27: em_sts:*

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29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rnd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	684	100.0	1704	6	E38399	E38399 NF-kappa B
2	684	100.0	1705	9	AB009358	AB009358 Homo sapi
3	684	100.0	1745	9	AF218074	AF218074 Homo sapi
4	684	100.0	1788	6	AR231198	AR231198 Sequence
5	684	100.0	1788	6	AR307979	AR307979 Sequence
6	684	100.0	2656	6	AR231192	AR231192 Sequence
7	684	100.0	2656	6	AR307973	AR307973 Sequence
8	684	100.0	2757	9	BC017715	BC017715 Homo sapi
9	684	100.0	2769	6	AX377912	AX377912 Sequence
10	684	100.0	2769	9	AB009356	AB009356 Homo sapi
11	684	100.0	2785	6	E38397	E38397 NF-kappa B
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13	684	100.0	2866	6	E38398	E38398 NF-kappa B
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15	586.4	85.7	3107	10	BC006665	BC006665 Mus muscu
16	523.6	76.5	135308	2	AC114407	AC114407 Mus muscu
17	498.4	72.9	2745	5	BC049005	BC049005 Xenopus lae
18	498.4	72.9	2812	5	XL092030	U92030 Xenopus lae
19	177.2	25.9	3349	3	AF199466	AF199466 Drosophil
20	175.6	25.9	3386	3	AY051953	AY051953 Drosophil
21	144.8	21.2	153168	2	AC025387	AC025387 Homo sapi
22	141.2	20.6	100994	9	HSJ154314	AL121964 Human DNA
23	141.2	20.6	200469	2	AL161435	AL161435 Homo sapi
24	140.2	20.5	153168	2	AC025387	AC025387 Homo sapi
25	140.2	20.5	200469	2	AL161435	AL161435 Homo sapi
26	138	20.2	3482	9	HSB000550	AL050393 Homo sapi
27	127	18.6	144836	2	AC011102	AC011102 Homo sapi
28	124.6	18.2	165700	10	AL833781	AL833781 Mouse DNA
29	124.6	18.2	233722	2	AC134067	AC134067 Rattus no
30	124.6	18.2	238817	2	AC134221	AC134221 Rattus no
31	124.6	18.2	242458	2	AC094220	AC094220 Rattus no
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36	97.4	14.2	192888	2	EX005296	EX005296 Danio rer
37	65.8	9.6	1611	3	AF145377	AF145377 Caenorhab
38	65.8	9.6	1993	3	AF143242	AF143242 Caenorhab
39	65.4	9.6	1428	6	AX506187	AX506187 Sequence
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ALIGNMENTS

RESULT 1

E38399

LOCUS

DEFINITION

NF-kappa B activation inhibitory drug targeting TAK1 and method for

identifying the same.

ACCESSION

E38399

VERSION

E38399.1 GI:18626979

KEYWORDS

JP 2000197500-A/5.

SOURCE

unidentified

ORGANISM

unclassified

REFERENCE

1 (bases 1 to 1704)

Sugita,N., Sakurai,H., Kageyama,N. and Hasegawa,H.

NF-kappa B activation inhibitory drug targeting TAK1 and method for

identifying the same

Pred. No. is the number of results predicted by chance to have a

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db 892 GAGCCATTACAGTATCCTTGTCTCAG 915

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DEFINITION	Sequence 1788 bp DNA	
ACCESSION	Sequence 14 from patent US 6451617.	
VERSION	AR231198.1 GI:27272086	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 1788)	
TITLE	Onc,K., Ohtomo,T. and Tsuchiya,M.	
JOURNAL	Method of screening TGF-.beta. inhibitory substances	
FEATURES	Patent: US 6451617-A 14 17-SEP-2002;	
source	Location/Qualifiers	
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QY	61	TGCTTGAATCCAGTGTGCTTGTGTGAATGAAATATGCTGAAGGGGCTCTTTATATAATGTG	120	
DB	292	TGCTTGAATCCAGTGTGCTTGTGTGAATGAAATATGCTGAAGGGGCTCTTTATATAATGTG	351	
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QY	181	CAGTGTTCCTCCAGGAGTGGCTTTATCTTCACAGCATGCAACCCAAAGCCGCTAATTCACAGG	240	
DB	412	CAGTGTTCCTCCAGGAGTGGCTTTATCTTCACAGCATGCAACCCAAAGCCGCTAATTCACAGG	471	
QY	241	GACCTGAACACCAACCACTTACTGCTGGTTGCAGGGGGACAGTTCTAAAAATTTGTGAT	300	
DB	472	GACCTGAACACCAACCACTTACTGCTGGTTGCAGGGGGACAGTTCTAAAAATTTGTGAT	531	
QY	301	TTTGGTACAGCCTGTGCATATTCAGACACACATGACCAATTAACAGGGGAGTCTGCTCTGG	360	
DB	532	TTTGGTACAGCCTGTGCATATTCAGACACACATGACCAATTAACAGGGGAGTCTGCTCTGG	591	
QY	361	ATGGCACCTGAAGTTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGTCTTCAGCTGG	420	
DB	592	ATGGCACCTGAAGTTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGTCTTCAGCTGG	651	
QY	421	GGTATTATTCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGATTGGTGGCCCA	480	
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QY	481	GCTTTCCGAATCATGTGGGCTGTTCTAATATGTTACTGACACCAACCTGATAAAAATTTA	540	
DB	712	GCTTTCCGAATCATGTGGGCTGTTCTAATATGTTACTGACACCAACCTGATAAAAATTTA	771	
QY	541	CCTAAGCCCATTCAGAGCCTGTGACTCGTTGTTGGTCTAAAGATCCCTTCCAGAGCCCTC	600	
DB	772	CCTAAGCCCATTCAGAGCCTGTGACTCGTTGTTGGTCTAAAGATCCCTTCCAGAGCCCTC	831	
QY	601	TCAATGGAGAAATTGTGAAAAATAATGACTCACTTGATGCGGTATCTTTCCAGAGCAGAT	660	
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LOCUS			linear
DEFINITION		Sequence 14 from patent US 6551840.	PAT 12-JUN-2003
ACCESSION		AR307979	
VERSION		AR307979.1	GI:31698736
KEYWORDS			
SOURCE		Unknown.	
ORGANISM		Unknown.	
REFERENCE		1 (bases 1 to 1788)	
AUTHORS		Ono, K., Ontomo, T. and Tsuchiya, M.	
TITLE		Method of screening TGF-beta-inhibiting substances	
JOURNAL		Patent: US 6551840-A 14 22-APR-2003;	
FEATURES		Location/Qualifiers	
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Gaps 0;			
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Db	232	GTGAGCTTCGGCAGTTATCCCGTGTGAACCATCCTAATATTGTAAAGCTTTATGGAGCC	291
Qy	61	TGCTTGAATCCAGTGTGCTTTGTGATGGAATATGCTGAAGGGGCTCTTTATAAATGTG	120
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Qy	121	CTGCAATGCTGTGAACCAATGCGCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA	180
Db	352	CTGCAATGCTGTGAACCAATGCGCATTTATATCTGCTGCCACGCAATGAGTTGGTGTTA	411
Qy	181	CAGTGTCCCAAGGAGTGGCTTATCTTCCACAGATGCAACCCAAAGCGCTAAATTCACAGG	240
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Qy	301	TTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTCTCTTGG	360
Db	532	TTTGGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTCTCTTGG	591
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Db	592	ATGCGACCTGAGTTTTTTGAGGTAGTAAATACAGTAAAAATGTGACGCTTTCAGCTGG	651
Qy	421	GGTATTATTCTTTGGGAAATGATAACGGGTGCGAAACCCCTTTGATGAGATTGGTGGCCCA	480
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Qy	481	GCTTTCCGAATCATGTGGCTGTTTCATTAATGTTACTCGACACCACTCATAAAAATTTA	540
Db	712	GCTTTCCGAATCATGTGGCTGTTTCATTAATGTTACTCGACACCACTCATAAAAATTTA	771
Qy	541	CCTAAGCCCATTTGAGACCTGATGACTGGTCTTGGTCTTAAAGATCCCTTCCAGAGCCCT	600
Db	772	CCTAAGCCCATTTGAGACCTGATGACTGGTCTTGGTCTTAAAGATCCCTTCCAGAGCCCT	831
Qy	601	TCAATGGAGGAATTTGTGAAAAATAATGACTCACTTGTATGCGGTACTTTCCAGAGAGAGAT	660
Db	832	TCAATGGAGGAATTTGTGAAAAATAATGACTCACTTGTATGCGGTACTTTCCAGAGAGAGAT	891


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QY 661 GAGCATTACAGTATCCCTGTGCAG 684
Db 1068 GAGCCATTACAGTATCCCTGTGCAG 1091

RESULT 8
LOCUS BC017715 2757 bp mRNA linear PRI 06-DEC-2001
DEFINITION Homo sapiens, mitogen-activated protein kinase kinase 7,
clone MGC:21263 IMAGE:3906837, mRNA, complete cds.
ACCESSION BC017715
VERSION BC017715.1 GI:17389342
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Strausberg, R.
TITLE Direct Submission
INSTITUTE National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 22 Row: 1 Column: 18
This clone was selected for full length sequencing because it
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Query Match 100.0%; Score 684; DB 9; Length 2757;
Best Local Similarity 100.0%; Pred. No. 1.9e-200;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TGCCTGAATCAGTGTCTTGTGTGATGAATATGCTGAAGGGGGCTCTTTATATAATGTS 120
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RESULT 9
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DEFINITION Sequence 107 from Patent WO0212338.
ACCESSION AX377912
VERSION AX377912.1 GI:19573976
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Gillen, C., Wetzel, I., Wrenndt, S., Weihe, E. and Schaefer, M.K.
TITLE Screening method
PATENT: WO 0212338-A 107 14-FEB-2002;
Gruenthal GmbH (DE)
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Query Match      100.0%; Score 684; DB 9; Length 2850;
Best Local Similarity 100.0%; Pred. No. 1.9e-200;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGAGCTTCGGCAGTTATCCGCTGTGAACCACTCCTAATATTGTAAAGCTTTATGGAGCC 60
Db 1 GTAGAGCTTCGGCAGTTATCCGCTGTGAACCACTCCTAATATTGTAAAGCTTTATGGAGCC 447
QY 61 TGCCTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 448 TGCCTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 507
QY 121 CTGATGTGTGTAACCACTTACTGCTGCTGCCAGCAATGAGTTGGTGTGTTA 180
Db 508 CTGATGTGTGTAACCACTTACTGCTGCTGCCAGCAATGAGTTGGTGTGTTA 567
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCCAAGCGCTTAATTCACAGG 240
Db 568 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCCAAGCGCTTAATTCACAGG 627
QY 241 GACCTGAAACCCCAACCACTTACTGCTGGTGGAGGGGGACAGTTCCTAAATAATTTGTAT 300
Db 628 GACCTGAAACCCCAACCACTTACTGCTGGTGGAGGGGGACAGTTCCTAAATAATTTGTAT 687
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTCTGTGG 360
Db 688 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTCTGTGG 747
QY 361 ATGGCACTGAACTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 420
Db 748 ATGGCACTGAACTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 807
QY 421 GGTATTATCTTTGGGAAGTGATACCGCTCGGAAACCTTTGATGAGATTGGTGCCCA 480
Db 808 GGTATTATCTTTGGGAAGTGATACCGCTCGGAAACCTTTGATGAGATTGGTGCCCA 867
QY 481 GCTTTCGAATCATGTGGGCTGTTTCAATAATGGTACTCGACACCACTGATATAAAATTTA 540
Db 868 GCTTTCGAATCATGTGGGCTGTTTCAATAATGGTACTCGACACCACTGATATAAAATTTA 927
QY 541 CCTAAGCCCATTCAGAGCTGTGATGCTGCTGTGTTGGTCTTAAAGATCCTTCCAGCGCCT 600
Db 928 CCTAAGCCCATTCAGAGCTGTGATGCTGCTGTGTTGGTCTTAAAGATCCTTCCAGCGCCT 987
QY 601 TCAATGAGGAAATTTGGAATAATGACATCACTTGTGATGGTACTTTCCAGAGCAGAT 660
Db 988 TCAATGAGGAAATTTGGAATAATGACATCACTTGTGATGGTACTTTCCAGAGCAGAT 1047
QY 661 GAGCCATTACAGTATCCTTGTCTAG 684
Db 1048 GAGCCATTACAGTATCCTTGTCTAG 1071
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RESULT 13

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E38398
LOCUS      E38398      2866 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION NP-kappa B activation inhibitory drug targeting TAK1 and method for
            identifying the same.
ACCESSION  E38398      GI:18626978
VERSION    E38398.1
KEYWORDS   JP 2000197500-A/4.
SOURCE     unidentified
           unclassified.
ORGANISM   1 (bases 1 to 2866)
            Sugita,N., Sakurai,H., Kageyama,N. and Hasegawa,H.
            NP-kappa B activation inhibitory drug targeting TAK1 and method for
            identifying the same
            Patent: JP 2000197500-A 4 18-JUL-2000;
            TANABE SEIVAKU CO LTD
COMMENT    OS Unidentified
           PN JP 2000197500-A/4
           PD 18-JUL-2000
           PF 04-FEB-1999 JP 1999026803
           PR
           PI NAOHISA SUGITA,HIROAKI SAKURAI,NORIKO KAGEYAMA, PI HIROSHI
            HASEGAWA
           PC C12Q1/48,A61K31/00,A61K31/00,A61K45/00,C12N5/10,C12N9/99,PC
            C12Q1/02,
           PC G01N33/15,G01N33/50,G01N33/566//C12N15/09,C12Q1/68,(C12N15/09,
            PC C12R1:91),
           PC C12N5/00,C12N15/00,(C12N15/00,C12R1:91)
           CC Strandedness: Double;
           CC Topology: Linear;
           FH Key Location/Qualifiers
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BASE COUNT      848 a  588 c  656 g      774 t
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Best Local Similarity 100.0%; Pred. No. 1.9e-200;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGAGCTTCGGCAGTTATCCGCTGTGAACCACTCCTAATATTGTAAAGCTTTATGGAGCC 60
Db 388 GTAGAGCTTCGGCAGTTATCCGCTGTGAACCACTCCTAATATTGTAAAGCTTTATGGAGCC 447
QY 61 TGCCTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 448 TGCCTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTCTTTATATAATGTG 507
QY 121 CTGATGTGTGTAACCACTTACTGCTGCTGCCAGCAATGAGTTGGTGTGTTA 180
Db 508 CTGATGTGTGTAACCACTTACTGCTGCTGCCAGCAATGAGTTGGTGTGTTA 567
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCCAAGCGCTTAATTCACAGG 240
Db 568 CAGTGTTCCTCAAGAGTGGCTTATCTTCAGCATGCAACCCCAAGCGCTTAATTCACAGG 627
QY 241 GACCTGAAACCCCAACCACTTACTGCTGGTGGAGGGGGACAGTTCCTAAATAATTTGTAT 300
Db 628 GACCTGAAACCCCAACCACTTACTGCTGGTGGAGGGGGACAGTTCCTAAATAATTTGTAT 687
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTCTGTGG 360
Db 688 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTCTGTGG 747
QY 361 ATGGCACTGAACTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 420
Db 748 ATGGCACTGAACTTTTGAAGGTAGTAATTAACAGTGAATAATGTGACGCTTTCAGCTGG 807
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 09:42:22 ; Search time 864.703 Seconds
(without alignments)
1911.298 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPFLTLQSTNTHQTSSSSS.....AEFYRLNSVDHGQSVVTAP 68

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em_estba: *
2: em_esthum: *
3: em_estmu: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_man: *
23: em_gss_mas: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gsal: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	359	100.0	757	13	BX393376	BX393376 BX393376
2	359	100.0	974	10	BE989567	BE989567 601681494
3	359	100.0	1021	13	BU152619	BU152619 AGENCOURT
4	356	99.2	496	9	AW258218	AW258218 uq31h07.y
5	356	99.2	578	13	BU609697	BU609697 UI-M-DJ2-
6	356	99.2	705	10	BE375985	BE375985 601229419
7	355	98.9	782	12	BI253992	BI253992 602975130
8	355	98.9	1385	13	BQ925425	BQ925425 AGENCOURT
9	353	98.3	997	10	BG115732	BG115732 602317018
10	352	98.1	851	13	BX347763	BX347763 BX347763
11	351	97.8	334	10	BF710376	BF710376 MI-P-AY1-
12	351	97.8	378	10	BG382061	BG382061 297803 MA
13	351	97.8	527	12	BI400511	BI400511 MI-P-AY1-
14	351	97.8	582	12	BI681846	BI681846 461334 MA
15	351	97.8	599	12	BI401530	BI401530 MI-P-CP0-
16	351	97.8	648	12	BI184403	BI184403 UNL-P-PN-
17	351	97.8	815	12	BI181306	BI181306 UNL-P-PN-
18	347	96.7	644	12	BM934363	BM934363 UI-M-CG0p
19	345	96.1	777	12	BI181203	BI181203 UNL-P-PN-
20	343	95.5	738	13	BU709271	BU709271 UI-M-EV0-
21	339	94.4	930	13	BX347740	BX347740 BX347740
22	336	93.6	912	13	BX347764	BX347764 BX347764
23	327	91.1	919	10	BF163305	BF163305 601771849
24	322	89.7	337	10	BF712308	BF712308 MI-P-A3-a
25	311	86.6	325	9	AW658281	AW658281 94183 MAR
26	309	86.1	617	13	BU443120	BU443120 604144467
27	309	86.1	772	13	BG710962	BG710962 pgl1n.pk0
28	309	86.1	772	13	BU229272	BU229272 60399682
29	309	86.1	941	13	BU427891	BU427891 603955296
30	307	85.5	934	13	BX347741	BX347741 BX347741
31	288	80.2	677	13	BU426433	BU426433 603954265
32	287	79.9	1107	10	BE902307	BE902307 601676585
33	275	76.6	1002	14	BY709101	BY709101 BY709101
34	275	76.6	1576	11	AK009321	AK009321 Mus muscu
35	268	74.7	795	13	BU109063	BU109063 603109730
36	267	74.4	450	9	AA674170	AA674170 vp9a05.r
37	252	70.2	584	10	BE901639	BE901639 601677788
38	251.5	70.1	610	13	BQ387712	BQ387712 NISC.mn25
39	247	68.8	695	13	BU256845	BU256845 603414291
40	245.5	68.4	818	10	BE746542	BE746542 601580107
41	245	68.2	654	13	BU417660	BU417660 603961557
42	213	59.3	997	13	BX367448	BX367448 BX367448
43	210.5	58.6	1243	14	CD501051	CD501051 CDA48-F08
44	187.5	52.2	931	14	CA469739	CA469739 AGENCOURT
45	185	51.5	626	13	BX278260	BX278260 BX278260

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
BX393376 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC002Y002 5-PRIME, mRNA sequence.
ACCESSION
BX393376
VERSION
BX393376.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 757)

Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCM2570 row: k column: 11
 High quality sequence start: 48
 High quality sequence stop: 601.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6381058"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_40"
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 205 a 386 c 259 g 165 t 6 others
 ORIGIN

Alignment Scores:
 Pred. No.: 8.93e-32 Length: 1021
 Score: 359.00 Matches: 68
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x BU152619 (1-1021)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 244 CAAGCCCGAGCTTAACCCCTGAGTCCACCAACAGCAGCAGCAGCAGCTCCAGC 303
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
 Db 304 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCCACCTCGTCCGCGGAGGACGGT 363
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 364 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 423
 QY 61 GluGlnSerValThrAlaPro 68
 Db 424 GAGCAGAGCGTGTGACAGCACCG 447

RESULT 4
 AW258218 496 bp mRNA linear EST 03-APR-2000
 LOCUS uq31h07.y1 NCI CGAP Mams Mus musculus cDNA clone IMAGE:2811037 5,
 DEFINITION similar to TR:Q15750 Q15750 TAKI BINDING PROTEIN. ;, mRNA sequence.
 ACCESSION AW258218
 VERSION AW258218.1 GI:6631199
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 496)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished

COMMENT

Other_ESTS: uq31h07.x1
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40RP from Gibco
 High quality sequence stop: 439.
 Location/Qualifiers

FEATURES

source

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 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:2811037"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam5"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
 BASE COUNT 113 a 158 c 140 g 85 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.71e-32 Length: 496
 Score: 356.00 Matches: 67
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.53% Mismatches: 0
 Query Match: 99.16% Indels: 0
 DB: 9 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x AW258218 (1-496)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 17 CAGAGCCCCACTCTGACCTCGAGTCCACCAACAGCAGCAGCAGCTCCAGC 76
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
 Db 77 TCTGACGAGGCGCTCTCCGCTCCAGCCGCTCCTCCTCCACCGAGGAGTGGC 136
 QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60
 Db 137 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 196
 QY 61 GluGlnSerValThrAlaPro 68
 Db 197 GAGCAGAGCGTGTGACGACCGCCT 220

RESULT 5

BU609697

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BU609697 578 bp mRNA linear EST 20-FEB-2003
 UI-M-DJ2-bvx-p-14-0-UI.r1 NIH BMAP DJ2 Mus musculus cDNA clone
 UI-M-DJ2-bvx-p-14-0-UI 5', mRNA sequence.
 BU609697
 BU609697.1 GI:23275912
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 578)
 Ronaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEst@mail.nih.gov
Tissue Procurement: Dr. Robin Davisson
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 REVERSE.

FEATURES
source
1. .578
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UI-M-DJ2-bv-p-14-0-UI"
/tissue_type="subfornical organ and postrema"
/dev_stage="Adult"
/lab_host="NIH BMAP DJ2"
/notes="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-M-DJ2 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subfornical organ and area postrema."
BASE COUNT 117 a 193 c 159 g 109 t
ORIGIN

Alignment Scores:
Pred. No.: 9.44e-32 Length: 578
Score: 356.00 Matches: 67
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.53% Mismatches: 0
Query Match: 99.16% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x BU609697 (1-578)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
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Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 234 TCTGACGGGGCCCTCTCCGCTCCAGACCGGCTCACTCACTCCACCCGGAGAGATGGC 293
Qy 41 ArgValGluProTyroValAspPheAlaGluPheTyroArgLeuTrpSerValAspHisGly 60
Db 294 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTCTACCGACTCTGTGAGCGTGGACACGGC 353
Qy 61 GluGlnSerValValThrAlaPro 68
Db 354 GAGCAGACGCGTGATGACGGCACCT 377
RESULT 6
BE375985 705 bp mRNA linear EST 21-JUL-2000
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

601229419F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3593452 5', mRNA sequence.
BE375985
BE375985.1 GI:9321350
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 705)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LHAM8766 row: e column: 05
High quality sequence stop: 583.

FEATURES
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1. .705
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/clone="IMAGE:3593452"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam1"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 159 a 231 c 194 g 121 t
ORIGIN

Alignment Scores:
Pred. No.: 1.23e-31 Length: 705
Score: 356.00 Matches: 67
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.53% Mismatches: 0
Query Match: 99.16% Indels: 0
DB: 10 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x BE375985 (1-705)

Qy 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 132 CAGAGCCCCACTCTGACCTGCAGTCCACCAACAGCACCCAGAGAGATCCAGC 191
Qy 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 192 TCTGACGGGGCCCTCTCCGCTCCAGACCGGCTCACTCACTCCACCCGGAGAGATGGC 251
Qy 41 ArgValGluProTyroValAspPheAlaGluPheTyroArgLeuTrpSerValAspHisGly 60
Db 252 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTCTACCGACTCTGTGAGCGTGGACACGGC 311
Qy 61 GluGlnSerValValThrAlaPro 68
Db 312 GAGCAGACGCGTGATGACGGCACCT 335
RESULT 7
BE375992 782 bp mRNA linear EST 17-JUL-2001
LOCUS
DEFINITION 602975130F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114622 5', mRNA sequence.

ACCESSION BI253992
 VERSION BI253992.1 GI:14805965
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 782)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11278 row: k column: 07
 High quality sequence stop: 657.
 High quality sequence stop: 657.
 FEATURES
 source
 Location/Qualifiers
 1..782
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5114622"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 BASE COUNT 162 a 288 c 214 g 118 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.84e-31 Length: 782
 Score: 355.00 Matches: 67
 Percent Similarity: 98.53% Conservative: 0
 Best Local Similarity: 98.53% Mismatches: 1
 Query Match: 98.89% Indels: 0
 DB: 12 Gaps: 0
 US-09-830-144-4_COPY_437_504 (1-68) x BI253992 (1-782)
 QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 306 CAAAGCCGACCTTAACTGAGTCCACCAACACGACGACGACGACGACGACGACG 365
 QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 366 TCTGAGGAGGCTCTTCCGCTCCGCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 425
 QY 41 ArgValGluProThrValAspPheAlaGluPheThrArgLeuTrpSerValAspHisGly 60
 Db 426 CGTGTGAGCCCTATGTGGACTTTGTGAGTTTACCGCTCTGGAGCGTGGACCATGC 485
 QY 61 GluGlnSerValThrAlaPro 68
 Db 486 GAGCAGAGCGTGGTACAGCACC 509
 RESULT 8
 BQ925425
 LOCUS 1385 bp mRNA linear EST 20-AUG-2002
 DEFINITION AGENCOURT 8801162 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6310974
 5', mRNA sequence.
 ACCESSION BQ925425
 VERSION BQ925425
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1385)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.
 cDNA Library Preparation: ResGen, Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13734 row: c column: 07
 High quality sequence start: 58
 High quality sequence stop: 404.
 High quality sequence stop: 404.
 FEATURES
 source
 Location/Qualifiers
 1..1385
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:6310974"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_129"
 /note="Organ: olfactory epithelium; Vector:
 pCMV-SPORT6.1.ccdB; Site 1: EcoRV; Site 2: NotI; Cloned
 unidirectionally. Primer: Oligo dT. Average insert size
 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
 is a NIH_MGC Library."
 BASE COUNT 257 a 536 c 337 g 253 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.93e-31 Length: 1385
 Score: 355.00 Matches: 67
 Percent Similarity: 98.53% Conservative: 0
 Best Local Similarity: 98.53% Mismatches: 1
 Query Match: 98.89% Indels: 0
 DB: 13 Gaps: 0
 US-09-830-144-4_COPY_437_504 (1-68) x BQ925425 (1-1385)
 QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 247 CAAAGCCGACCTTAACTGAGTCCACCAACACGACGACGACGACGACGACG 306
 QY 21 SerAspGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
 Db 307 TCTGAGGAGGCTCTTCCGCTCCGCGCTCCGCTCCGCTCCGCTCCGCTCCG 366
 QY 41 ArgValGluProThrValAspPheAlaGluPheThrArgLeuTrpSerValAspHisGly 60
 Db 367 CGTGTGAGCCCTATGTGGACTTTGTGAGTTTACCGCTCTGGAGCGTGGACCATGC 426
 QY 61 GluGlnSerValThrAlaPro 68
 Db 427 GAGCAGAGCGTGGCAGCACC 450
 RESULT 9
 BQ115732
 LOCUS 997 bp mRNA linear EST 30-JAN-2001
 DEFINITION 602317018F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4417108 5',
 mRNA sequence.
 ACCESSION BQ115732
 VERSION BQ115732.1 GI:12609238
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 997)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA library Preparation: Life Technologies, Inc.
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM0149 row: d column: 05
 High quality sequence stop: 659.
 Location/Qualifiers
 1..997
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4417108"
 /issue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6;
 Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."
 BASE COUNT 251 a 310 c 296 g 140 t
 ORIGIN
 Alignment Scores: 4.36e-31 Length: 997
 Pred. No.: 353.00 Matches: 67
 Score: 98.53% Conservativeness: 0
 Percent Similarity: 98.53% Mismatches: 1
 Best Local Similarity: 98.33% Indels: 0
 Query Match: 10 Gaps: 0
 DB:
 US-09-830-144-4_COPY_437_504 (1-68) x BG115732 (1-997)
 QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 194 CAATTCCGACCTTAACCTTGAGTCCACCAACGACGACGACGACGACGACGACG 253
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
 Db 254 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCGCCACTCGCTCCGCGCTGGCGAGGCGGT 313
 QY 41 ArgValGluProThrValAspPheAlaGluPheThrArgLeuThrSerValAspHisGly 60
 Db 314 CGTGTTCAGCGCTATGTGGACTTTGCTGAGTTTACCGCTTCTGGAGCGTGGACCATGGC 373
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 374 GAGCAGAGCGGTGGTACAGCACC 397
 RESULT 10
 BX347763 851 bp mRNA linear EST 05-MAY-2003
 LOCUS BX347763 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC018YG07 5-PRIME, mRNA sequence.
 ACCESSION BX347763
 VERSION BX347763.1 GI:30375210
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 851)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization

JOURNAL COMMENT

Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 invitrogen. This sequence belongs to sequence cluster 10651.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BAE0082G12 AE00768 1&cluster=10651.f.
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0BAE0082G12_AE00768_1.

FEATURES

source

1..851
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC018YG07"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 172 a 284 c 253 g 140 t 2 others
 ORIGIN

Alignment Scores:

Pred. No.: 4.63e-31 Length: 851
 Score: 352.00 Matches: 67
 Percent Similarity: 98.53% Conservativeness: 0
 Best Local Similarity: 98.53% Mismatches: 1
 Query Match: 98.05% Indels: 0
 DB: 13 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x BX347763 (1-851)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
 Db 544 CAAGCCGACCTTAACCTTGAGTCCACCAACGACGACGACGACGACGACGACG 603
 QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
 Db 604 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCGCCACTCGCTCCGCGCTGGCGAGGCGGT 663
 QY 41 ArgValGluProThrValAspPheAlaGluPheThrArgLeuThrSerValAspHisGly 60
 Db 664 CGTGTTCAGCGCTATGTGGACTTTGCTGAGTTTACCGCTTCTGGAGCGTGGACCATGGC 723
 QY 61 GluGlnSerValValThrAlaPro 68
 Db 724 GAGCAGAGCGGTGGTACAGCACC 747

RESULT 11

BX347763/c

LOCUS BX347763

DEFINITION MI-P-AV1-nqr-c-02-0-UI.s1 MI-P-AV1 Sus scrofa cDNA clone

MI-P-AV1-nqr-c-02-0-UI 3', mRNA sequence.

ACCESSION BF710376

VERSION BF710376.1

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ctuggle@iastate.edu
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 61-111,
>GC rich#Low complexity
Seq primer: M13 Forward
POLYA=No.

FEATURES

source

Location/Qualifiers
1..334
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-Ayl-ngr-c-02-0-UI"
/lab_host="DHI08 (Life Technologies)"
/clone_lib="MI-P-Ayl"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ayl
library is normalized library derived from the MI-P-Ayl
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described (Ronald
, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_SEQ=None found"

BASE COUNT

43 a 111 c 136 g 44 t

ORIGIN

Alignment Scores:

Pred. No.:	1.76e-31	Length:	334
Score:	351.00	Matches:	66
Percent Similarity:	97.06%	Conservative:	0
Best Local Similarity:	97.06%	Mismatches:	2
Query Match:	97.77%	Indels:	0
DB:	10	Gaps:	0

US-09-830-144-4_COPY_437_504 (1-68) x BF710376 (1-334)

Qy	1	GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer	20
Db	317	CAGAGCCGACCCCTGACCTTGACCTCCACCAACACCCACAGAGCAGCAGCTCCAGC	258
Qy	21	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	40
Db	257	TCCGACGGGGCCCTCTTCGCTCCGGCCACCCACCTCGCTCCGCCGCGGAGATGGC	198
Qy	41	ArgValGluProTrValAspPheAlaGluPheTyArgLeuTrpSerValAspHisGly	60
Db	197	CGGTGGAGCCCTACGTGGACTTCGCGGAGTTCTACCGCTGTGGAGCGTGGACCGGC	138
Qy	61	GluGlnSerValValThrAlaPro	68
Db	137	GAGCAGAGTGTGGCAGCGCGCG 114	

RESULT 12

BG382061

LOCUS

297803 MARC 1P1G Sus scrofa cDNA 5', mRNA linear EST 12-MAR-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 378)
Fahrenkrug,S.C., Smith,T.P.I., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Perlea,G., Sultana,R., Quackenbush
J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGC
Plate: 2 row: 0 column: 16
Seq primer: ATTAGTGACATATAG.
Location/Qualifiers
1..378
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DHI08"
/clone_lib="MARC 1P1G"
/note="Vector: pQWV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

FEATURES

source

BASE COUNT 52 a 154 c 123 g 49 t

ORIGIN

Alignment Scores:

Pred. No.:	2.07e-31	Length:	378
Score:	351.00	Matches:	66
Percent Similarity:	97.06%	Conservative:	0
Best Local Similarity:	97.06%	Mismatches:	2
Query Match:	97.77%	Indels:	0
DB:	10	Gaps:	0

US-09-830-144-4_COPY_437_504 (1-68) x BG382061 (1-378)

Qy	1	GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer	20
Db	71	CAGAGCCGACCCCTGACCTTGACCTCCACCAACACCCACAGCAGCAGCTCCAGC	130
Qy	21	SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly	40
Db	131	TCCGACGGGGCCCTCTTCGCTCCGGCCACCCACCTCGCTCCGCCGCGGAGATGGC	190
Qy	41	ArgValGluProTrValAspPheAlaGluPheTyArgLeuTrpSerValAspHisGly	60
Db	191	CGGTGGAGCCCTACGTGGACTTCGCGGAGTTCTACCGCTGTGGAGCGTGGACCGGC	250
Qy	61	GluGlnSerValValThrAlaPro	68
Db	251	GAGCAGAGTGTGGCAGCGCGCG 274	

RESULT 13

BI400511/c

LOCUS

MI-P-Ayl-nge-a-03-0-UI.61 MI-P-Ayl Sus scrofa cDNA clone linear EST 14-AUG-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 527)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Tuggle CK
8889548
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Oligo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 62-112,
>GC rich/Low complexity
Seq primer: M13 Forward
POLYA=No.

FEATURES
source
1..527
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-AY1-ngc-a-03-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MI-P-AY1"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1
library is normalized library derived from the MI-P-AY0
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG SEQ=None found"
BASE COUNT 67 a 166 c 216 g 78 t
ORIGIN
Alignment Scores:
Pred. No.: 3.22e-31 Length: 527
Score: 351.00 Matches: 66
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 2
Query Match: 97.77% Indels: 0
DB: 12 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x BI400511 (1-527)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 318 CAGAGCCGACCTTGACCTCGAGTCCACCAACACCCACAGAGCAGCAGCTCCAGC 259
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 258 TCCGACGGGGCCCTTTTCGCTCCGGCCACCCACCTCGCTCCCGCCGGGAGATGGC 199
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 198 CGCGTGGAGCCCTACGTGGACTTCGCGGAGTTCTACCGCTGTGGAGGTGGACACCGC 139
QY 61 GluGlnSerValValThrAlaPro 68

Db 138 GAGCAGAGTGTGGCAGCGCGCGC 115
RESULT 14
BI681846
LOCUS
DEFINITION
461334 MARC 1BOV Bos taurus cDNA 5', mRNA linear EST 17-SEP-2001
ACCESSION
BI681846
VERSION
BI681846.1 GI:15634771
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
REFERENCE
1 (bases 1 to 582)
AUTHORS
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.B., White, J., Cho, J., Fahrrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Perteira, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 135 row: 0 column: 15
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..582
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1BOV"
/notes="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 93 a 212 c 179 g 98 t
ORIGIN
Alignment Scores:
Pred. No.: 3.67e-31 Length: 582
Score: 351.00 Matches: 67
Percent Similarity: 98.53% Conservative: 0
Best Local Similarity: 98.53% Mismatches: 1
Query Match: 97.77% Indels: 0
DB: 12 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x BI681846 (1-582)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
Db 80 CAGAGCCGACCTTGACCTCGAGTCCACCAACACCCACAGAGCAGCAGCTCCAGC 139
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
Db 140 TCCGACGGGGCCCTTTTCGCTCCGGCCACCCACCTCGCTCCCGCCGGGAGATGGC 199
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60

Db 200 CCGGTGGAGCCCTACGTGGACTTTGCCGAGTTCTACCGCTCTGGAGCGTGGACCATGGC 259

QY 61 GluInSerValThrAlaPro 68

Db 260 GAGCAGAGTGTGTGACGGCGCG 283

RESULT 15

BI401530/c

LOCUS

DEFINITION MI-P-CP0-nvn-g-07-0-UI.s1 MI-P-CP0 Sus scrofa cDNA clone

ACCESSION BI401530

VERSION BI401530.1 GI:15180591

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 599)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Tuggle CK

Molecular Genetics Laboratory, Department of Animal Science

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201 Kildee Hall, Ames, IA 50011-3150, USA

Tel: 5152944252

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Email: cktuggle@iastate.edu

Oligo-dT track not found. Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares lab, University of Iowa EST sequencing: M.B. Soares lab, University of Iowa Clone Distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 60-110,

>GC rich#Low complexity

Seq primer: M13 Forward

POLYA=No.

FEATURES

Location/Qualifiers

1..599

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="MI-P-CP0-nvn-g-07-0-UI"

/lab_host="DH10B (Life Technologies)"

/clone_lib="MI-P-CP0"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0 library is derived from uterus. For a detailed description of the library from which this clone was derived, please visit our web site at <http://pigest.genome.iastate.edu/>. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_SEQ=None found"

BASE COUNT 77 a 193 c 238 g 91 t

ORIGIN

Alignment Scores:

Pred. No.: 3..81e-31 Length: 599

Score: 351.00 Matches: 66

Percent Similarity: 97.06% Conservative: 0

Best Local Similarity: 97.06% Mismatches: 2

Query Match: 97.77% Indels: 0

DB: 12 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x BI401530 (1-599)

QY 1 GluSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20

Db 316 CAGAGCCCCACCCCTGACCTGCAGTCCACCAACACCCACCCAGAGCAGCTCCAGC 257

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40

Db 256 TCCGACGGGGGCTCTTTTCGCTCCCGGCCACCCACTCGCTCCCGCCCGGAGATGGC 197

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60

Db 196 CCGGTGGAGCCCTACGTGGACTTCGGGAGTTCTACCGCTCTGGAGCGTGGACCATGGC 137

QY 61 GluInSerValThrAlaPro 68

Db 136 GAGCAGAGTGTGGCCACGGCGCCG 113

Search completed: December 4, 2003, 12:42:52

Job time : 867.703 secs

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2003, 09:21:16 ; Search time 28.4865 seconds
(without alignments)
615.997 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPTLTQSTNTHQTSSSSS.....AEFVRLWSVDHGEQSWVTAP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	356	99.2	500	11 Q8R0D1	Q8rd1 mus musculus
2	356	99.2	502	11 Q8CF89	Q8cf89 mus musculus
3	275	76.6	52	11 Q9CV62	Q9cv62 mus musculus
4	260.5	72.6	498	13 Q73614	Q73614 xenopus lae
5	74.5	20.8	329	4 Q96S04	Q96s04 homo sapien
6	70	19.5	1034	5 Q81QW0	Q81qw0 drosophila
7	70	19.5	1162	5 Q9VW87	Q9vw87 drosophila
8	69.5	19.4	389	12 Q9DXA1	Q9dxa1 avian pneum
9	69.5	19.4	389	12 Q9DXA0	Q9dxa0 avian pneum
10	67.5	18.8	703	4 Q9H451	Q9h451 homo sapien
11	67.5	18.8	739	4 Q43584	Q43584 homo sapien
12	67.5	18.8	862	4 Q9BV75	Q9bv75 homo sapien
13	67.5	18.8	903	4 Q96E66	Q96f66 homo sapien
14	66.5	18.5	497	16 Q8P7D0	Q8p7d0 xanthomonas
15	66	18.4	591	16 Q9RKD3	Q9rkd3 streptomyce
16	65.5	18.2	634	11 Q925Q8	Q925q8 mus musculus

17	65	18.1	452	12 Q91TB9	Q91tb9 hepatitis c
18	65	18.1	452	12 Q91TC8	Q91tc8 hepatitis c
19	65	18.1	452	12 Q91TC1	Q91tc1 hepatitis c
20	64.5	18.0	673	3 Q9C2H6	Q9c2h6 neurospora
21	64	17.8	452	12 Q91TC6	Q91tc6 hepatitis c
22	64	17.8	5604	4 Q8WZ53	Q8wz53 homo sapien
23	63.5	17.7	780	13 Q9FUI4	Q9fui4 xenopus lae
24	63.5	17.7	3021	12 Q92933	Q92933 hepatitis c
25	63.5	17.7	2152	4 Q8WXI7	Q8wxi7 homo sapien
26	63	17.5	452	12 Q91TC4	Q91tc4 hepatitis c
27	63	17.5	452	12 Q91TD5	Q91td5 hepatitis c
28	63	17.5	452	12 Q91TB8	Q91tb8 hepatitis c
29	63	17.5	452	12 Q91TB3	Q91td3 hepatitis c
30	63	17.5	452	12 Q91TC3	Q91tc3 hepatitis c
31	63	17.5	452	12 Q91TB6	Q91tb6 hepatitis c
32	63	17.5	452	12 Q91TB4	Q91tb4 hepatitis c
33	63	17.5	2112	5 Q9VEL9	Q9vel9 drosophila
34	63	17.5	3021	12 Q81258	Q81258 hepatitis c
35	63	17.5	3021	12 Q68870	Q68870 hepatitis c
36	62.5	17.4	262	5 Q8MYC6	Q8myc6 apis mellif
37	62.5	17.4	268	5 Q8MYC4	Q8myc4 apis mellif
38	62.5	17.4	300	5 Q8MYC8	Q8myc8 apis mellif
39	62.5	17.4	303	5 Q8MYC7	Q8myc7 apis mellif
40	62.5	17.4	358	4 Q96BE7	Q96be7 homo sapien
41	62.5	17.4	393	2 Q8KY29	Q8ky29 streptomyce
42	62.5	17.4	1656	10 Q9LGS1	Q9lgs1 oryza sativ
43	62.5	17.4	1910	5 Q9V768	Q9v768 drosophila
44	62	17.3	172	10 Q9FGW8	Q9fgw8 arabidopsis
45	62	17.3	266	16 Q8FRA6	Q8fra6 corynebacte

ALIGNMENTS

RESULT 1

Q8R0D1 PRELIMINARY; PRT: 500 AA.
ID Q8R0D1
AC Q8R0D1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to mitogen-activated protein kinase kinase 7
DE interacting protein 1 (fragment).
GN 2310012M03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC027054; AAH27054.1; -
DR MGD; MGI:1913763; 2310012M03RIK.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
KW Kinase.
FT NON TER 1
SQ SEQUENCE 500 AA; 54413 MW; 97529D2E2AE4DA34 CRC64;
YQ

Query Match 99.2%; Score 356; DB 11; Length 500;
Best Local Similarity 98.5%; Pred. No. 2e-34;
Matches 67; Conservative 1; Mismatches 0; Gaps 0;
QY 1 QSPTLTQSTNTHQTSSSSSSDGLFRSPAHSPLPFGEDGRVEPYVDFAEFVRLWSVDHG 60
Db 433 QSPTLTQSTNTHQTSSSSSSDGLFRSPAHSPLPFGEDGRVEPYVDFAEFVRLWSVDHG 492
QY 61 EQSWVTAP 68
Db 493 EQSWVTAP 500

RA Hayashizaki Y.;
RT "functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK009321; BAB26215.1; -;
DR MGI; MGI:1913763; 2310012M03Rik.
FT NON_TER 1
SQ SEQUENCE 52 AA; 5712 MW; 813E29B1639920A6 CRC64;

Query Match 76.6%; Score 275; DB 11; Length 52;
Best Local Similarity 98.1%; Pred. No. 8.2e-26;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 SSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHGQSVVTAP 68
Db 1 SSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHGQSVVTAP 52
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RESULT 4
073614 PRELIMINARY; PRT; 498 AA.
ID 073614
AC 073614
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE TAB1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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RN SEQUENCE FROM N.A.
RP MEDLINE-98120593; PubMed-9463380;
RX Shibuya H., Iwata H., Masuyama N., Gotoh Y., Yamaguchi K., Irie K.,
RA Matsumoto K., Nishida E., Ueno N.;
RT "Role of TAK1 and TAB1 in BMP signaling in early Xenopus
development."
RL EMBO J. 17:1019-1028(1998).
DR EMBL; U92031; RAC14009.1; -;
DR InterPro; IPR001932; PF2C-like.
DR Pfam; PF00481; PF2C; 1.
DR SMART; SMC0332; PF2CC; 1.
SQ SEQUENCE 498 AA; 54450 MW; 654AB8DE2353524 CRC64;

Query Match 72.6%; Score 260.5; DB 13; Length 498;
Best Local Similarity 73.5%; Pred. No. 6e-23;
Matches 50; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 1 QSPTLTQSTNTHTQSSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 60
Db 430 QSPSATLQSTNTHTQSSSSSDGLFRSRPLPSLPQDGEDGRVEPYVDFYRLWNAHN 489
[1]
QY 61 EQ-SVWTA 67
Db 490 DPGTLTA 497
[1]

RESULT 5
Q96S04 PRELIMINARY; PRT; 329 AA.
ID Q96S04
AC Q96S04
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN GS78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE-21096910; PubMed-11157797;

RA Hayashizaki Y.;
RT "functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK009321; BAB26215.1; -;
DR MGI; MGI:1913763; 2310012M03Rik.
FT NON_TER 1
SQ SEQUENCE 52 AA; 5712 MW; 813E29B1639920A6 CRC64;

Query Match 76.6%; Score 275; DB 11; Length 52;
Best Local Similarity 98.1%; Pred. No. 8.2e-26;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 SSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHGQSVVTAP 68
Db 1 SSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHGQSVVTAP 52
[1]

RESULT 4
073614 PRELIMINARY; PRT; 498 AA.
ID 073614
AC 073614
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE TAB1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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RN SEQUENCE FROM N.A.
RP MEDLINE-98120593; PubMed-9463380;
RX Shibuya H., Iwata H., Masuyama N., Gotoh Y., Yamaguchi K., Irie K.,
RA Matsumoto K., Nishida E., Ueno N.;
RT "Role of TAK1 and TAB1 in BMP signaling in early Xenopus
development."
RL EMBO J. 17:1019-1028(1998).
DR EMBL; U92031; RAC14009.1; -;
DR InterPro; IPR001932; PF2C-like.
DR Pfam; PF00481; PF2C; 1.
DR SMART; SMC0332; PF2CC; 1.
SQ SEQUENCE 498 AA; 54450 MW; 654AB8DE2353524 CRC64;

Query Match 72.6%; Score 260.5; DB 13; Length 498;
Best Local Similarity 73.5%; Pred. No. 6e-23;
Matches 50; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 1 QSPTLTQSTNTHTQSSSSSDGLFRSRPAHSLPPGEGRVEPYVDFAEFYRLWSVDHG 60
Db 430 QSPSATLQSTNTHTQSSSSSDGLFRSRPLPSLPQDGEDGRVEPYVDFYRLWNAHN 489
[1]
QY 61 EQ-SVWTA 67
Db 490 DPGTLTA 497
[1]

RESULT 5
Q96S04 PRELIMINARY; PRT; 329 AA.
ID Q96S04
AC Q96S04
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN GS78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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RN SEQUENCE FROM N.A.
RP MEDLINE-21096910; PubMed-11157797;

RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL, AF006465; AAK61262.1; -;
KW Hypothetical protein.
SQ SEQUENCE 329 AA; 35799 MW; 890FE4B3D1C5976D CRC64;
Query Match 20.8%; Score 74.5; DB 4; Length 329;
Best Local Similarity 28.6%; Pred. No. 0.9;
Matches 22; Conservative 8; Mismatches 28; Indels 19; Gaps 2;
QY 2 SPTLTQSTNTHTQSSSSSDGGLFRSPAHSLPPGDEG-----RVEPY 45
Db 138 APTREICRTRCHPQSSGELSDG--RNRCPHASESNHGRPGSSPVLGYFTRICKVERN 194
QY 46 VDFAEFYRLWSVDHGEQ 62
Db 195 IPECEDFRTWLTGSGEK 211
RESULT 6
Q81QW0 PRELIMINARY; PRT; 1034 AA.
AC Q81QW0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG11940-PB.
GN CG11940.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Aghayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Fosler K., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleeb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003513; AAN09520.1; -;
SQ SEQUENCE 1034 AA; 111096 MW; 827491ADDE5E4661 CRC64;
Query Match 19.5%; Score 70; DB 5; Length 1034;
Best Local Similarity 32.8%; Pred. No. 12;
Matches 22; Conservative 9; Mismatches 24; Indels 12; Gaps 2;
QY 3 PTLTQSTNTHTQSSSSSDGGLFRSPAHSLPPGDEGRVYDFAEFYRLWSVDHGE 61
Db 932 FVLFPQRSPSTLTSCHSSSSAGSAYQTYAPGPMPLPPR-----ADVARLSSLSNGS 880
QY 62 QSVVTAP 68
Db 881 SSEVTSP 887
RESULT 7
Q9VWB7 PRELIMINARY; PRT; 1162 AA.
ID Q9VWB7
AC Q9VWB7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG11940 protein.
GN CG11940.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDJ databases.
DR EMBL; AL109923; CAC09387.2;
DR HSP; Q13526; 1PIN.
DR InterPro; IPR000569; HECT_domain.
DR InterPro; IPR002349; WW.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00632; HECT; 1.
DR Pfam; PF00397; WW; 4.
DR PRINTS; PR00403; WWDOMAIN.
DR SMART; SM00119; HECTc; 1.
DR SMART; SM00456; WW; 4.
DR PROSITE; PS0237; HECT; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 4.
DR PROSITE; PS0020; WW_DOMAIN_2; 2.
FT NON_TER 1
SQ SEQUENCE 703 AA; 81304 MW; B021DF172A9F1449 CRC64;

Query Match 18.8%; Score 67.5; DB 4; Length 703;
Best Local Similarity 31.1%; Pred. No. 15;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;

QY 2 SPTLTOSTNTHTQSSSSSDG-----GLFRSRPAH-----SLPGEGRVPEYVDF 48
Db 119 SSTGSLPPTNTNTSEGATSLIPLTISGSGRPLNVTQAPLPGEQRVD----- 173
QY 49 AEFYRLMSVDHGEQ 62
Db 174 -QHGRVYVDHVEK 186

RESULT 12
Q9BY75 PRELIMINARY; PRT; 862 AA.
AC Q9BY75;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ubiquitin protein ligase Itch.
GN ITCH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazaki K., Okamoto Y., Sakamoto M., Nakagawara A.;
RT "Homo sapiens mRNA for ubiquitin protein ligase Itch, complete cds.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20549573; PubMed=10940313;
RA Qiu L., Joazeiro C., Fang N., Wang H.Y., Elly C., Altman Y., Fang D.,
RA Hunter T., Liu Y.C.;
RT "Recognition and ubiquitination of Notch by Itch, a hect-type E3
RT ubiquitin ligase.";
RL J. Biol. Chem. 275:35734-35737(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=98122574; PubMed=9462742;
RA Perry W.L., Hustad C.M., Swing D.A., O'Sullivan T.N., Jenkins N.A.,
RA Copeland N.G.;
RT "The itchy locus encodes a novel ubiquitin protein ligase that is
RT disrupted in at18H mice.";
RL Nat. Genet. 18:143-146(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=20501262; PubMed=11046148;
RA Winberg G., Matskova L., Chen F., Plant P., Rotin D., Gish G.,
RA Ingham R., Ernberg I., Pawson T.;
RT "Latent membrane protein 2A of Epstein-Barr virus binds WW domain E3
RT protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases.";
RL Mol. Cell. Biol. 20:8526-8535(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA MEDLINE=98313405; PubMed=9647693;
RA Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kushi J.,
RA Kaminsky Z., Kleiderlein J.J., Sharp A.H., Ross C.A.;
RT "Atrophin-1, the DRPLA gene product, interacts with two families of WW
RT domain-containing proteins.";
RL Mol. Cell. Neurosci. 11:149-160(1998).
RN [6]
RP SEQUENCE FROM N.A.
RA MEDLINE=21218930; PubMed=11318614;
RA Chen X., Wen S.C., Fukuda M.N., Gavva N.R., Hsu D.W., Akama T.O.,
RA Yang-Peng T.L., Shen C.K.J.;
RT "Human ITCH is a Co-regulator of the Hematopoietic Transcription
RT Factor NF-E2.";
RL Genomics 73:238-241(2001).
CC -/- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AB056663; BAB39389.1;
DR EMBL; AF095745; AAK39399.1;
DR HSP; Q13526; 1PIN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000569; HECT_domain.

```

DR InterPro; IPR002349; WW.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00632; HECT; 1.
DR Pfam; PF00397; WW; 4.
DR PRINTS; PR00403; WWDOMAIN.
DR SMART; SM00239; C2; 1.
DR SMART; SM00119; HECT; 1.
DR SMART; SM00456; WW; 4.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50237; HECT; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 4.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
KW Ligase.
SQ SEQUENCE 862 AA; 98675 MW; A3D960E7F4DBF9D3 CRC64;

Query Match 18.8%; Score 67.5; DB 4; Length 862;
Best Local Similarity 31.1%; Pred. No. 19;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;

QY 2 SPTLTQSTNTHQTSSSSSDG-----GLFRSRPAH-----SLPPGEGRVEPYVDF 48
Db 242 SSTGSLPPTNTINTSEGATGLIPLTISGSGRPLNPVTQAPLPQWGEQRVD----- 296

QY 49 AEFYRLWSVDHGQ 62
Db 297 -QHGRVYVDHVEK 309

RESULT 13
Q96F66 PRELIMINARY; PRT; 903 AA.
ID Q96F66
AC Q96F66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to itchy (Mouse homolog) E3 ubiquitin protein ligase.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Scrausberg R.;
RA TISSUE=Kidney;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; BC011571; AAH11571.1; -.
DR Genew; HGNC:13890; ITCH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000563; HECT_domain.
DR InterPro; IPR002349; WW.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00632; HECT; 1.
DR Pfam; PF00397; WW; 4.
DR PRINTS; PR00403; WWDOMAIN.
DR SMART; SM00239; C2; 1.
DR SMART; SM00119; HECT; 1.
DR SMART; SM00456; WW; 4.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50237; HECT; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 4.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 903 AA; 102802 MW; 6777A2043C7B67BC CRC64;

Query Match 18.8%; Score 67.5; DB 4; Length 903;
Best Local Similarity 31.1%; Pred. No. 20;
Matches 23; Conservative 12; Mismatches 20; Indels 19; Gaps 3;

QY 2 SPTLTQSTNTHQTSSSSSDG-----GLFRSRPAH-----SLPPGEGRVEPYVDF 48
Db 283 SSTGSLPPTNTINTSEGATGLIPLTISGSGRPLNPVTQAPLPQWGEQRVD----- 337

QY 49 AEFYRLWSVDHGQ 62
Db 338 -QHGRVYVDHVEK 350

RESULT 14
Q9F7D0 PRELIMINARY; PRT; 497 AA.
ID Q9F7D0
AC Q9F7D0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN OPRM OR XCC2681.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.T.T.,
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012380; AAM41953.1; -.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
DR Complete proteome.
KW SEQUENCE 497 AA; 53173 MW; D41D5A1419B44C60 CRC64;

Query Match 18.5%; Score 66.5; DB 16; Length 497;
Best Local Similarity 36.1%; Pred. No. 13;
Matches 26; Conservative 8; Mismatches 27; Indels 11; Gaps 2;

QY 3 PTLTQSTNTHQTSSSSSDGGLFRSR-----PAHSLPPGEGRVEPYVDFAEFVRLW 55
Db 327 PSISL-----TATLGSSSSSSLSGLFESGTRAWSFVQLTLPLFNAGRANLDMKANEDI 382

QY 56 SVDHGQSVVTA 67
Db 383 EVARYEKSQTA 394

RESULT 15
Q9RKD3 PRELIMINARY; PRT; 591 AA.
ID Q9RKD3
AC Q9RKD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative integral membrane protein.
GN SCO3154 OR SCE87.05.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;


```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939115; CAB59650.1; -.
DR InterPro: IPR003342; Glyco_trans_39.
DR Pfam: PF02366; PMT; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 66289 MW; DE7F1707C0071897 CRC64;
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Query Match 18.4%; Score 66; DB 16; Length 591;
Best Local Similarity 47.4%; Pred. NO. 19;
Matches 18; Conservative 2; Mismatches 14; Indels 4; Gaps 1;
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```
Qy 27 RSRPAHSLPPGCDGRVPEYVDFAEFYRL----WSVDHG 60
||| |:||| ||||| ||||| |
Db 255 RSLAALPYDEDEGRVPEDAHVETLGLGWRPRLAG 292
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Search completed: December 4, 2003, 09:33:04
Job time : 30.4865 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 09:23:11 ; Search time 11.7162 Seconds
(without alignments)
558.155 Million cell updates/sec

Title: US-09-830-144-4_COPY_437_504

Perfect score: 359

Sequence: 1 QSPFTLTQSTNTHTQSSSS.....AEFYRLWSVDHGQSVVTAP 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63.5	17.7	243	D84792	probable protein t
2	62	17.3	541	S51799	nucleoporin NUP57
3	62	17.3	679	H95036	glycosyl hydrolase
4	62	17.3	737	D97907	alpha-xylosidase (
5	62	17.3	4957	T03455	ALR protein - huma
6	62	17.3	5262	T03454	ALR protein - huma
7	61.5	17.1	238	T52505	hypothetical prote
8	61.5	17.1	737	I39547	S-protein secretio
9	61	17.0	267	S74415	hypothetical prote
10	61	17.0	665	B82506	proteinase II VCA0
11	61	17.0	909	T06246	aspartate kinase (
12	61	17.0	951	B88042	protein F56D12.6 [
13	61	17.0	1511	A53351	pleiotropic drug r
14	60	16.7	1260	S60896	agglutinin-like pr
15	60	16.7	1576	AE0249	probable hemolysin
16	59.5	16.6	1369	T32338	hypothetical prote
17	59	16.4	173	G86861	hypothetical prote
18	59	16.4	329	S61884	carbonate dehydrat
19	59	16.4	330	S61883	carbonate dehydrat
20	59	16.4	330	S61882	carbonate dehydrat
21	59	16.4	429	T38146	dihydrofolate redu
22	59	16.4	651	JC7705	death receptor-6
23	58.5	16.3	338	H72679	hypothetical prote
24	58.5	16.3	378	A84161	hypothetical prote
25	58.5	16.3	608	I53269	prolactin receptor
26	58.5	16.3	1093	I38533	AP17 protein - hum
27	58.5	16.3	1099	T18257	phospholipase C -
28	58.5	16.3	2897	B48666	cell proliferation
29	58.5	16.3	3256	A48666	cell proliferation

30 58 16.2 142 2 D69891 yneK protein - Bac
31 58 16.2 277 2 D69158 sensory transducti
32 58 16.2 532 2 B35621 spore germination
33 57.5 16.0 172 2 T36107 probable serine/ar
34 57.5 16.0 232 1 A25108 homeotic protein H
35 57.5 16.0 366 2 A86392 hypothetical prote
36 57.5 16.0 394 2 H65010 hypothetical prote
37 57.5 16.0 396 2 A57090 CSA protein - huma
38 57.5 16.0 629 2 B83107 chemotactic transd
39 57.5 16.0 686 2 JC5708 villin-like protei
40 57 15.9 762 2 S67765 probable membrane
41 57 15.9 778 2 H84678 hypothetical prote
42 56.5 15.7 276 2 T06331 photosystem II 22K
43 56.5 15.7 283 2 H83860 pantothenate synth
44 56.5 15.7 343 2 E83673 sorbitol dehydroge
45 56.5 15.7 457 2 B64790 yclB protein - Esc

ALIGNMENTS

RESULT 1

D84792

probable protein translocase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: D84792

R.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84792

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-243 <SFO>

A:Cross-references: GB:AE002093; NID:g4056494; PIDN:AAC98060.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g37410

A:Map position: 2

Query Match 17.7%; Score 63.5; DB 2; Length 243;
Best Local Similarity 39.0%; Pred. No. 7.9;
Matches 16; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 8 QSTNTHTQSSSSSDGGLFRSPAHSLPPCGEDGRVEPYVDF 48

Db 193 QNQTASSSSSSSWFGGLF-DKKKEVQPSKTEVLESF 232

RESULT 2

S51799

nucleoporin NUP57 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G6320; protein YGR119C

C:Species: Saccharomyces cerevisiae

C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C:Accession: S51799; S51800; S64428; S64427; S55976; S72192

R.;Schlauch, N.L.

submitted to the EMBL Data Library, August 1994

A:Reference number: S51799

A:Accession: S51799

A:Molecule type: DNA

A:Residues: 1-541 <SCH>

A:Cross-references: EMBL:X81155; NID:g671635; PID:g671636

R.;Grandi, P.; Schlaich, N.; Tekotte, H.; Hurt, E.C.

EMBO J. 14, 76-87, 1995

A:Title: Functional interaction of Nic96p with a core nucleoporin complex consisting of

A:Reference number: S51800; MUID:95129554; PMID:7828598

A:Accession: S51800

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-446, 'RL', 449-541 <GRA>

A;Cross-references: EMBL:X81155
R;Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.; Del
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64428
A;Accession: S64428
A;Molecule type: DNA
A;Residues: 1-353 <VAN>
A;Cross-references: EMBL:Z72904; MIPS:YGR119C
A;Experimental source: strain S288C
R;Hansen, M.; Albers, M.; Backes, U.; Coblenz, A.; Leuther, H.; Neu, R.; Schreer, A.; Sc
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64417
A;Accession: S64427
A;Molecule type: DNA
A;Residues: 300-541 <HAN>
A;Cross-references: EMBL:Z72904; MIPS:YGR119C
A;Experimental source: strain S288C
R;van Dyck, L.; Goffeau, A.
submitted to the EMBL Data Library, December 1994
A;Description: Genes for an asn synthase, a GLFG-motif nucleoporin and a putative homeo
e new ORFs, remnants of Ty and three tRNA genes.
A;Reference number: S55976
A;Accession: S55976
A;Molecule type: DNA
A;Residues: 1-353 <VAV>
A;Cross-references: EMBL:X83099
R;Hansen, M.; Albers, M.; Backes, U.; Coblenz, A.; Leuther, H.; Neu, R.; Schreer, A.; Sc
Yeast 12, 1273-1277, 1996
A;Title: The sequence of a 23.4 kb segment on the right arm of chromosome VII from Sacch
A;Reference number: S72179; MUID:97061913; PMID:8905931
A;Accession: S72192
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-541 <HAN>
A;Cross-references: EMBL:Z72904; MID:g1323182; PIDN:CBA97129.1; PID:g1323193
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1996
C;Genetics:
A;Gene: SGD:NUP57
A;Cross-references: SGD:S0003351; MIPS:YGR119C
A;Map position: 7R

Query Match 17.3%; Score 62; DB 2; Length 541;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 8 QSTWHTQSSSSSDGGLFRSRPA 31
| | | | : | : | : | : | : | : |
Db 60 QATNFGSNQQSSTGGGLFGNKPA 83

RESULT 3
H95036
glycosyl hydrolase, family 31 SP0312 [imported] - Streptococcus pneumoniae (strain TIGR4
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: H95036
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:I1463916
A;Accession: H95036
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-679 <KUR>
A;Cross-references: GB:A8005672; PIDN:AAK74489.1; PID:g14371785; GSPDB:GN00164; TIGR:SPA
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0312

Query Match 17.3%; Score 62; DB 2; Length 679;

A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: E82506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-665 <HEI>
 A:Cross-references: GB:AE004349; GB:AE003853; NID:g9657434; PIDN:AAF95977.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
 C:Genetics:
 A:Gene: VCA0063
 A:Map position: 2

Query Match 17.0%; Score 61; DB 2; Length 665;
 Best Local Similarity 31.8%; Pred. No. 49;
 Matches 14; Conservative 10; Mismatches 12; Indels 8; Gaps 2;

QY 32 HSLPFGEDGRVFPYVDF-----EFYRL--WSVDHGEQSVVTA 67
 Db 96 HIVKIGACQIEPLNLSARAPFDYVQLASWSLDRSQVQVALA 139

RESULT 11
 T06246
 N:Contains: aspartate kinase (EC 2.7.2.4) / homoserine dehydrogenase (EC 1.1.1.3) precursor - soybean
 C:Species: Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
 C:Accession: T06246
 R:Gebhardt, J.S.; Weisemann, J.M.; Matthews, B.F.
 A:Description: Genes encoding the bifunctional aspartokinase-homoserine dehydrogenase fr
 A:Reference number: Z15563
 A:Accession: T06246
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-909 <GEB>
 A:Cross-references: EMBL:AF049708; NID:g2970554; PIDN:AAC05983.1; PID:g2970556
 A:Experimental source: cultivar Century
 C:Genetics:
 A:Gene: AK-HSDH
 A:Introns: 47/2; 69/1; 194/1; 223/3; 325/1; 342/3; 414/2; 443/3; 481/3; 514/3; 579/3; 60
 C:Function: <AK>
 A:Description: catalyzes phosphorylation of aspartate
 C:Function: <HDH>
 A:Description: catalyzes reduction of aspartate beta-semialdehyde into homoserine
 C:Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydroge
 C:Keywords: multifunctional enzyme; oxidoreductase; phosphotransferase
 F:87-552/Domain: aspartate kinase homology <DKI>
 F:555-813/Domain: homoserine dehydrogenase homology <HSD>

Query Match 17.0%; Score 61; DB 2; Length 909;
 Best Local Similarity 41.3%; Pred. No. 71;
 Matches 19; Conservative 5; Mismatches 18; Indels 4; Gaps 2;

QY 2 SPTLTQSTNTHTQSSSSDGLFRSPAHSLPPG---EDGRVEP 44
 Db 15 SPTLTLLHSHDRLEPHSQCRFFFLSRPSHSLKGLTLPGRGAP 59

RESULT 12
 E88042
 protein F56D12.6 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: E88042
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: E88042
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-951 <STO>
 A:Cross-references: GB:chr_11; PIDN:AB66120.1; PID:g2315677; GSPDB:GN00020; CESP:F56D12
 C:Genetics:
 A:Gene: F56D12.6
 A:Map position: 2

Query Match 17.0%; Score 61; DB 2; Length 951;
 Best Local Similarity 43.9%; Pred. No. 74;
 Matches 18; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

QY 11 NTHQTSSSSSDGGLFR-SRPAHSL---PPGEDGRVPEPVD 47
 Db 420 DTHSTASSKSDDKMLNGSAPAHSLDAPIDEKPKNLPVVD 460

RESULT 13
 A53151
 pleiotropic drug resistance protein PDR5 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: drug resistance protein YDR1; protein O3542; protein YOR153w; sporide
 C:Species: Saccharomyces cerevisiae
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 02-Feb-2001
 C:Accession: A53151; A49730; B49730; S48224; S55359; S67041; S34702
 R:Bissinger, P.H.; Kuchler, K.
 J. Biol. Chem. 269, 4180-4186, 1994
 A:Title: Molecular cloning and expression of the Saccharomyces cerevisiae STS1 gene prod
 A:Reference number: A53151; MUID:94140838; PMID:8307980
 A:Accession: A53151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1511 <BIS>
 A:Cross-references: GB:X74113; NID:g395258; PIDN:CAA52212.1; PID:g395259
 R:Balzi, E.; Wang, M.; Leternie, S.; Van Dycck, L.; Goffeau, A.
 J. Biol. Chem. 269, 2206-2214, 1994
 A:Title: PDR5, a novel yeast multidrug resistance conferring transporter controlled by
 A:Reference number: A49730; MUID:94124579; PMID:8294477
 A:Accession: A49730
 A:Molecule type: DNA
 A:Residues: 1-1511 <BAL>
 A:Cross-references: GB:L11922; NID:g402500; PIDN:AAB53769.1; PID:g402501
 A:Accession: B49730
 A:Molecule type: protein
 A:Residues: 2-12 <BAW>
 R:Hirata, D.; Yano, K.; Miyahara, K.; Miyakawa, T.
 Curr. Genet. 26, 285-294, 1994
 A:Title: Saccharomyces cerevisiae YDR1, which encodes a member of the ATP-binding casse
 A:Reference number: S48224; MUID:95188264; PMID:7882421
 A:Accession: S48224
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-1511 <HIR>
 R:Miyakawa, T.
 submitted to the EMBL Data Library, January 1994
 A:Reference number: S55359
 A:Accession: S55359
 A:Molecule type: DNA
 A:Residues: 'M' 62-170, 'L', 172-189, 'I', 191-213, 'T', 215-307, 'V', 309-338, 345-475, 'H', 477-6
 A:Cross-references: EMBL:D26548; NID:g57724; PIDN:BA05547.1; PID:d1006091; PID:g132166
 R:Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Wins
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67032
 A:Accession: S67041
 A:Molecule type: DNA
 A:Residues: 1-1511 <BOR>
 A:Cross-references: EMBL:Z75061; NID:g1420382; PIDN:CAA93359.1; PID:e252040; PID:g142038
 C:Genetics:
 A:Gene: SGD:PDR5; STS1; YDR1
 A:Cross-references: SGD:S0005679; MIPS:YOR153w
 A:Map position: 15R
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
 C:Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
 F:176-386/Domain: ATP-binding cassette homology <ABC1>
 F:520-536/Domain: transmembrane #status predicted <TM1>

C;Genetics: A:Gene: YPO2045

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GenCore version 5.1.6
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Run on: December 4, 2003, 09:43:02 ; Search time 91.6622 Seconds
(without alignments)
1097.894 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303
Perfect score: 1252
Sequence: 1 VELQSLRVNHPNIVKLYGA.....MTHLMRYFPGADEPLQYPCQ 228

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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1252	100.0	1788	4	US-10-158-895-14
3	1252	100.0	2656	2	US-08-685-625A-5
4	1252	100.0	2656	4	US-09-529-279-3
5	1252	100.0	2656	4	US-10-158-895-3
6	1247	99.6	2443	2	US-08-685-625A-1
7	371	29.6	1365	3	US-09-221-235-6
8	371	29.6	1365	3	US-09-221-235-6
9	371	29.6	1365	3	US-09-221-235-6
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13	371	29.6	1365	3	US-09-163-115-6	Sequence 6, Appli
14	371	29.6	1365	3	US-09-221-528-6	Sequence 6, Appli
15	371	29.6	1365	3	US-09-593-553-6	Sequence 6, Appli
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17	371	29.6	2119	4	US-09-399-588-1	Sequence 1, Appli
18	371	29.6	2120	3	US-09-221-235-4	Sequence 4, Appli
19	371	29.6	2120	3	US-09-221-928-4	Sequence 4, Appli
20	371	29.6	2120	3	US-09-221-527-4	Sequence 4, Appli
21	371	29.6	2120	3	US-09-221-236-4	Sequence 4, Appli
22	371	29.6	2120	3	US-09-221-416-4	Sequence 4, Appli
23	371	29.6	2120	3	US-09-221-245-4	Sequence 4, Appli
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28	353.5	28.2	3389	1	US-08-395-580-1	Sequence 1, Appli
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30	338.5	27.0	2505	3	US-09-291-839-3	Sequence 3, Appli
31	338.5	27.0	2505	4	US-09-458-457-3	Sequence 3, Appli
32	338.5	27.0	3025	3	US-09-291-839-1	Sequence 1, Appli
33	338.5	27.0	3025	4	US-09-458-457-1	Sequence 1, Appli
34	335.5	26.8	2505	4	US-09-458-457-9	Sequence 9, Appli
35	335.5	26.8	3026	4	US-09-458-457-7	Sequence 7, Appli
36	323	25.8	2890	1	US-07-928-464-1	Sequence 1, Appli
37	323	25.8	2890	5	PCT-US93-07347-1	Sequence 1, Appli
38	323	25.8	3033	1	US-08-003-311B-1	Sequence 1, Appli
39	323	25.8	3033	1	US-08-261-432-1	Sequence 1, Appli
40	305.5	24.4	1774	4	US-09-312-283C-403	Sequence 403, App
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42	305.5	24.4	3516	3	US-09-188-930-257	Sequence 257, App
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45	294	23.5	1888	3	US-09-188-930-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-529-279-14
; Sequence 14, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-09-529-279-14

Alignment Scores:
Pred. No.: 4e-140
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1788
Matches: 228
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-09-529-279-14 (1-1788)

Qy	1	ValGluLeuArgGlnLeuSerArgValAlaAsnHisProAsnIleValIysLeuTyrGlyAla	20
Db	232	GTAGAGCTTCGGCAGTTATCCGCTGTGAACCATCTCTATATTGTAAAGCTTTATGGAGCC	291
Qy	21	CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal	40
Db	292	TGCTTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGGCTCTTTATATATATGTG	351
Qy	41	LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu	60
Db	352	CTGCATGTGTCTGAACCAATGCCATATTATCTGCTGCCACCAATGAGTTGGTGTTTA	411
Qy	61	GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg	80
Db	412	CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG	471
Qy	81	AspLeuIysProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp	100
Db	472	GACCTGAAACCACCAAACTTACTGCTGGTTGAGGGGGACAGTTCCTAAAAATTTGTGAT	531
Qy	101	PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr	120
Db	532	TTTGGTACAGCTGTGCATTCAGACACATGACCATAACAGGGAGTCTGCTTGG	591
Qy	121	MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr	140
Db	592	ATGGCACCTGAAGTTTTCGAGGTAGTAAATTCACAGTGAAAAATGTGACGCTCTCAGCTCG	651
Qy	141	GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro	160
Db	652	GGTATATTCTTTGGGAAGTGATAACGCTCGAAACCCCTTTGATGAGATTGGTGGCCCA	711
Qy	161	AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu	180
Db	712	GCTTTCGAAATCATGTGGGCTGTTCTATAATGGTACTCGACCACTGATAAAAAATTTA	771
Qy	181	ProIysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro	200
Db	772	CCTAAGCCCATTTGAGAGCCCTGATGACTCGTTGTTGGTCTTAAAGATCCTTCCACAGCGCCCT	831
Qy	201	SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp	220
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Qy	221	GluProLeuGlnTyrProCysGln	228
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RESULT 2
US-10-158-895-14
Sequence 14, Application US/10158895
Patent No. 6551840
GENERAL INFORMATION:
APPLICANT: ONO, KOICHIRO
APPLICANT: OTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/10/158,895
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/529,279
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/230188
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patenlin Ver. 2.1
SEQ ID NO 14
LENGTH: 1788
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Alignment Scores:
Pred. No.: 4e-140 Length: 1788
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservatives: 0
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US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-14 (1-1788)

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Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db 352 CTGCATGGTGTGAACCATTTGCCATATATATACTGCTGCCACGCAATGAGTTGGTGT 411
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
Db 412 CAGTGTTCCTCCAAAGAGTGGCTATCTTCACAGCATGCAACCCAAAGCGCTTAATTCACAGG 471
Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 472 GACCTGAAACACCACCAACTTACTCTGTTGACGGGGGACAGTTCTAAAAATTTGTGAT 531
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Db 532 TTTGGTACAGCCTGTGACATTCACAGACACATGACCAATAACAAGGGAGTGCTGCTTGG 591
Qy 121 MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 140
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Qy 141 GlyIleIleLeuTrpGluValIleThrArgArgLysPropheAspGluIleGlyPro 160
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Qy 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 712 GCTTTCCGAATCATGTGGGCTGTTCAATAATGCTACTCGACACCACTCATATAAAATTTA 771
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTGAGCGCTGATGACTGCTGTTGGTCTAAGAATCCTTCCAGCGCCCT 831
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 832 TCAATGGAGGAATTTGTGAAATAATATGACTCACTTGTATCGCGGTACTTTTCCAGGACGAGAT 891
Qy 221 GluProLeuGlnTrpProCysGln 228
Db 892 GAGCCATTCAGATATCTTGTGCAG 915

RESULT 3
US-08-685-625A-5
; Sequence 5, Application US/08685625A
; Patent No, 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MATSUMOTO, Kunhiro
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
; TITLE OF INVENTION: TRANSDUCTION SYSTEM

```

NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,625A
 FILING DATE: 24-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-253549
 FILING DATE: 29-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M.
 REGISTRATION NUMBER: 36,607
 REFERENCE/DOCKET NUMBER: 001560-267
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2656 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 183..1922
 US-08-685-625A-5

Alignment Scores:
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 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
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 Db 408 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGCC 467
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
 Db 468 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATAATG 527
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 528 CTCATGGGTGCTGAACCATTCGCATATTACTGTGCTGCCACGCAATGAGTTGGTGT 587
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
 Db 588 CAGTGTTCACAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTTAATTCACAGG 647
 QY 81 AspLeuLysProAsnLeuLeuValAlaGlyThrValLeuLysIleCysAsp 100
 Db 648 GACCTGAACACCAACCACTTACTGCTGGTTGAGGGGGGACACTTCTAAAAATTTGTGAT 707
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
 Db 708 TTTGGTACAGCTGTGACATTCACACATGACCAATAACAAGGGGAGTGTCTGTGG 767

QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
 Db 768 ATGCACCTTGAAGTTTGTGAAGGTAGTAATTACAGTGAATAATGTACGTCTTCAGCTGG 827
 QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
 Db 828 GGTATTATTCTTTGGGAAGTGATAACCGTGGAAACCCCTTTGATGAGATTGGTGGCCCA 887
 QY 161 AlaPheArgIleMetTyrPheAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
 Db 888 GCTTTCCGAATCATGTGGCTGTTTCAATAATGTTACTCGACCCACCTGATAAAAAATTTA 947
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
 Db 948 CCTAAGCCCATTTGAGACCTGATGACTCGTGTGTGGTCTAAAGATCTCTCCACGCGCT 1007
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
 Db 1008 TCAATGGAGGAATTTGAAAAATAATGACTCACTTGAATGCGTACTTTCAGGAGCAGAT 1067
 QY 221 GluProLeuGlnTyrProCysGln 228
 Db 1068 GAGCCATTACAGTATCTCTGTCTCAG 1091
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 US-09-529-279-3
 ; Sequence 3, Application US/09529279
 ; Patent No. 6451617
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/09/529,279
 ; CURRENT FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 2656
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (183)..(1919)
 US-09-529-279-3

Alignment Scores:
 Pred. No.: 7,26e-140 Length: 2656
 Score: 1252.00 Matches: 228
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-830-144-2_COPY_76_303 (1-228) x US-09-529-279-3 (1-2656)
 QY 1 ValGluLeuArgGlnLeuSerArgValAlaHisProAsnIleValLysLeuTyrGlyAla 20
 Db 408 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGCC 467
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
 Db 468 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATAATG 527
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 Db 528 CTCATGGGTGCTGAACCATTCGCATATTACTGTGCTGCCACGCAATGAGTTGGTGT 587

QY	61	GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuLeHisArg	80
Db	588	CAGTGTTCACAGGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAATTCACAGG	647
QY	81	AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp	100
Db	648	GACCTGAAACCCAACTTACTGCTGGTTGCAGGGGGGACAGTCTCTAAAAAATTTGTGAT	707
QY	101	PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr	120
Db	708	TTTGGTACAGCCTGTGACATTCAGACACACATGACCAATAACAGGGGAGTGTCTGTGG	767
QY	121	MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr	140
Db	768	ATGGCACCTGAGATTTTGAAGGTAGTAATTCAGTGAATAATCTGACGCTCTTCAGCTGG	827
QY	141	GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro	160
Db	828	GGTATTATTCTTTGGGAAGTGATAACGCGTCGAAACCCCTTTGATGAGATGTGGTGCCCA	887
QY	161	AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu	180
Db	888	GCITTCGAATCATGTGGCGTGTTCATPAATGTGACTCGACACACCATGATATAAAAAATT	947
QY	181	ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro	200
Db	948	CCATAAGCCCAATTGAGACCGCTGATGACTCGTGTGTGTGGTCTTAAGAGATCTTCCAGCGCCCT	1007
QY	201	SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp	220
Db	1008	TCAATGAGGAATTTGGAAATAATGACTCACTCTTGATGCGGTACTTTCCAGGACGAGAT	1067
QY	221	GluProLeuGlnTyrProCysGln	228
Db	1068	GAGCCATTACAGTATCTCTGTGCAG	1091

5 T.11153a

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US-10-158-895-3
; Sequence 3, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)..(1919)
US-10-158-895-3

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Alignment Scores:		
Pred. No.:	7.26e-140	Length: 2656
Score:	1252.00	Matches: 228
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	4	Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-3 (1-2656)

Qy	1	ValGluLeuArgGlnLeuSerArgValAenHisProAsnIleValLysIleuTyrGlyAla	20
Db	408	GTAGACCTTCGGCAGTTATCCCGTGTGAACCACTCTAATATTGTAAGCTTTATGAGCC	467
Qy	21	CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyCysSerLeuTyrAsnVal	40
Db	468	TGCTTGAATCCAGTGTGTCTGTGATGGAAATAGCTGGAAGGGGGCTCTTTATATAATGTG	527
Qy	41	LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu	60
Db	528	CTGCATGGTGCTGAACCATGGCCATATATACCTGCTGCCACCACCAATGAGTGGTGTTA	587
Qy	61	GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg	80
Db	588	CAGTGTTCACAGAGTGGCTATCTTCACAGATGCACACCCCAAGCGCTAATTCACAGG	647
Qy	81	AspLeuIleProProLeuLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp	100
Db	648	GACCTGAACCAACCAACTTACTGCTGGTTGTCAGGGGGACAGTTCTTAAAAATTTGTGAT	707
Qy	101	PheClyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr	120
Db	708	TTTGGTACAGCCCTGTGACATTCAGACACACATCACCAATAACAGGGAGTGTCTGTGG	767
Qy	121	MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr	140
Db	768	ATGGCACTCGAAGTTTTTGAAGGTAGTAATTACAGTGAAAAATGTGACGCTCTTCAGCTGG	827
Qy	141	GlyIleLeuLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro	160
Db	828	GGTATTATTCTTTGGGAAGTGATAACGCGTCGGAACCCCTTGTATGAGATTGCTGGGCCCA	887
Qy	161	AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu	180
Db	888	GCITTCGAATCATGTGGGCTGTTCATAATGGTATCTCACACACCATGATAAAAAATTTTA	947
Qy	181	ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro	200
Db	948	CCTAAGGCCCATGTGAGGCCGTGATGACTCGTTTGTGTCTTAAGATCCCTCCACGGCCCT	1007
Qy	201	SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp	220
Db	1008	TCAATGAGGAAATGTGAAAAATAATGACTCACTTGATGCGGTACTTTCCAGGAGCAGAT	1067
Qy	221	GluProLeuGlnTyrProCysGln	228
Db	1068	GAGCCATTACAGTATCTCTGTGAG	1091

DEPT. 6

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RESJULI 6
US-08-685-625A-1
; Sequence 1, Application US/08685625A
; Patent No. 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
; TITLE OF INVENTION: TRANSDUCTION SYSTEM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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Db 562 GACACATATCTCTAGGTGTGCTCTCGGAGATGCTTACAGGAGGTCCCTTTTAAA 621
QY 156 GluileGlyProAlaPheArgileMetTrp---AlaValHisAsnGlyThrArgPro 174
Db 622 GGTITGGAAGA-----TTACAAGTAGCTTGGCTTGTAGTGGAAGGAGAGATTA 675
QY 175 ProLeuileLysAsnLeuProLysProileGluSerLeuMetThrArgCysTrpSerLys 194
Db 676 ACCATTCCAAGCAGTGGCCCAAGAGTTTGTCTGAAGTGTATACATCAGTGTGGGAAGCT 735
QY 195 AspProSerGlnArgProSerMetGluLluileValLysIleMet 209
Db 736 GATGCCAAGAAACGGCCATCATTCACGCAAAATCAITTCATCTG 780

RESULT 8

US-09-221-928-6
; Sequence 6, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,928
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-928-6

Alignment Scores:
Pred. No.: 9,19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-928-6 (1-1365)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAlaCys 21
Db 157 GAGCGAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGAGTAATT 216
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyzAlaGluGlyGlySerLeuTyAsn 39
Db 217 CTTGAACCTCCCACTATGCAATGTGCACAGATATGCTTCTCGGATCACTCTATGAT 276
QY 40 ValLeuHisGly-----AlaGluProLeuProTyTyThrAlaAlaHisAlaMetSer 57
Db 277 TACATTAAACAGTAACAGAGTGAGGAGATG-----GATATGGATCATCATATGACC 327
QY 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyzLeuHisSerMetGlnProLysAlaLeu 77
Db 328 TGGGCCACTGATGTAGCCAAAGGATGCATTTATATATGAGGCTCTCTCAAGGTG 387
QY 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
Db 388 ATTACAGAGACCTCAAGTCAGAAAGGTTGTTATATAGTCTGTATGGA---GTACTGAAG 444
QY 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db 445 ATCTGTGACTTTGGT---GCTCTCGGTTCCATTAACCATACACACACATGCTCTGGTT 501
QY 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTySerGluLysCys 135

Db 502 GGAACCTTTCCATGATGGCTCCAGAACTTATCCAGAGTCTCCCTGTGTGCAGAAACTTGT 561
QY 136 AspValPheSerTrpGlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db 562 GACACATATCTCTAGGTGTGCTCTCGGAGATGCTTACAGGAGGTCCCTTTTAAA 621
QY 156 GluileGlyProAlaPheArgileMetTrp---AlaValHisAsnGlyThrArgPro 174
Db 622 GGTITGGAAGA-----TTACAAGTAGCTTGGCTTGTAGTGGAAGGAGAGATTA 675
QY 175 ProLeuileLysAsnLeuProLysProileGluSerLeuMetThrArgCysTrpSerLys 194
Db 676 ACCATTCCAAGCAGTGGCCCAAGAGTTTGTCTGAAGTGTATACATCAGTGTGGGAAGCT 735
QY 195 AspProSerGlnArgProSerMetGluLluileValLysIleMet 209
Db 736 GATGCCAAGAAACGGCCATCATTCACGCAAAATCAITTCATCTG 780

RESULT 9

US-09-221-527-6
; Sequence 6, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; CURRENT FILING DATE: 1998-12-28
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-527-6

Alignment Scores:
Pred. No.: 9,19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-527-6 (1-1365)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAlaCys 21
Db 157 GAGCGAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGAGTAATT 216
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyzAlaGluGlyGlySerLeuTyAsn 39
Db 217 CTTGAACCTCCCACTATGCAATGTGCACAGATATGCTTCTCGGATCACTCTATGAT 276
QY 40 ValLeuHisGly-----AlaGluProLeuProTyTyThrAlaAlaHisAlaMetSer 57
Db 277 TACATTAAACAGTAACAGAGTGAGGAGATG-----GATATGGATCATCATATGACC 327
QY 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyzLeuHisSerMetGlnProLysAlaLeu 77
Db 328 TGGGCCACTGATGTAGCCAAAGGATGCATTTATATATGAGGCTCTCTCAAGGTG 387
QY 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
Db 388 ATTACAGAGACCTCAAGTCAGAAAGGTTGTTATATAGTCTGTATGGA---GTACTGAAG 444
QY 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115

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Db      445 ATCTGTGACATTGGT---GCCTCTCGGTTCCATAACCAACACACACATGTCCTTGGTT 501
Qy      116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
Db      502 GGAATCTTCCCATGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTCCAGAAACTTGT 561
Qy      136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgAlaGlyGlyProPheAsp 155
Db      562 GACACATATCTATGTTGGTTCTCTGGGAGATGCTTAACAGGAGGTCCTCCCTTTTAAA 621
Qy      156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db      622 GGTTTGAAGGA-----TTACAAGTAGCTTGGCTTGTAGTGGAAACACAGAGATT 675
Qy      175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db      676 ACCATTCCAAAGCAGTTCCTCCAGAAAGTTTCTGGAAGTGTACATCATGTTGGGAAGCT 735
Qy      195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db      736 GATGCCAAGAAACGCCCATCATTTCAAGCAATCATTTCAATCCTG 780

RESULT 10
US-09-221-236-6
; Sequence 6, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-236-6

Alignment Scores:
Pred. No.: 9.19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-236-6 (1-1365)
Qy      2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db      157 GAGCGCAAAATACTCAGTGTCTCCAGTACAGAAACATCATCCAGTTTATGAGTAATT 216
Qy      22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsn 39
Db      217 CTTGAACCTCCCAACTATGCGCATGTCCAGAAATATGCTTCTCGGATCCTCTATGAT 276
Qy      40 ValLeuHisGly-----AlaGluProLeuProTyrThrAlaAlaHisAlaMetSer 57
Db      277 TACATTAAACAGTAACAGAAGTAGGAGATG-----GATATGATCACATTATGACC 327
Qy      58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
Db      328 TGGGCCACTGATGATGCCAAAGGAATGCAATATTATCATATGAGGCTCCTGCAAGGTG 387
Qy      78 IleHisArgAspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97

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Db      388 ATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGTCTGTATGGA---GTACTGAAG 444
Qy      98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db      445 ATCTGTGACATTGGT---GCCTCTCGGTTCCATAACCAACACACATGTCCTTGGTT 501
Qy      116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
Db      502 GGAATCTTCCCATGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTCCAGAAACTTGT 561
Qy      136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgAlaGlyGlyProPheAsp 155
Db      562 GACACATATCTATGTTGGTTCTCTGGGAGATGCTTAACAGGAGGTCCTCCCTTTTAAA 621
Qy      156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db      622 GGTTTGAAGGA-----TTACAAGTAGCTTGGCTTGTAGTGGAAACACAGAGATT 675
Qy      175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db      676 ACCATTCCAAAGCAGTTCCTCCAGAAAGTTTCTGGAAGTGTACATCATGTTGGGAAGCT 735
Qy      195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db      736 GATGCCAAGAAACGCCCATCATTTCAAGCAATCATTTCAATCCTG 780

RESULT 11
US-09-221-416-6
; Sequence 6, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-416-6

Alignment Scores:
Pred. No.: 9.19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-416-6 (1-1365)
Qy      2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db      157 GAGCGCAAAATACTCAGTGTCTCCAGTACAGAAACATCATCCAGTTTATGAGTAATT 216
Qy      22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsn 39
Db      217 CTTGAACCTCCCAACTATGCGCATGTCCAGAAATATGCTTCTCGGATCCTCTATGAT 276
Qy      40 ValLeuHisGly-----AlaGluProLeuProTyrThrAlaAlaHisAlaMetSer 57
Db      277 TACATTAAACAGTAACAGAAGTAGGAGATG-----GATATGATCACATTATGACC 327
Qy      58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77

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Db 328 TGGGCCACTGATGTACCAAGGAATGCAATATTTACATATGAGGCTCCTCTCAGGTG 387
      ::::::::::::::::::::
Qy 78 IleHisArgAspLeuLeuValAlaGlyThrValLeuLys 97
      ::::::::::::::::::::
Db 388 ATTCACAGAGACTCAAGTCAAGAAACGTTGTATAGCTGCTGATGGA---GTACTGAAG 444
      ::::::::::::::::::::
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
      ::::::::::::::::::::
Db 445 ATCTGTGACTTTGGT---GCCTCTCGTTCCTCAATACACACACACATGCTCCTTGGTT 501
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Qy 116 GlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
      ::::::::::::::::::::
Db 502 GGAACATTTCCCATGGATGCTCCAGAAAGTTATCCAGAGTCTCCTGTGTCAGAACTTGT 561
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Qy 136 AspValPheSerTyrGlyIleLeuTyrGluValIleThrArgArgLysPropheAsp 155
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Db 562 GACACATATTCCTATGTTGGTTCCTCTGGAGATGCTAACAAAGGAGGTCCCTTTAAA 621
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Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
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Db 622 GGTTTGGAAGGA-----TTACAAGTAGCTTGGCTTGTAGTGGAATAAACGAGAGATTA 675
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Qy 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrSerLys 194
      ::::::::::::::::::::
Db 676 ACCATTCCAAGCAGTTGCCCAAGATTTTGTCTGAACTGTTCATCATCGTTGGGAAGCT 735
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Qy 195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
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Db 736 GATGCCAAGAAACGGCCATCATTCACGAATCATTTCAATCTCTG 780
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RESULT 12

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US-09-221-245-6
; Sequence 6, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; EARLIER FILING DATE: 1998-12-28
; CURRENT APPLICATION NUMBER: US 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-245-6
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Alignment Scores:
Pred. No.: 9.19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8
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US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-245-6 (1-1365)

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Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
      ::::::::::::::::::::
Db 157 GAGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 216
      ::::::::::::::::::::
Qy 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
      ::::::::::::::::::::
Db 217 CTTGAACCTCCCAACTATGGCAATGTCACAGAATATGCTCTCTGGGATCACTCTATGAT 276
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Qy 40 ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
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Db 277 TACATTAAAGTAAACAGAAAGTGAGGAGATG-----GATATGGATCACATTATGACC 327
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Qy 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
      ::::::::::::::::::::
Db 328 TGGGCCACTGATGTACCAAGGAATGCAATATTTACATATGAGGCTCCTCTCAGGTG 387
      ::::::::::::::::::::
Qy 78 IleHisArgAspLeuLeuValAlaGlyThrValLeuLys 97
      ::::::::::::::::::::
Db 388 ATTCACAGAGACTCAAGTCAAGAAACGTTGTATAGCTGCTGATGGA---GTACTGAAG 444
      ::::::::::::::::::::
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
      ::::::::::::::::::::
Db 445 ATCTGTGACTTTGGT---GCCTCTCGTTCCTCAATACACACACACATGCTCCTTGGTT 501
      ::::::::::::::::::::
Qy 116 GlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
      ::::::::::::::::::::
Db 502 GGAACATTTCCCATGGATGCTCCAGAAAGTTATCCAGAGTCTCCTGTGTCAGAACTTGT 561
      ::::::::::::::::::::
Qy 136 AspValPheSerTyrGlyIleLeuTyrGluValIleThrArgArgLysPropheAsp 155
      ::::::::::::::::::::
Db 562 GACACATATTCCTATGTTGGTTCCTCTGGAGATGCTAACAAAGGAGGTCCCTTTAAA 621
      ::::::::::::::::::::
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
      ::::::::::::::::::::
Db 622 GGTTTGGAAGGA-----TTACAAGTAGCTTGGCTTGTAGTGGAATAAACGAGAGATTA 675
      ::::::::::::::::::::
Qy 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrSerLys 194
      ::::::::::::::::::::
Db 676 ACCATTCCAAGCAGTTGCCCAAGATTTTGTCTGAACTGTTCATCATCGTTGGGAAGCT 735
      ::::::::::::::::::::
Qy 195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
      ::::::::::::::::::::
Db 736 GATGCCAAGAAACGGCCATCATTCACGAATCATTTCAATCTCTG 780
      ::::::::::::::::::::
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RESULT 13

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US-09-163-115-6
; Sequence 6, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-163-115-6
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Alignment Scores:
Pred. No.: 9.19e-35 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8
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US-09-830-144-2_COPY_76_303 (1-228) x US-09-163-115-6 (1-1365)

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Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
      ::::::::::::::::::::
Db 157 GAGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 216
      ::::::::::::::::::::
Qy 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
      ::::::::::::::::::::
Db 217 CTTGAACCTCCCAACTATGGCAATGTCACAGAATATGCTCTCTGGGATCACTCTATGAT 276
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Search completed: December 4, 2003, 12:44:58
Job time : 97.6622 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:36:53 ; Search time 84.7297 Seconds
(without alignments)
3563.166 Million cell updates/sec

Title: US-09-830-144-1_COPY_408_1091

Perfect score: 684

Sequence: 1 gttagagcttggcagttatc.....cattacagttacgttgcag 684

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	1788	4	US-09-529-279-14
2	684	100.0	1788	4	US-10-158-895-14
3	684	100.0	2656	2	US-08-685-625A-5
4	684	100.0	2656	4	US-09-529-279-3
5	684	100.0	2656	4	US-10-158-895-3
6	585.4	85.6	2443	2	US-08-685-625A-1
7	54.6	8.0	1365	3	US-09-221-235-6
8	54.6	8.0	1365	3	US-09-221-928-6
9	54.6	8.0	1365	3	US-09-221-527-6
10	54.6	8.0	1365	3	US-09-221-236-6
11	54.6	8.0	1365	3	US-09-221-416-6
12	54.6	8.0	1365	3	US-09-221-245-6
13	54.6	8.0	1365	3	US-09-163-115-6
14	54.6	8.0	1365	3	US-09-221-528-6
15	54.6	8.0	1365	3	US-09-593-553-6
16	54.6	8.0	1365	3	US-09-221-237-6
17	54.6	8.0	2119	4	US-09-399-588-1
18	54.6	8.0	2120	3	US-09-221-235-4
19	54.6	8.0	2120	3	US-09-221-928-4
20	54.6	8.0	2120	3	US-09-221-527-4
21	54.6	8.0	2120	3	US-09-221-236-4
22	54.6	8.0	2120	3	US-09-221-416-4
23	54.6	8.0	2120	3	US-09-221-245-4
24	54.6	8.0	2120	3	US-09-163-115-4
25	54.6	8.0	2120	3	US-09-221-528-4
26	54.6	8.0	2120	3	US-09-593-553-4
27	54.6	8.0	2120	3	US-09-221-237-4

28	52	7.6	1251	2	US-09-211-930-2	Sequence 2, Appli
29	52	7.6	1251	3	US-09-340-993-2	Sequence 2, Appli
30	52	7.6	1251	4	US-09-468-442-2	Sequence 2, Appli
31	52	7.6	1353	2	US-09-211-930-8	Sequence 8, Appli
32	52	7.6	1353	3	US-09-340-993-8	Sequence 8, Appli
33	52	7.6	1353	4	US-09-468-442-8	Sequence 8, Appli
34	52	7.6	1542	4	US-09-345-473E-13	Sequence 13, Appli
35	52	7.6	3201	2	US-09-211-930-1	Sequence 1, Appli
36	52	7.6	3201	3	US-09-340-993-1	Sequence 1, Appli
37	52	7.6	3201	4	US-09-468-442-1	Sequence 1, Appli
38	49.4	7.2	1979	4	US-09-685-462-3	Sequence 3, Appli
39	49.4	7.2	2028	2	US-09-211-930-12	Sequence 12, Appli
40	49.4	7.2	2028	3	US-09-340-993-12	Sequence 12, Appli
41	49.4	7.2	2028	4	US-09-468-442-12	Sequence 12, Appli
42	45.2	6.6	2890	1	US-07-928-464-1	Sequence 1, Appli
43	45.2	6.6	2890	5	PCT-US93-07347-1	Sequence 1, Appli
44	45.2	6.6	3033	1	US-08-003-311B-1	Sequence 1, Appli
45	45.2	6.6	3033	1	US-08-261-432-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-529-279-14
; Sequence 14, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(1776)
US-09-529-279-14

Query Match	100.0%;	Score 684;	DB 4;	Length 1788;
Best Local Similarity	100.0%;	Pred. No. 1.6e-218;		
Matches 684;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GTAGAGCTTGGCAGTATCCCGTGTGAACCAATCTTAATTTGTAAGCTTTATGAGCC	60	
Db	232	GTAGAGCTTGGCAGTATCCCGTGTGAACCAATCTTAATTTGTAAGCTTTATGAGCC	291	
QY	61	TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTTTATATATG	120	
Db	292	TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGGCTTTATATATG	351	
QY	121	CTGCATGGTGTGAACCAATTCATATATCTGCTGCCACGCAATGAGTTGGTTT	180	
Db	352	CTGCATGGTGTGAACCAATTCATATATCTGCTGCCACGCAATGAGTTGGTTT	411	
QY	181	CAGTGTTCACAGAGTGCTTATCTTACAGCATGCAACCCAAAGCGTAAATTCACAG	240	
Db	412	CAGTGTTCACAGAGTGCTTATCTTACAGCATGCAACCCAAAGCGTAAATTCACAG	471	
QY	241	GACCTGAACCAACCAACTTACTGCTGTCAGGGGGACAGTTCTTAAATTTGTGAT	300	
Db	472	GACCTGAACCAACCAACTTACTGCTGTCAGGGGGACAGTTCTTAAATTTGTGAT	531	

Db 352 CTGCATGCTGCTGAACCAATGCCATATATATATCTGCTGCCACGCAATGAGTTGGTGTTA 411
Qy 181 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGCATGCAACCAAGGCGTAAATTCACAGG 240
Db 412 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGCATGCAACCAAGGCGTAAATTCACAGG 471
Qy 241 GACCTGAACCAACCAACTTACTGCTGTTGCGAGGGGACAGTTTCTAAAAATTTGTGAT 300
Db 472 GACCTGAACCAACCAACTTACTGCTGTTGCGAGGGGACAGTTTCTAAAAATTTGTGAT 531
Qy 301 TTTGTCAGAGCTGTGACATTCAGACACACATGACCAATACAGAGGAGTGTCTGCTGG 360
Db 532 TTTGTCAGAGCTGTGACATTCAGACACACATGACCAATACAGAGGAGTGTCTGCTGG 591
Qy 361 ATGGCACCCTGAGTTTTCGAGGTAGTAAATACAGTGAATAATGACGCTTTCAGCTGG 420
Db 592 ATGGCACCCTGAGTTTTCGAGGTAGTAAATACAGTGAATAATGACGCTTTCAGCTGG 651
Qy 421 GGTATTATTTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGTAGTGAATTCGTCGCCA 480
Db 652 GGTATTATTTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGTAGTGAATTCGTCGCCA 711
Qy 481 GCTTTCCGAATCATGTGGGCTCTTCAATATGCTGACACACCTGATGATAAAATTTA 540
Db 712 GCTTTCCGAATCATGTGGGCTCTTCAATATGCTGACACACCTGATGATAAAATTTA 771
Qy 541 CTTAAGCCCATTCAGAGCTGATGACTCGTTGCTGCTAAAGATCCTTCCAGAGCCCT 600
Db 772 CTTAAGCCCATTCAGAGCTGATGACTCGTTGCTGCTAAAGATCCTTCCAGAGCCCT 831
Qy 601 TCAATGGAGGAAATTTGAAATAATGACTCACTTTGATCGGTACTTTCCAGAGCAGAT 660
Db 832 TCAATGGAGGAAATTTGAAATAATGACTCACTTTGATCGGTACTTTCCAGAGCAGAT 891
Qy 661 GAGCCATTACAGTATCCTTTGTGAC 684
Db 892 GAGCCATTACAGTATCCTTTGTGAC 915

RESULT 3
US-08-685-625A-5
; Sequence 5, Application US/08685625A
; Patent No. 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MAISUMOTO, Kunihiro
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
; TITLE OF INVENTION: TRANSDUCTION SYSTEM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,625A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 7-253549
; FILING DATE: 29-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M. 36,607
; REGISTRATION NUMBER: 001560-267
; REFERENCE/DOCKET NUMBER: 001560-267

1091/99 210

1022

Qy 301 TTTGTCAGAGCTGTGACATTCAGACACACATGACCAATACAGAGGAGTGTCTGCTGG 360
Db 532 TTTGTCAGAGCTGTGACATTCAGACACACATGACCAATACAGAGGAGTGTCTGCTGG 591
Qy 361 ATGGCACCCTGAGTTTTCGAGGTAGTAAATACAGTGAATAATGACGCTTTCAGCTGG 420
Db 592 ATGGCACCCTGAGTTTTCGAGGTAGTAAATACAGTGAATAATGACGCTTTCAGCTGG 651
Qy 421 GGTATTATTTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGTAGTGAATTCGTCGCCA 480
Db 652 GGTATTATTTCTTTGGGAAGTGATAACGGCTCGGAAACCTTTTGTAGTGAATTCGTCGCCA 711
Qy 481 GCTTTCCGAATCATGTGGGCTCTTCAATATGCTGACACACCTGATGATAAAATTTA 540
Db 712 GCTTTCCGAATCATGTGGGCTCTTCAATATGCTGACACACCTGATGATAAAATTTA 771
Qy 541 CTTAAGCCCATTCAGAGCTGATGACTCGTTGCTGCTAAAGATCCTTCCAGAGCCCT 600
Db 772 CTTAAGCCCATTCAGAGCTGATGACTCGTTGCTGCTAAAGATCCTTCCAGAGCCCT 831
Qy 601 TCAATGGAGGAAATTTGAAATAATGACTCACTTTGATCGGTACTTTCCAGAGCAGAT 660
Db 832 TCAATGGAGGAAATTTGAAATAATGACTCACTTTGATCGGTACTTTCCAGAGCAGAT 891
Qy 661 GAGCCATTACAGTATCCTTTGTGAC 684
Db 892 GAGCCATTACAGTATCCTTTGTGAC 915

RESULT 2
US-10-158-895-14
; Sequence 14, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Query Match 100.0%; Score 684; DB 4; Length 1788;
Best Local Similarity 100.0%; Pred. No. 1.6e-218;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCCTAATATGTAAGCTTTATGAGCC 60
Db 232 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCCTAATATGTAAGCTTTATGAGCC 291
Qy 61 TGCTTGAATCCAGTGTCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 292 TGCTTGAATCCAGTGTCTGTCATGATGATGATGATGATGATGATGATGATGATGATG 351
Qy 121 CTGCATGCTGCTGAACCAATGCCATATATATATCTGCTGCCACGCAATGAGTTGGTGTTA 180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2656 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 183..1922
US-08-685-625A-5

APPLICANT: ONO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/09/529,279
CURRENT FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/290188
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 3
LENGTH: 2656
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (183)..(1919)
US-09-529-279-3

Query Match 100.0%; Score 684; DB 2; Length 2656;
Best Local Similarity 100.0%; Pred. No. 2e-218;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
DB GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 467

QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
DB TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527

QY 121 CTGCATGCTGTGAACCATTCGCATATATATCTGTCGCCACGCAATGAGTTGGTGTGTTA 180
DB CTGCATGCTGTGAACCATTCGCATATATATCTGTCGCCACGCAATGAGTTGGTGTGTTA 587

QY 181 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 240
DB CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 647

QY 241 GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAATAATTTGTGAT 300
DB GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAATAATTTGTGAT 707

QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 360
DB TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 767

QY 361 ATGGCACCCTGAAGTTTGTGAAGGTAGTAATTACAGTGCAAAAATGTGACGCTTCAGCTGG 420
DB ATGGCACCCTGAAGTTTGTGAAGGTAGTAATTACAGTGCAAAAATGTGACGCTTCAGCTGG 827

QY 421 GGTATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGATTGGTGCCCA 480
DB GGTATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGATTGGTGCCCA 887

QY 481 GCCTTCGGAATCATGTGGGCTGTTCAATATGTTGCTAAGATCCTTCCAGCGCCCT 600
DB GCCTTCGGAATCATGTGGGCTGTTCAATATGTTGCTAAGATCCTTCCAGCGCCCT 1007

QY 541 CCTAAGCCCATTCAGAGCTGATGACTCGTGTGTTGGTCTAAGATCCTTCCAGCGCCCT 600
DB CCTAAGCCCATTCAGAGCTGATGACTCGTGTGTTGGTCTAAGATCCTTCCAGCGCCCT 1007

QY 601 TCNATGGAGAAATTTGTAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 660
DB TCNATGGAGAAATTTGTAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 1067

QY 661 GAGCCATTACAGTATCCTTGTGAC 684
DB GAGCCATTACAGTATCCTTGTGAC 1091

RESULT 4

US-09-529-279-3
Sequence 3, Application US/09529279
Patent No. 6451617
GENERAL INFORMATION:

Query Match 100.0%; Score 684; DB 4; Length 2656;
Best Local Similarity 100.0%; Pred. No. 2e-218;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 60
DB GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGGAGCC 467

QY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
DB TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527

QY 121 CTGCATGCTGTGAACCATTCGCATATATATCTGTCGCCACGCAATGAGTTGGTGTGTTA 180
DB CTGCATGCTGTGAACCATTCGCATATATATCTGTCGCCACGCAATGAGTTGGTGTGTTA 587

QY 181 CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 240
DB CAGTGTTCCTCCAAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 647

QY 241 GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAATAATTTGTGAT 300
DB GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTAATAATTTGTGAT 707

QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 360
DB TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTGG 767

QY 361 ATGGCACCCTGAAGTTTGTGAAGGTAGTAATTACAGTGCAAAAATGTGACGCTTCAGCTGG 420
DB ATGGCACCCTGAAGTTTGTGAAGGTAGTAATTACAGTGCAAAAATGTGACGCTTCAGCTGG 827

QY 421 GGTATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGATTGGTGCCCA 480
DB GGTATTATCTTTGGGAAGTGATAACCGCTCGGAAACCCCTTTGATGAGATTGGTGCCCA 887

QY 481 GCCTTCGGAATCATGTGGGCTGTTCAATATGTTGCTAAGATCCTTCCAGCGCCCT 600
DB GCCTTCGGAATCATGTGGGCTGTTCAATATGTTGCTAAGATCCTTCCAGCGCCCT 1007

QY 541 CCTAAGCCCATTCAGAGCTGATGACTCGTGTGTTGGTCTAAGATCCTTCCAGCGCCCT 600
DB CCTAAGCCCATTCAGAGCTGATGACTCGTGTGTTGGTCTAAGATCCTTCCAGCGCCCT 1007

QY 601 TCNATGGAGAAATTTGTAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 660
DB TCNATGGAGAAATTTGTAATAATGACTCACTTGTGCGGTACTTTCCAGGAGCAGAT 1067

QY 661 GAGCCATTACAGTATCCTTGTGAC 684
DB GAGCCATTACAGTATCCTTGTGAC 1091

Db 948 CCTAAGCCATTGAGAGCCTGATGACTCGTTGTTGGTCTTAAAGATCCTTCCAGGCGCCCT 1007
Qy 601 TCATGGAGGAAATGTGAAATATGATGACTCATTGATGCGGTACTTTCCAGGAGCAGAT 660
Db 1008 TCATGGAGGAAATGTGAAATATGATGACTCATTGATGCGGTACTTTCCAGGAGCAGAT 1067
Qy 661 GAGCCATTACAGTATCCTTTGTCAG 684
Db 1068 GAGCCATTACAGTATCCTTTGTCAG 1091

NO

RESULT 6
US-08-685-625A-1
; Sequence 1, Application US/08685625A
; Patent No. 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MATSUMOTO, Kunihiko
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
; TITLE OF INVENTION: TRANSDUCTION SYSTEM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,625A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-253549
; FILING DATE: 29-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-8620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 157..1893
; US-08-685-625A-1

Query Match 85.6%; Score 585.4; DB 2; Length 2443;
Best Local Similarity 91.1%; Pred. No. 1.8e-185;
Matches 622; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGGCAGTTATCCGCTGTCGACCACTTAAATTTGTAAGCTTTATGGAGCC 60
Db 382 GTGAGCTCCGGCAGTTATCCGCTGTCGACCACTTAAATTTGTAAGCTTTATGGAGCC 441
Qy 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 442 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 501
Qy 121 CTGCATGTGTGTGAACCAATTGCCATATTTATCTGCTGCCACCAATGAGTTGGTTTA 180

US-10-158-895-3
; Sequence 3, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)..(1919)
; US-10-158-895-3

Query Match 100.0%; Score 684; DB 4; Length 2656;
Best Local Similarity 100.0%; Pred. No. 2e-218;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGGCAGTTATCCGCTGTCGACCACTTAAATTTGTAAGCTTTATGGAGCC 60
Db 408 GTAGAGCTTCGGCAGTTATCCGCTGTCGACCACTTAAATTTGTAAGCTTTATGGAGCC 467
Qy 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 120
Db 468 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 527
Qy 121 CTGCATGTGTGAAACCAATTGCCATATTTATCTGCTGCCACCAATGAGTTGGTTTA 180
Db 528 CTGCATGTGTGAAACCAATTGCCATATTTATCTGCTGCCACCAATGAGTTGGTTTA 587
Qy 181 CAGTGTTCCTCAAGGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGCTAAATTCACAGG 240
Db 588 CAGTGTTCCTCAAGGAGTGGCTTATCTTCAGCATGCAACCCAAAGCGCTAAATTCACAGG 647
Qy 241 GACCTGAAACCAACCAACTTACTGCTGTTGCAGGGGGGACAGTTCTTAAATTTGTGAT 300
Db 648 GACCTGAAACCAACCAACTTACTGCTGTTGCAGGGGGGACAGTTCTTAAATTTGTGAT 707
Qy 301 TTGTTGACAGCTGTGACATTCAGACACATGACCAATACAGGGGAGTGTCTGTGG 360
Db 708 TTGTTGACAGCTGTGACATTCAGACACATGACCAATACAGGGGAGTGTCTGTGG 767
Qy 361 ATGGCAGCTGAAGTTTGTGAAGGTAGTAAATACAGTGAATAATGTGACGCTTTCAGCTGG 420
Db 768 ATGGCAGCTGAAGTTTGTGAAGGTAGTAAATACAGTGAATAATGTGACGCTTTCAGCTGG 827
Qy 421 GGTATTATCTTTGGGAAGTATACCGCTGCGAAACCCCTTTGATGAGATTGTTGGCCCA 480
Db 828 GGTATTATCTTTGGGAAGTATACCGCTGCGAAACCCCTTTGATGAGATTGTTGGCCCA 887
Qy 481 GCTTTCCGAATCATGTGGGCTGTTCAATGCTGACCACTGACCACTGATATAAATTTA 540
Db 888 GCTTTCCGAATCATGTGGGCTGTTCAATGCTGACCACTGACCACTGATATAAATTTA 947
Qy 541 CCTAAGCCATTGAGAGCCTGATGACTCGTTGTTGGTCTTAAAGATCCTTCCAGGCGCCT 600

Db 502 CTGCAATGGTCTGAACCAATTCCTTACTACATCTGCTGCTCATGCCATGAGTGGTGTATA 561
QY 181 CAGTGTTCCTCAAGGAGTGGCTTATCTTACACAGATGCAACCAAGCGCTAATTCACAGG 240
Db 562 CAGTGTTCCTCAAGGAGTGGCTTATCTTACACAGATGCAACCAAGCGCTAATTCACAGG 621
QY 241 GACCTGAAACCAACCAACTTACTGCTGTTGAGGGGGGACAGTCTTAAATAATTTGTGAT 300
Db 622 GACCTCAAGCTCCAACTTGTCTGTTGAGGGGGGACAGTCTTAAATAATTTGTGAT 681
QY 301 TTTGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTCTGCTTGG 360
Db 682 TTTGTACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTCTGCTTGG 741
QY 361 ATGGCACTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGACGTCTTCAAGTGG 420
Db 742 ATGGCCCTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGACGTCTTCAAGTGG 801
QY 421 GGTATTAATCTTTGGGAAGTGAACCGGTGCGAAACCTTTGATGAGATGGTGGCCCA 480
Db 802 GGTATTAATCTTTGGGAAGTGAACCGGTGCGAAACCTTTGATGAGATGGTGGCCCA 861
QY 481 GCTTCCGAATCATGTGGGCTGTTCAATGATGACTGACCACTGACCACTGATCAAAAATTTA 540
Db 862 GCTTCCGAATCATGTGGGCTGTTCAATGATGACTGACCACTGACCACTGATCAAAAATTTA 921
QY 541 CCTAAGCCCATTTGAGAGCTGATGACTGTTGGTCTAAGATCCTTCCAGGCGCT 600
Db 922 CCTAAGCCCATTTGAGAGCTGATGACAGCTGTTGGTCTAAGGACCCATCTCAGGCGCT 981
QY 601 TCAATGAGGAAATTTGAAATAATGACTCACTTGTGATGCGGTACTTTCCAGGAGCAGAT 660
Db 982 TCAATGAGGAAATTTGAAATAATGACTCACTTGTGATGCGGTACTTTCCAGGAGCAGAT 1041
QY 661 GAGCCATTACAGTCTCTGTCA 683
Db 1042 GAGCCATTACAGTCTCTGTCA 1064

RESULT 7
US-09-221-235-6
; Sequence 6, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/221,235
; EARLIER FILING DATE: 1998-12-28
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-235-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTATACAGTGTCCCAAGGAGTGGCTTATCTTACAGATGCAA 219
Db 316 CACATTATGACCTGGGCCCATGATGAGCAAGGAATGCAATTTATACATATGAGGCT 375
QY 220 CCAAAAGCGCTAATTCACAGGAGCTGAAACCAACCACTTACTGCTGGTTCAGGGGG 279
Db 376 CCGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAAGTGTGTATAGTCTGTATGGA 435
QY 280 ACAGTCTAAAATTTGTGATTTTGTACAGCTTTGTGACATTCAGACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTGTGCTCTCGGTTCCATAACCATACACACATGTCC 495
QY 340 AACAGGGGAGTGGCTTGGATGGACCTGAGTGTGAGGGTGTATTAACAGTGA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGTGAGAA 555
QY 400 AAATGTGAGCTCTTACAGCTGGGGTATTATTCTTTGGGAAGTGTATACCGGTGCGAAACCC 459
Db 556 ACTTGTGACACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAGGGAGGTCCCC 615
QY 460 TTTGATGAGATGGTGG 476
Db 616 TTTAAAGGTTTGAAGG 632

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTATACAGTGTCCCAAGGAGTGGCTTATCTTACAGATGCAA 219
Db 316 CACATTATGACCTGGGCCCATGATGAGCAAGGAATGCAATTTATACATATGAGGCT 375
QY 220 CCAAAAGCGCTAATTCACAGGAGCTGAAACCAACCACTTACTGCTGGTTCAGGGGG 279

Db 376 CCGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTATAGTCTGTATGGA 435
QY 280 ACAGTCTTAAAATTTGTGATTTGGTACAGCTGTGACATTTCAGACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTGGTCCCTTCCATTAACATACACACATGTGTC 495
QY 340 AACAGGGGAGTGGCTGCTTGGATGGACCTGAAGTTTTTGAAGGTAGTAAATACAGTGA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGTGAGAA 555
QY 400 AAATGTGAGCTCTTACAGCTGGGGTATTATTCTTTGGGAAGTGTATACCGGTGCGAAACCC 459
Db 556 ACTTGTGACACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAGGGAGGTCCCC 615
QY 460 TTTGATGAGATGGTGG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 8
US-09-221-928-6
; Sequence 6, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,928
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-928-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTATACAGTGTCCCAAGGAGTGGCTTATCTTACAGATGCAA 219
Db 316 CACATTATGACCTGGGCCCATGATGAGCAAGGAATGCAATTTATACATATGAGGCT 375
QY 220 CCAAAAGCGCTAATTCACAGGAGCTGAAACCAACCACTTACTGCTGGTTCAGGGGG 279
Db 376 CCGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAAGTGTGTATAGTCTGTATGGA 435
QY 280 ACAGTCTAAAATTTGTGATTTTGTACAGCTTTGTGACATTCAGACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTGTGCTCTCGGTTCCATAACCATACACACATGTCC 495
QY 340 AACAGGGGAGTGGCTTGGATGGACCTGAGTGTGAGGGTGTATTAACAGTGA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGTGAGAA 555
QY 400 AAATGTGAGCTCTTACAGCTGGGGTATTATTCTTTGGGAAGTGTATACCGGTGCGAAACCC 459
Db 556 ACTTGTGACACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAGGGAGGTCCCC 615
QY 460 TTTGATGAGATGGTGG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 9
US-09-221-527-6

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; Sequence 6, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-527-6

Query Match      8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CAGCAATGAGTTGGTGTTCACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGGCCACTGATGACCAAGGAATGCATTATTACATATGAGGCT 375
QY 220 CCCAAGCGCTAATTCACAGGACCTGAAACACCAAACTTACTGCTGGTTCAGGGGG 279
Db 376 CCTGTCAAGTGATTCACAGACCTCAAGTCAAGAAAGTGTGTATAGTCTGCTGATGA 435
QY 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCTGTGACATTCACAGACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTTGGTCCCTCTCCATAACCAACACACATGTCC 495
QY 340 AACAAAGGGAGTGTCTGTGATGGACCTGAAAGTTTGAAGGTAGTAAATACAGTGAA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTCAGAA 555
QY 400 AAATGTGACGCTCTTCAGCTGGGGTATTATTCTTTGGGAAGTGATAACGGTTCGGAACCC 459
Db 556 ACTGTGACACATATTCCTATGTTGGTTCCTGCGAGATGCTAACAAAGGAGGTCCCC 615
QY 460 TTTGATGAGATTGGTG 476
Db 616 TTTAAAGTTTGAAGG 632

RESULT 11
US-09-221-416-6
; Sequence 6, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-416-6

Query Match      8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CAGCAATGAGTTGGTGTTCACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGGCCACTGATGACCAAGGAATGCATTATTACATATGAGGCT 375
QY 220 CCCAAGCGCTAATTCACAGGACCTGAAACACCAAACTTACTGCTGGTTCAGGGGG 279
Db 376 CCTGTCAAGTGATTCACAGACCTCAAGTCAAGAAAGTGTGTATAGTCTGCTGATGA 435
QY 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCTGTGACATTCACAGACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTTGGTCCCTCTCCATAACCAACACACATGTCC 495
QY 340 AACAAAGGGAGTGTCTGTGATGGACCTGAAAGTTTGAAGGTAGTAAATACAGTGAA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTCAGAA 555
QY 400 AAATGTGACGCTCTTCAGCTGGGGTATTATTCTTTGGGAAGTGATAACGGTTCGGAACCC 459

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; Sequence 6, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-236-6

Query Match      8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CAGCAATGAGTTGGTGTTCACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGGCCACTGATGACCAAGGAATGCATTATTACATATGAGGCT 375
QY 220 CCCAAGCGCTAATTCACAGGACCTGAAACACCAAACTTACTGCTGGTTCAGGGGG 279
Db 376 CCTGTCAAGTGATTCACAGACCTCAAGTCAAGAAAGTGTGTATAGTCTGCTGATGA 435
QY 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCTGTGACATTCACAGACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTTGGTCCCTCTCCATAACCAACACACATGTCC 495
QY 340 AACAAAGGGAGTGTCTGTGATGGACCTGAAAGTTTGAAGGTAGTAAATACAGTGAA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTCAGAA 555
QY 400 AAATGTGACGCTCTTCAGCTGGGGTATTATTCTTTGGGAAGTGATAACGGTTCGGAACCC 459
Db 556 ACTGTGACACATATTCCTATGTTGGTTCCTGCGAGATGCTAACAAAGGAGGTCCCC 615
QY 460 TTTGATGAGATTGGTG 476
Db 616 TTTAAAGTTTGAAGG 632

RESULT 10
US-09-221-236-6
; Sequence 6, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-236-6

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Db 556 ACTTGTGACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAAAGGAGGTCCCC 615
Qy 460 TTGTGATGAGATTGGGG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 12

US-09-221-245-6
; Sequence 6, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: US 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-245-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
Qy 160 CACGCAATGAGTTGGTGTACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGCCACTGATGTAGCCAAAGGAATGCATTATTACATATGGAGCT 375
Qy 220 CCCAAAGCGCTAATTCACAGGACCTGAACACCAACCAACTTACTGCTGGTTCAGAGGGGG 279
Db 376 CCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTATAGCTGCTGATGA 435
Qy 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCCTGTGACATTTCAGACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTGGTGGCTCTCGGTTCCATACCATACACACATGTCC 495
Qy 340 AACAAAGGGAGTGTCTGTGGATGGCACCTGAAGTTTTTGAAGGTAGTAATTACAGTGAA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTGAGA 555
Qy 400 AAATGTGACGCTTTCAGCTGGGTATTTCTTTGGGAAGTATTAACGGCTCGGAAACCC 459
Db 556 ACTTGTGACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAAAGGAGGTCCCC 615
Qy 460 TTGTGATGAGATTGGTG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 13

US-09-163-115-6
; Sequence 6, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-163-115-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
Qy 160 CACGCAATGAGTTGGTGTACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGCCACTGATGTAGCCAAAGGAATGCATTATTACATATGGAGCT 375
Qy 220 CCCAAAGCGCTAATTCACAGGACCTGAACACCAACCAACTTACTGCTGGTTCAGAGGGGG 279
Db 376 CCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTATAGCTGCTGATGA 435
Qy 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCCTGTGACATTTCAGACACACATGACCAAT 339
Db 436 GTACTGAAGATCTGTGACTTTGGTGGCTCTCGGTTCCATACCATACACACATGTCC 495
Qy 340 AACAAAGGGAGTGTCTGTGGATGGCACCTGAAGTTTTTGAAGGTAGTAATTACAGTGAA 399
Db 496 TTGGTTGGAACCTTCCCATGGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTGAGA 555
Qy 400 AAATGTGACGCTTTCAGCTGGGTATTTCTTTGGGAAGTATTAACGGCTCGGAAACCC 459
Db 556 ACTTGTGACATATTCCTATGTTGTTCTCTGGGAGATGCTAACAAAGGAGGTCCCC 615
Qy 460 TTGTGATGAGATTGGTG 476
Db 616 TTTAAAGGTTTGAAGG 632

RESULT 14

US-09-221-528-6
; Sequence 6, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-528-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
Qy 160 CACGCAATGAGTTGGTGTACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
Db 316 CACATTATGACCTGGCCACTGATGTAGCCAAAGGAATGCATTATTACATATGGAGCT 375
Qy 220 CCCAAAGCGCTAATTCACAGGACCTGAACACCAACCAACTTACTGCTGGTTCAGAGGGGG 279
Db 376 CCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTATAGCTGCTGATGA 435
Qy 280 ACAGTTCTAAAAATTTGTGATTTTGGTACAGCCTGTGACATTTCAGACACACATGACCAAT 339

Thu Dec 4 17:00:20 2003

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Db      436 GTACTGAAGATCTGTGACTTTGGTCCCTCTCGGTTCCATTAACCATACACACATGTCC 495
Qy      340 AACAGGGGAGTGTGCTGTGATGACCTGAAGTTTTTGAAGGTAGTAAATTACAGTGAA 399
Db      496 TTGGTTGGAACCTTCCCAATGATGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGAGAA 555
Qy      400 AAATGTGACGCTTTCAGTGGGGTATTAATCTTTGGGAAGTGAATAACGGTCGGAAACCC 459
Db      556 ACTTGTGACACATATTCCTATGTTGTTCTCTGGAGATGCTTAACAAGGGAGGTCCCC 615
Qy      460 TTTGATGAGATTGGTGG 476
Db      616 TTTAAAGGTTTGAAGG 632

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RESULT 15
US-09-593-553-6
; Sequence 6, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-593-553-6

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Query Match      8.0%; Score 54.6; DB 3; Length 1365;
Best Local Similarity 48.3%; Pred. No. 3.8e-08;
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy      160 CACCAATAGTGGTGTACAGTGTCCCAAGGAGTGGCTTATCTTCACAGCATGCAA 219
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Qy      220 CCCAAGCGCTAATTCACAGGACCTGAACCCAACTTACTCTGTTGCGAGGGGG 279
Db      376 CCTGTCAGGTGATTCACAGAGACCTCAAGTCAAGAACGTTGTATAGCTGTGATGGA 435
Qy      280 ACAGTCTCTAAAATTTGTGATTTTGGTACAGCCCTGTGACATTCAGACACATGACCAAT 339
Db      436 GTACTGAAGATCTGTGACTTTGGTGGCTCTCGGTTCCATAACCATACACACATGTCC 495
Qy      340 AACAGGGGAGTGTGCTGTGATGACCTGAAGTTTTTGAAGGTAGTAAATTACAGTGAA 399
Db      496 TTGGTTGGAACCTTCCCAATGATGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGAGAA 555
Qy      400 AAATGTGACGCTTTCAGTGGGGTATTAATCTTTGGGAAGTGAATAACGGTCGGAAACCC 459
Db      556 ACTTGTGACACATATTCCTATGTTGTTCTCTGGAGATGCTTAACAAGGGAGGTCCCC 615
Qy      460 TTTGATGAGATTGGTGG 476
Db      616 TTTAAAGGTTTGAAGG 632

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Search completed: December 4, 2003, 07:06:36
Job time : 89.7297 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:21:38 ; Search time 730.77 Seconds
(without alignments)
6784.777 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 204

Sequence: 1 caaagccgcacctaaccct.....agagcgtgtgacagcaccg 204

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*

1: em_estba:**
2: em_esthum:**
3: em_estin:**
4: em_estmu:**
5: em_estov:**
6: em_estpl:**
7: em_estro:**
8: em_hic:**
9: gb_est1:**
10: gb_est2:**
11: gb_hic:**
12: gb_est3:**
13: gb_est4:**
14: gb_est5:**
15: em_estfun:**
16: em_estom:**
17: em_gss_hum:**
18: em_gss_inv:**
19: em_gss_pln:**
20: em_gss_vrt:**
21: em_gss_fun:**
22: em_gss_mam:**
23: em_gss_mus:**
24: em_gss_pro:**
25: em_gss_rod:**
26: em_gss_phg:**
27: em_gss_vrl:**
28: gb_gss1:**
29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	757	13	BX393376
2	204	100.0	974	10	BE988567
3	204	100.0	1021	13	BUI52619
4	203	99.5	851	13	BX347763

5	200.8	98.4	782	12	BI253992
6	200.8	98.4	997	10	BGI15732
7	200.8	98.4	1385	13	BQ925425
8	194.4	95.3	930	13	BX347740
9	192.8	94.5	912	13	BX347764
10	184.8	90.6	934	13	BX347741
11	172	84.3	582	12	BI681846
12	165.6	81.2	378	10	BG382061
13	165.6	81.2	527	12	BI400511
14	165.6	81.2	599	12	BI401530
15	165.6	81.2	648	12	BI184403
16	165.6	81.2	815	12	BI181306
17	164.6	80.7	496	9	AM258218
18	164.6	80.7	578	13	BU060967
19	164.6	80.7	705	10	BE375985
20	164.6	80.7	777	12	BI181203
21	164	80.4	334	10	BF710376
22	160.2	78.5	644	12	BM934363
23	158	77.5	1107	10	BE902307
24	155.2	76.1	337	10	BF712308
25	153.6	75.3	738	13	BU709271
26	152.6	74.8	919	10	BF163305
27	145.8	71.5	325	9	AM658281
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29	141.2	69.2	818	10	BE746542
30	139.8	68.5	617	10	BE710962
31	139.8	68.5	772	13	BU229272
32	138.2	67.7	587	13	BU443120
33	138.2	67.7	941	13	BU427891
34	134.6	66.0	997	13	BX367448
35	130.4	63.9	677	13	BU426433
36	126.2	61.9	1002	14	BY709101
37	126.2	61.9	1576	11	AK009321
38	122.6	60.1	795	13	BU109063
39	120.4	59.0	450	9	AA674170
40	114.4	56.1	695	13	BU256845
41	113	55.4	654	13	BU417660
42	103	50.5	417	10	BE167965
43	102.4	50.2	614	12	BG913752
44	92.2	45.2	610	13	BQ387712
45	86.8	42.5	626	13	BX278260

ALIGNMENTS

RESULT 1
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LOCUS BX393376 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DC002Y002 5-PRIME, mRNA sequence.
ACCESSION BX393376
VERSION BX393376.1 GI:30619996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10651.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAM001ZC05 AM029_1&cluster=10651.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." 6 others

BASE COUNT 205 a 386 c 259 g 165 t
ORIGIN

Query Match 100.0%; Score 204; DB 13; Length 1021;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGAGTCCAGC 60
DB 244 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGTCCAGC 303
QY 61 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 120
DB 304 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 363
QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGCACCATGGC 180
DB 364 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGCACCATGGC 423
QY 181 GAGCAGAGCGTGTGACAGCACC 204
DB 424 GAGCAGAGCGTGTGACAGCACC 447

RESULT 4
BX347763
LOCUS BX347763 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DC018YG07 5-PRIME, mRNA sequence.
ACCESSION BX347763
VERSION BX347763.1 GI:30375210
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
AUTHORS Li, W.B., Gruber, C., Jesses, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE008ZG12_AE00768_1&cluster=10651.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE008ZG12_AE00768_1.
Location/Qualifiers

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC018YG07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 172 a 284 c 253 g 140 t 2 others
ORIGIN

Query Match 99.5%; Score 203; DB 13; Length 851;
Best Local Similarity 99.5%; Pred. No. 2.4e-40;
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGTCCAGC 60
DB 544 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGTCCAGC 603
QY 61 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 120
DB 604 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 663
QY 121 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGCACCATGGC 180
DB 664 CGTGTGAGCCCTATGTGGACTTTGCTGAGTTTACCGCCCTCTGGAGCGTGCACCATGGC 723
QY 181 GAGCAGAGCGTGTGACAGCACC 204
DB 724 GAGCAGAGCGTGTGACAGCACC 747

RESULT 5
BX253992
LOCUS BX253992 602975130F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114622 5',
DEFINITION mRNA sequence.
ACCESSION BX253992
VERSION BX253992.1 GI:14805965
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 782)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11278 row: k column: 07
High quality sequence stop: 657.
Location/Qualifiers

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1..782
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5114622"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 162 a 288 c 214 g 118 t
ORIGIN

Query Match 98.4%; Score 200.8; DB 12; Length 782;
Best Local Similarity 99.0%; Pred. No. 8.5e-40;
Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGTCCAGC 60
DB 306 CAAGCCGAGCCTTAACCCCTGAGTCCACCAACGACGACGAGAGAGTCCAGC 365
QY 61 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 120
DB 366 TCTGACGAGGAGCCTTCTCCGCTCCCGGCCGCCCACTCGCTCCCGCTGGGAGACGGT 425

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QY 121 CQTGTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
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Db 426 CQTGTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 485
    |||||||
QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
    |||||||
Db 486 GAGCAGAGCGTGGTGACAGCACCG 509
    |||||||

RESULT 6
BG115732
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 997)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10149 row: d column: 05
High quality sequence stop: 659.
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4417108"
        /tissue_type="duodenal adenocarcinoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC 88"
        /note="Organ: Small intestine; Vector: pCMV-SPORT6;
        Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
        oligo-dT primed. Average insert size 1.767 kb. Library
        enriched for full-length clones and constructed by Life
        Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 251 a 310 c 296 g 140 t
ORIGIN
Query Match 98.4%; Score 200.8; DB 10; Length 997;
Best Local Similarity 99.0%; Pred. No. 8.9e-40;
Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1  CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCAGCTCCAGC 60
Db 194 CAATTCGCCAGCTTAACCTCGAGTCACCAACACGACGACGAGCAGCAGCTCCAGC 253
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QY 61  TCTGACGAGGCGCTCTTCGCTCCCGCCGCGCCACTCGCTCCCGCTGGGAGGACGGT 120
Db 254 TCTGACGAGGCGCTCTTCGCTCCCGCCGCGCCACTCGCTCCCGCTGGGAGGACGGT 313
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QY 121 CGTCTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db 314 CGTCTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 373
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QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
Db 374 GAGCAGAGCGTGGTGACAGCACCG 397
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RESULT 7
BQ925425
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1385)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13734 row: c column: 07
High quality sequence start: 68
High quality sequence stop: 404.
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        /clone_lib="NIH_MGC 129"
        /note="Organ: olfactory epithelium; Vector:
        pCMV-SPORT6.1.ccdB; Site 1: EcoRV; Site 2: NotI; Cloned
        unidirectionally. Primer: Oligo dT. Average insert size
        2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
        is a NIH_MGC Library."
BASE COUNT 257 a 536 c 337 g 253 t 2 others
ORIGIN
Query Match 98.4%; Score 200.8; DB 13; Length 1385;
Best Local Similarity 99.0%; Pred. No. 9.5e-40;
Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1  CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCAGCTCCAGC 60
Db 247 CAAAGCCGACCTTAACCTCGAGTCACCAACACGACGACGAGCAGCAGCTCCAGC 306
    |||||||
QY 61  TCTGACGAGGCGCTCTTCGCTCCCGCCGCGCCACTCGCTCCCGCTGGGAGGACGGT 120
Db 307 TCTGACGAGGCGCTCTTCGCTCCCGCCGCGCCACTCGCTCCCGCTGGGAGGACGGT 366
    |||||||
QY 121 CGTCTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 180
Db 367 CGTCTTGAGCCCTATGTGAGCTTTCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 426
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QY 181 GAGCAGAGCGTGGTGACAGCACCG 204
Db 427 GAGCAGAGCGTGGTGACAGCACCG 450
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RESULT 8
BX347740
LOCUS
DEFINITION
ACCESSION
VERSION

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BX347740 930 bp mRNA linear EST 05-MAY-2003
BX347740 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC002Y002 5--PRIME, mRNA sequence.
BX347740
BX347740.1 GI:30369230

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 910)
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE007ZE10_AE00654_1&cluster=10651.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE007ZE10_AE00654_1.
FEATURES Location/Qualifiers
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1..930
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 168 a 316 c 224 g 219 t 3 others
ORIGIN
Query Match 95.3%; Score 194.4; DB 13; Length 930;
Best Local Similarity 97.1%; Pred. No. 3.4e-38;
Matches 198; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 60
Db 429 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 488
QY 61 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 120
Db 489 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 548
QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 180
Db 549 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGT 608
QY 181 GACGAGGCGTGTCAGACACCG 204
Db 609 GACGAGGCGTGTCAGACATACG 632
RESULT 9
BX347764
LOCUS
DEFINITION BX347764 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC018YG07 5-PRIME, mRNA sequence.
ACCESSION BX347764
VERSION BX347764.1 GI:30375211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 912)
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE008ZG12_AE00768_2&cluster=10651.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE008ZG12_AE00768_2.
FEATURES Location/Qualifiers
source
1..912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC018YG07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 181 a 298 c 269 g 159 t 5 others
ORIGIN
Query Match 94.5%; Score 192.8; DB 13; Length 912;
Best Local Similarity 96.6%; Pred. No. 8.4e-38;
Matches 197; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 60
Db 542 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 601
QY 61 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 120
Db 602 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 661
QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 180
Db 662 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 721
QY 181 GACGAGGCGTGTCAGACACCG 204
Db 722 GACGAGGCGTGTCAGACACCG 745
RESULT 10
BX347741
LOCUS
DEFINITION BX347741 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC002Y002 5-PRIME, mRNA sequence.
ACCESSION BX347741
VERSION BX347741.1 GI:30369231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 934)
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE007ZE10_AE00654_2&cluster=10651.f.

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE008ZG12_AE00768_2&cluster=10651.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAE008ZG12_AE00768_2.
FEATURES Location/Qualifiers
source
1..912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC018YG07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 181 a 298 c 269 g 159 t 5 others
ORIGIN

Query Match 94.5%; Score 192.8; DB 13; Length 912;
Best Local Similarity 96.6%; Pred. No. 8.4e-38;
Matches 197; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 60
Db 542 CAAGCCGACCTTAACCTTGCAGTCCACCAACGACGACGACGACGACGACG 601
QY 61 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 120
Db 602 TCTGACGAGGCGCTTTCGCTCCGCGCCGACCTCGCTCCGCGCTCGGAGGACG 661
QY 121 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 180
Db 662 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGACCATGGC 721
QY 181 GACGAGGCGTGTCAGACACCG 204
Db 722 GACGAGGCGTGTCAGACACCG 745

RESULT 10
BX347741
LOCUS
DEFINITION BX347741 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC002Y002 5-PRIME, mRNA sequence.
ACCESSION BX347741
VERSION BX347741.1 GI:30369231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 934)
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10651.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAE007ZE10_AE00654_2&cluster=10651.f.

Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AB007ZB10_AE00654_2.

FEATURES
source
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC002Y002"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 164 a 308 c 205 g 253 t 4 others
ORIGIN

Query Match 90.6%; Score 184.8; DB 13; Length 934;
Best Local Similarity 94.1%; Pred. No. 8.1e-36;
Matches 192; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 CAAGCCGACCTTAACCTGCGAGTCCACCAACAGCAGCAGAGCAGCAGCTCCAGC 60
DB 430 CAAGCCGACCTTAACCTGCGAGTCCACCAACAGCAGCAGAGCAGCAGCTCCAGC 489
QY 61 TCTGACGGAGGCGCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 120
DB 490 TCTGACGGAGGCGCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 549
QY 121 CGTGTGACCCCTATGTGACCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 180
DB 550 CGTGTGACCCCTATGTGACCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 609
QY 181 GAGCAGAGCGTGTGACAGCAGCG 204
DB 610 GTGACAGCGTGTGACAGTTCGG 533

RESULT 11
BI681846 582 bp mRNA linear EST 17-SEP-2001
LOCUS
DEFINITION
461334 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BI681846
VERSION
BI681846.1 GI:15634771
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 582)
Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrnkung, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG
Plate: 135 row: 0 column: 15
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..582
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/clone_lib="MARC 1BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 93 a 212 c 179 g 98 t
ORIGIN

Query Match 84.3%; Score 172; DB 12; Length 582;
Best Local Similarity 90.2%; Pred. No. 1.1e-32;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 CAAGCCGACCTTAACCTGCGAGTCCACCAACAGCAGCAGAGCAGCAGCTCCAGC 60
DB 80 CAAGCCGACCTTAACCTGCGAGTCCACCAACAGCAGCAGAGCAGCAGCTCCAGC 139
QY 61 TCTGACGGAGGCGCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 120
DB 140 TCGACGGGGCGCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGATGC 199
QY 121 CGTGTGACCCCTATGTGACCTTTCGCTCCCGGCCGCCACTCGCTCCCGCTCGCGAGGACGGT 180
DB 200 CGGTGGAGCCCTACGTGACCTTTCGCGAGTTCACCGCTCTGGAGCGTGGACCATGGC 259
QY 181 GAGCAGAGCGTGTGACAGCAGCG 204
DB 260 GAGCAGAGTGTGTGACGGCGCG 283

RESULT 12
BG382061 378 bp mRNA linear EST 12-MAR-2001
LOCUS
DEFINITION
297803 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
BG382061
VERSION
BG382061.1 GI:13306533
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 378)
Fahrnkung, S.C., Smith, T.P.L., Preking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Perte, G., Sultana, R., Quackenbush
J. and Keele, J.W.
TITLE
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG
Plate: 135 row: 0 column: 15
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1..582
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/clone_lib="MARC 1BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 93 a 212 c 179 g 98 t
ORIGIN

FEATURES


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POLYA-No.      Location/Qualifiers
1. .648
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-cn-c-04-0-UNL"
/dev_stage="ADULT"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="UNL-P-FN"
/note="Vector: pTYT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996.

BASE COUNT      TAG_SEQ=None found"      99 t      7 others
85 a      205 C      252 G

ORIGIN
Query Match      81.2%; Score 165.6; DB 12; Length 648;
Best Local Similarity 88.2%; Pred. NO. 4.3e-31;
Matches 180; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      1      CAAAGCCGACCTTAACCTGCAGTCCACACACACAGCAGACGAGCAGCTCCAGC 60
Db      317      CAGAGCCGACCTGACCTGCAGTCCACACACACAGCAGACGAGCAGCTCCAGC 258
QY      61      TCTGAGGAGGCTCTTCGCTCCCGGCCCGCCACTCGCTCCCGCTCGCGAGGACGTT 120
Db      257      TCGACGGGGGCTCTTTCGCTCCGGCCACCCACTCGCTCCCGCCGGCGAGGATGGC 198
QY      121      CGTGTGTGAGCCCTATGTGGACTTTGTGAGTTTATCGGCTCTGGAGCTGGACCATGGC 180
Db      197      CGCGTGGAGCCCTACGTGGACTTTCGGGGAGTTCTACCGCTGTGGAGCTGGACCATGGC 138
QY      181      GACACAGCGTGTGGACAGCAGC 204
Db      137      GAGCAGAGTGTGGACGGCGCG 114

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POLYA-No.					
Location/Qualifiers					
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/mol_type="mRNA"					
/db_xref="taxon:9823"					
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/lab_host="DH10B (Life Technologies)"					
/clone_lib="MI-P-CP0"					
/note=Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0 library is derived from uterus. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)					
TAG_SEQ=None found"					
77 a _193 c 238 g 91 t					
BASE COUNT					
ORIGIN					
Query Match 81.2%; Score 155.6; DB 12; Length 599;					
Best Local Similarity 88.2%; Pred. NO. 4.3e-31;					
Matches 180; Conservative 0; Mismatches 24; Indels 0; Gaps 0;					
QY	1	C A A G C C C G A C C T T A A C C C T G C A G T C C A C C A C G C A C A C G A G A G A G A G A G C T C C A G C 60			
DB	316	C A G A G C C C G A C C C T G A C C T G A C T C A C C A C C C A C C A C C A C C A G A G A G A G A G C T C C A G C 257			
QY	61	T C T G A C G A G G A G G C C T T C C G T T C C C G G C C C G C C A C T C G C T C C C G C T G C G A G A G C G T 120			
DB	256	T C C G A C G G G G C C T C T T T G C T C C C G G C C C A C C A C C A C T C G C T C C C G C C G G G A G A T G G C 197			
QY	121	C G T G T G A G C C C A T A T G T G A C T T C T G A G T T T A C C G C C T C T G A G A G C G T G G A C C A T G G C 180			
DB	196	C G C G T G G A G C C C T A G T G G A C T T C G G A G T T C T A C C G C C T G T G A G C G T G A C C A C G C 137			
QY	181	G A G C A G A G G T G G T G A C A C C G C 204			
DB	136	G A C A G A G T G G G A G C G G C G C G 113			
RESULT 15					
BI184403/C					
LOCUS					
UNL-P-FN-cn-c-04-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone					
DEFINITION UNL-P-FN-cn-c-04-0-UNL 3', mRNA sequence.					
ACCESSION BI184403					
VERSION BI184403.1 GI:14658812					
KEYWORDS EST.					
SOURCE Sus scrofa (pig)					
ORGANISM Sus scrofa					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
REFERENCE Caetano,A.R., Johnson,R.K. and Pomp,D.					
AUTHORS 1 (bases 1 to 648)					
TITLE Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles					
JOURNAL Mamm. Genome 14 (1), 65-70 (2003)					
MEDLINE 22419904					
PUBMED 12532269					
COMMENT Contact: Pomp, D					
Department of Animal Science					
University of Nebraska, Lincoln					
Lincoln, NE 68583-0908, USA					
Tel.: 402 472 6416					
Fax: 402 472 6362					
Email: dpomp@unl.edu					
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. The following repetitive elements were found in this cDNA sequence: 61-111,					
>GC rich#Low complexity					
Seq primer: M13 -29					

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 08:22:54 ; Search time 23.2027 Seconds
(without alignments)
4537.638 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541

Perfect score: 361

Sequence: 1 caaagccgacctaaccct.....agagcgtggtgacagcaccg 204

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2 1/USPTO.spool/US09830144/runat_03122003_122344_21277/app_query.fasta_1.1230
-DB=SPTRMBL_23 -CPMP=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144 @CGN 1 1 100 @runat_03122003_122344_21277 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	356	98.6	500	11	Q8R0D1	Q8r0d1 mus musculus

ID	Q8R0D1	PRELIMINARY;	PRT;	500 AA.
AC	Q8R0D1			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Similar to mitogen-activated protein kinase kinase 7			
DE	Interacting protein 1 (Fragment).			
GN	2310012M03RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Strausberg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC027054; AAH27054.1; -			
DR	MGD; MGI:1913763; 2310012M03RIK.			
DR	InterPro; IPR001932; PP2C-like.			
DR	Pfam; PF00481; PP2C; 1.			
DR	SMART; SM00332; PP2CC; 1.			
KW	Kinase.			

ALIGNMENTS

RESULT 1

ID	Q8R0D1	PRELIMINARY;	PRT;	500 AA.
AC	Q8R0D1			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Similar to mitogen-activated protein kinase kinase 7			
DE	Interacting protein 1 (Fragment).			
GN	2310012M03RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Strausberg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC027054; AAH27054.1; -			
DR	MGD; MGI:1913763; 2310012M03RIK.			
DR	InterPro; IPR001932; PP2C-like.			
DR	Pfam; PF00481; PP2C; 1.			
DR	SMART; SM00332; PP2CC; 1.			
KW	Kinase.			

QY	121	CGTGTGACCCCTATGCGA	UJ3614	PRELIMINARY;	PRT; 498 AA.
	121	CTGTGTTTACCGCTCTGGAGCGTGGACCATGGC	ID 073614		

Thu Dec 4 17:00:26 2003

us-09-830-144-3_copy_1338_1541.rspt

RT "Functional Analysis of the Profilaggrin N-Terminal Peptide:
RT Identification of Domains that Regulate Nuclear and Cytoplasmic
RT Distribution";
RT J. Invest. Dermatol. 119:661-669(2002).
DR EMBL; AY102923; AAM54369.1; -.
FT NON TER 501 501
SQ SEQUENCE 501 AA; 55418 MW; 7317F95F907FD235 CRC64;

Alignment Scores:
Pred. No.: 3.15 Length: 501
Score: 79.50 Matches: 24
Percent Similarity: 47.46% Conservative: 4
Best Local Similarity: 40.68% Mismatches: 14
Query Match: 21.14% Indels: 17
DB: 11 Gaps: 3

US-09-830-144-3_COPY_1338_1541 (1-204) x Q8CIU0 (1-501)

QY 196 TCACACGCTCTGCTCGCATGTCACGCTCCAGAGCGGTAAACT-----CAGCAA 143
DB 295 ThrProGlySerThrArgThrGlySerArgGlyArgGlyGluSerProAlaGlyGlnGln 314
QY 142 AGTCCACATAGGCTCAACAC-----GACCGTCTCGCCAGGCGGAGCG 98
DB 315 SerProAspArgAlaArgHisIleGluSerArgArgGlyArgThrArgGluAlaGlyAla 334
QY 97 AGT-----GGCGCGCGCGGAGCGGAGAGGC 71
DB 335 SerGlnSerSerAspSerGluAlaIleSerGlyAlaHisAlaGlyIleGlyGlnGly 353

RESULT 9

ID Q94E81 PRELIMINARY; PRT; 531 AA.
AC Q94E81; 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative 3-dehydroquinase dehydratase.
GN B111C09.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
clone:B111C09.4";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003204; BAB61159.1; -.
DR Gramene; Q94E81; -.
DR InterPro; IPR001381; DHQuinase_I.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR006152; Shikimate.
DR InterPro; IPR006151; Shikimate_DH.
DR Pfam; PF01487; DHQuinase_I; 1.
DR Pfam; PF01488; Shikimate_DH; 1.
DR ProDom; PD005337; DHQuinase_I; 1.
DR TIGRFAMs; TIGR01093; aroD; 1.
DR TIGRFAMs; TIGR00507; aroE; 1.
SQ SEQUENCE 531 AA; 56905 MW; 17E3491DC42CE95A CRC64;

Alignment Scores:
Pred. No.: 4.07 Length: 531
Score: 78.50 Matches: 23
Percent Similarity: 46.34% Conservative: 15
Best Local Similarity: 28.05% Mismatches: 23
Query Match: 20.88% Indels: 21
DB: 10 Gaps: 4

US-09-830-144-3_COPY_1338_1541 (1-204) x Q94E81 (1-531)

QY 28 ---TGGACTGCAGG 17
DB 57 ArgTrpThrSerGly 61

RESULT 7

Q99053 PRELIMINARY; PRT; 625 AA.

AC Q99053; 23, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Profilaggrin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Haydock P.V., Dale B.A.;
RT "Filaggrin, an intermediate filament-associated protein: Structural
and functional implications from the sequence of a cDNA from rat.";
RL DNA Cell Biol. 9:251-261(1990).
DR EMBL; M21759; AAA41161.1; -.
FT NON TER 1 1
FT CHAIN 1 406 FILAGGRIN.
SQ SEQUENCE 625 AA; 65957 MW; 8424342E121CB105 CRC64;

Alignment Scores:
Pred. No.: 2.48 Length: 625
Score: 80.50 Matches: 28
Percent Similarity: 47.44% Conservative: 9
Best Local Similarity: 35.90% Mismatches: 27
Query Match: 21.41% Indels: 14
DB: 11 Gaps: 3

US-09-830-144-3_COPY_1338_1541 (1-204) x Q99053 (1-625)

QY 196 TCACACGCTCTGCTCGCATGTCACGCTCCAGAGCGGTAAACT-----CAGCAA 143
DB 116 ThrProGlySerThrArgThrGlySerArgGlyArgGlyGluSerProAlaGlyGlnGln 135
QY 142 AGTCCACATAGGCTCAACAC-----GACCGTCTCGCCAGGCGGAGCG 98
DB 136 SerProAspArgAlaArgHisIleGluSerArgArgGlyArgThrArgGluAlaSerAla 155
QY 97 AGT-----GGCGCGCGCGGAGCGGAGAGGC 56
DB 156 SerGlnSerSerAspSerGluGlyHisSerGlyAlaHisAlaGlyIleGlyGlnGlyGln 175
QY 55 AGCTGCTCTGCTGCGTGCGGTGGTGGAGTGCAGCGGTAAAGTCGGGCT 4
DB 176 Thr-SerThrIleHisArgArgAlaGlySerSerSerGlySerGlnArgAla 192

RESULT 8

Q8CIU0 PRELIMINARY; PRT; 501 AA.

AC Q8CIU0; 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Profilaggrin (Fragment).
GN FLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RX MEDLINE=2218272; PubMed=12230510;
RA Pearson D.J., Dale B.A., Presland R.B.;

RP SEQUENCE FROM N.A.
 RC STRAIN=FaCl;
 RA Oh B., Twigg P., Hong J., Mullin B., An C.S.;
 RT "nifv is contiguous to nifHDK in Frankia strain FaCl.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53363; AAB36873.1; -;
 SQ SEQUENCE 349 AA; 37915 MW; 6650CAB1684F67C4 CRC64;

Alignment Scores:
 Pred. No.: 8.46 Length: 349
 Score: 75.50 Matches: 32
 Percent Similarity: 46.84% Conservative: 5
 Best Local Similarity: 40.51% Mismatches: 26
 Query Match: 20.08% Indels: 16
 DB: 2 Gaps: 4

US-09-830-144-3_COPY_1338_1541 (1-204) x Q47925 (1-349)

```

QY 193 CCACGCTCTGCTCGCATGGTCCACGCTCCAGAGCGGTAAACTCAG----- 146
Db ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
11 ProGlySerAlaArgGlyProArgArgSerArgGlyGlyArgGluGlnGlyGluAspArg 30
QY 145 ---CAAAGTCCACATAGGGCTCAACACGACCGCTCTCGCCAGGCGGAGCGAGTG----- 94
Db ||| ||| : : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
31 GlyGlySerAlaValSerSerGluHisAspArgPro-ProAlaArgAspArgThrGlySe 50
QY 93 -----GGCGGGCGCGGAGCGGAGAGCGCTCCGTCAGAGCTGGAGC 53
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 rArgArgAlaPheThrArgGlyGlyAlaGlyGlyAlaValGlyProPheArgArgGlyAl 70
QY 52 TGCT---GCTCTCGGTGTGGCT---GTTGGTGACTCAGGGTTAAGGTCGGGCT 4
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 aSerValAlaGlyArgGlyArgProProGlyGlyGlyGlnGlyArgSerArgAla 88

```

Search completed: December 4, 2003, 09:07:17
 Job time : 28.2027 secs

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 4, 2003, 08:37:54 ; Search time 8.95946 Seconds
(without alignments)
4379.374 Million cell updates/sec

Title: US-09-830-144-3_COPY_1338_1541
Perfect score: 361
Sequence: 1 caaagccgcgaaccttaacct.....agagcgtggtgacagcaccg 204

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q/cgn2 1/USPTO.spool/US09830144/runat_03122003_122345_21308/app.query.fasta_1.1230
-DB-pir 76 -QWMT-fascan -SUFFIX=rpr -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USPR=US09830144 @CGN 1 1 35 @runat_03122003_122345_21308 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	80.5	21.4	625	2	A34615
C 2	74	19.7	111	2	T14306
C 3	74	19.7	273	2	A86280
C 4	73	20.2	518	1	P2WL47
C 5	72	19.1	383	2	S32975
C 6	72	19.9	574	2	T43556
C 7	72	19.9	574	2	T38819
C 8	72	19.9	1139	2	A40670
C 9	71	19.7	132	1	S15618
C 10	71	18.9	152	2	T34649
C 11	71	18.9	219	2	B84326
C 12	71	19.7	240	2	G83401
C 13	71	19.7	519	2	S36471
C 14	71	19.7	521	2	S36571

15	70.5	19.5	518	2	S36542	L2 protein - human
C 16	70	18.6	142	2	T00616	probable nucleic a
C 17	70	18.6	256	2	A84437	probable PHD-type
C 18	70	19.4	520	2	S36489	L2 protein - human
C 19	70	18.6	606	2	G75302	orotidine 5'-phosp
C 20	69.5	18.5	177	2	C87614	hypothetical prote
C 21	69.5	18.5	1146	2	A38587	collagen, cornea-s
C 22	69.5	19.3	1198	2	T28678	polyketide synthas
C 23	68.5	18.2	537	2	B46535	interleukin 2 rece
C 24	68.5	18.2	824	2	B38423	protein-glutamine
C 25	68.5	18.2	993	2	F84774	probable ATP-depen
C 26	68	18.1	190	2	C72532	hypothetical prote
C 27	68	18.1	511	2	S24345	Balbani ring 1 pr
C 28	68	18.8	667	2	S63587	gene pacc protein
C 29	68	18.1	1428	2	T13926	probable translati
C 30	68	18.1	1666	2	T09072	E4 protein - human
C 31	67.5	18.7	125	1	A46315	retrovirus-related
C 32	67.5	18.0	386	2	A41950	BRcore-NS-Z3 prote
C 33	67.5	18.7	704	2	S21911	hypothetical prote
C 34	67	17.8	682	2	T28899	hypothetical prote
C 35	67	18.6	989	2	C83035	probable zinc fing
C 36	67	18.6	1083	2	T05689	probable serine/th
C 37	66.5	17.7	257	2	T09646	TEA domain-contain
C 38	66.5	18.4	550	2	T36746	L2 protein - human
C 39	66	18.3	384	2	JC5255	L2 protein - human
C 40	66	18.3	427	2	JC5254	protein-glutamine
C 41	66	18.3	518	1	P2WL8	hypothetical orf5
C 42	66	18.3	518	1	P2WL5	ORF2 protein - Orf
C 43	66	17.6	817	1	TGHUM1	
C 44	65.5	17.4	102	4	JC5161	
C 45	65.5	17.4	221	2	C34768	

ALIGNMENTS

RESULT 1

A34615

profilaggrin - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 04-Feb-2000

C:Accession: A34615

R:Haydock, P.V.; Dale, B.A.

DNA Cell Biol. 9, 251-261, 1990

A:Title: Filaggrin, an intermediate filament-associated protein: structural and functions

A:Reference number: A34615; MUID:90274870; PMID:1693512

A:Accession: A34615

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-625 <HAY>

A:Cross-references: GB:M21759; NID:G204143; PIDN:AAA41161.1; PID:G204144

A>Note: the authors translated the codon GAA for residue 568 as Gln

C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology

C:Keywords: EF hand; epidermis

Alignment Scores:

Pred. No.:	0.826	Length:	625
Score:	80.50	Matches:	28
Percent Similarity:	47.44%	Conservative:	9
Best Local Similarity:	35.90%	Mismatches:	27
Query Match:	21.41%	Indels:	14
DB:	2	Gaps:	3

US-09-830-144-3_COPY_1338_1541 (1-204) x A34615 (1-625)

QY 196 TCACACAGCTCTGCTCGCATGGTCCACGTCAGAGCGGTAAACT-----CAGCAA 143

Db 116 ThrProGlySerThrArgThrGlySerArgGlyGluSerProAlaGlyGlnGln 135

QY 142 AGTCACATAGGCTCAACAC-----GACCGTCTCGCAGCGGGAGGG 98

Db 136 SerProAspArgAlaArgHisIleGluSerArgGlyArgThrArgGluAlaSerAla 155

QY 97 AGT-----GGGCGGCGGGAGCGGAAGAGCGCTCGTCAGACTCG 56

UC-09-830-144-3 COPY 1338 1541 (1-204) x A86280 (1-273)

[illegible]

RESULT 4
P2ML47
L2 protein - human papillomavirus type 47
C:Species: human papillomavirus type 47
A:Host: host Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: F35324
R:Kiyono, T.; Adachi, A.; Ishibashi, M.
Virology 177, 401-405, 1990
A:Title: Genome organization and taxonomic position of human papillomavirus type 47
A:Reference number: A35324; MUID:90281611; PMID:2162112
A:Accession: F35324
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-518 <GR>
A:Cross-references: KB:23305; NID:G333062; PIDN:AAA46981.1; PID:G333069
C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

Alignment Scores:		
Pred. No.:	5.68	Length:
Score:	73.00	Matches:
Percent Similarity:	49.21%	Conservative:
Best Local Similarity:	34.92%	Mismatches:
Query Match:	20.22%	Indels:
DB:	1	Gaps:
		2
		518

US-09-830-144-3_COPY_1338_1541 (1-204) x 2_WNL47 (1-518)

Qy	11	CGTTAAACCGCTCAGTCCA-----CCACACGCACGCAGCAGCAGCAGCTCCA	58
Db	141	ProIleProGluGlyProThrIleAspSerProValValThrThrThrGlySerSer	160
Qy	59	GCTCTGACGAGGCGCTCTTCGCTCCGCCGCCACCTCGTCCGCCGCTGCGCAGACG	118
Db	161	AlaValLeuGluValAlaProGluProValProThrArgValargIleAlaArgThr	180
Qy	119	GTCGTGTGTGAGCCCTATGTGGACTTGTGTG-----AGTTTACCGCCCTCTGCAGCGTGG	172
Db	191	GlnTyrHisAsnProSerPheGlnIleLeuThrGluSerThrProAlaGlnGlyGluSer	200
Qy	173	ACCATGGCG	181
Db	201	SerLeuAla	203

RESULT 5
S32975
gene BCRF2 protein - human herpesvirus 4
N-Alternate names: gene BWRF1 protein

RESULT 6
T43556
Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C.Accession: T43556
R.Zankel, T.C.; Ow, D.W.
A.Submitted to the EMBL Data Library, December 1997
A.Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces pombe,
A.A.Reference number: Z22575
A.Accession: T43556
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-574 <ZAN>
A.Cross-references: EMBL:AF038575; PIDN:AAB92587.1
A.Experimental source: strain JS21
C.Genetics:
A.Gene: wsp1
A.Map position: I
A.Introns: 72/3; 519/3; 564/1

RESULT 8
A40670
nuclear envelope protein POM 121 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A40670
R:Hallberg, E.; Wozniak, R.W.; Blobel, G.
J. Cell Biol. 122, 513-521, 1993
A:Title: An integral membrane protein of the pore membrane domain of the nuclea


```
Db 11 SerProArgSerThrArgThrArgCysGlyArgSerArgThrProThrAlaArg 30
QY 142 ACTCCACATAGGCTCAACACAGCGCTCTCCAGCGGGAGTGGGGCGGGCGG 83
Db 31 ArgArgHisArgGlyValGlnProArgPro-----ThrAlaArgArgProThr 46
QY 82 ACCGGAAGAGGCTCGTCAGAGCTGGAGCTGCTCTGCGTGTGCGTGT----- 32
Db 47 ThrGlyArg-----ArgProSerTrpSerArgValSerValMetAlaValArgThrLeu 64
QY 31 -----TGTTGGAGT 23
Db 65 ProArgArgArgArgTrpAlaAlaProThrArgAlaArgArgSerArgArgTrpThr 84
RESULT 12
G83401
hypothetical protein PA1960 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83401
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bu-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A:Reference number: A82950; MUID:2043737; PMID:10984043
A:Accession: G83401
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <STO>
A/Cross-references: GB:AB004622; GB:AB004091; NID:g9947948; PIDN:AAG05348.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1960
Alignment Scores:
Pred. No.: 9.7 Length: 240
Score: 71.00 Matches: 21
Percent Similarity: 50.00% Conservative: 5
Best Local Similarity: 40.38% Mismatches: 24
Query Match: 19.67% Indels: 2
DB: 2 Gaps: 2
US-09-830-144-3_COPY_1338_1541 (1-204) x G83401 (1-240)
QY 26 CCACCAACAGCGACAGCAGCAGCAGCTCCAGCTCTGAGGAGGCTCTTCGCTCC 85
Db 86 ProProThrValArgArgGlyAlaGlnAlaPro----ValThrArgAlaGlnAlaArgPro 104
QY 86 GGCCCGCCCACTCGCTCCCGCTGGCGAGGAGCTGTG---TTGAGCCCTATGTGGACT 142
Db 105 AlaProThrProProSerAlaLeuGlnArgProLeuAlaLysLeuValLeuLeu 124
QY 143 TTGCTGAGTTTACCGCTCTGAGGCTGGACCATG 178
Db 125 LeuCysValLeuProAlaAlaGlyAlaTrpArgMet 136
RESULT 13
S36471
L2 protein - human papillomavirus type 14D
C:Species: human papillomavirus type 14D
C>Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S36471
R:DeLius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36471
A:Molecule type: DNA
A:Residues: 1-519 <DEL>
A/Cross-references: EMBL:X74467; NID:g396918; PIDN:CAA52504.1; PID:g396922
A:Experimental source: strain 14D
```

C:Superfamily: papillomavirus L2 protein
C:Keywords: late protein

Alignment Scores:
Pred. No.: 9.48 Length: 519
Score: 71.00 Matches: 16
Percent Similarity: 50.00% Conservative: 11
Best Local Similarity: 29.63% Mismatches: 23
Query Match: 19.67% Indels: 4
DB: 2 Gaps: 1

US-09-830-144-3_COPY_1338_1541 (1-204) x S36471 (1-519)

QY 2 AAAGCCGACCTTAACCTGCAGTCCACCAACA-----CGCACACCGCAGCA 49
Db 138 GluValHisProGlyProSerArgProProThrAspThrProValThrThrSerThrGly 157
QY 50 GCAGCTCCAGCTCTGACGAGGCTTCGCTCCGCGCGCCGCCACCTGCTCCGCTCG 109
Db 158 GlySerSerAlaIleLeuGluValAlaProGluProThrProProSerArgValArgVal 177
QY 110 GCGAGGAGCGTGTGTTGAGCCCTATGTGACTTTGCTGAGT 151
Db 178 ThrArgThrGlnTyrHisAsnProSerPheGlnValIleThr 191
RESULT 14
S36571

L2 protein - human papillomavirus type 49

C:Species: human papillomavirus type 49

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36571

R:DeLius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36571

A:Molecule type: DNA

A:Residues: 1-521

A/Cross-references: EMBL:X74480; NID:g397030; PIDN:CAA52583.1; PID:g397036

C:Superfamily: papillomavirus L2 protein

C:Keywords: late protein

Alignment Scores:
Pred. No.: 9.48 Length: 521
Score: 71.00 Matches: 14
Percent Similarity: 63.16% Conservative: 10
Best Local Similarity: 36.84% Mismatches: 14
Query Match: 19.67% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-3_COPY_1338_1541 (1-204) x S36571 (1-521)

QY 38 ACACGACGAGCAGCAGCTCCAGCTCTGAGGAGGCTCTTCGCTCCGCGCCGCGCACT 97

Db 153 ThrThrSerArgGlySerAlaValLeuValAlaSerGluProThrProProThr 172

QY 98 CGCTCCCGCTGGCGAGGAGCGTGTGAGCCCTATGTGGACTTTGCTGAGT 151

Db 173 ArgThrArgIleSerArgThrGlnTyrHisAsnProSerPheGlnIleLeuThr 190

RESULT 15

S36542

L2 protein - human papillomavirus type 12

C:Species: human papillomavirus type 12

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36542

R:DeLius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36542

A:Molecule type: DNA

A:Residues: 1-518

Thu Dec 4 17:00:26 2003

A;Cross-references: EMBL:X74466; NID:G396910; PIDN:CAA52500.1; PID:G396916
 C;Superfamily: papillomavirus L2 protein
 C;Keywords: late protein

Alignment Scores:
 Pred. No.: 10.8 Length: 518
 Score: 70.50 Matches: 20
 Percent Similarity: 56.36% Conservative: 11
 Best Local Similarity: 36.36% Mismatches: 21
 Query Match: 19.53% Indels: 3
 DB: 2 Gaps: 2

US-09-830-144-3_COPY_1338_1541 (1-204) x S36542 (1-518)

QY	23	AGTCCACCAACACGACGACGACGACGCTCTGACGAGCCCTCTTCCGCT	82
Db	150	SerProValValThrThrSerArgGlySerSer---AlaIleLeuGluValAlaProAsp	168
QY	83	CCCGGCCCGCCACTCGCTCCCGCCTGGCGAGGACGCTGTTGAGCCCTATGTGGACT	142
Db	169	ProIleProProThrArgValArgValAlaArgThrGlnTyrHisAsnProAlaPheGln	188
QY	143	TTGCTG-----AGTTTACCGCTCTGGAGCGTGACCATGGCG	181
Db	189	IleIleThrGluSerThrProAlaGlnGlyGluThrSerLeuAla	203

Search completed: December 4, 2003, 09:08:41
 Job time : 11.9595 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2003, 09:42:22 ; Search time 2899.3 seconds
(without alignments)
1911.298 Million cell updates/sec

Title: US-09-830-144-2_COPY_76_303

Perfect score: 1252

Sequence: 1 VELQLSRVHPNIVKLYGA.....MTHLMRYPGADEPLQVPCQ 228

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09830144/runat_03122003_122509_23332/app_query.fasta_1.654
-DB=EST -QPM=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPFCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09830144 @CGN 1.1 3596 @runat_03122003_122509_23332 -NCPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
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3: em_estin:*
4: em_estnu:*
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6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	2994	11	AK053911 Mus muscu
2	1246	99.5	1221	13	BUS11353 AGENCOURT
3	1236	98.7	2976	11	AK046565 Mus muscu
4	1167	93.2	739	12	B1696710 603347214
5	1099	87.8	1201	13	BX364931 BX364931
6	1069	85.4	604	12	BM426610 BM426610
7	1041	83.1	839	13	BU418819 BU418819
8	1024	81.8	1157	14	CD508913 CD508913
9	1016	81.2	1062	12	BM554120 BM554120
10	998	79.7	750	13	BU104161 BU104161
11	984	78.6	646	12	BJ073883 BJ073883
12	982	78.4	688	12	BJ062988 BJ062988
13	982	78.4	696	12	BJ074867 BJ074867
14	966	77.2	600	14	CH112561 CH112561
15	953.5	76.2	910	10	BF780358 BF780358
16	932.5	74.5	1087	9	AL525728 AL525728
17	924	73.8	590	14	CB583299 CB583299
18	849.5	67.9	1118	9	AL550589 AL550589
19	847	67.7	542	10	AW960377 AW960377
20	824	65.8	668	13	BUS29310 BUS29310
21	823	65.7	641	13	BQ386875 BQ386875
22	802.5	64.1	742	13	BUS58580 BUS58580
23	753	60.1	1006	13	BQ219348 BQ219348
24	748	59.7	686	10	BG548917 BG548917
25	741	59.2	771	12	BI093821 BI093821
26	737	58.9	682	9	AV398933 AV398933
27	723	57.7	924	14	CA984799 CA984799
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ALIGNMENTS

RESULT 1
AK053911

LOCUS

DEFINITION

AK053911 2994 bp mRNA linear HTC 05-DEC-2002
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
library, clone:EI30320K22 product:mitogen activated protein kinase
kinase kinase 7, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AK053911.1 GI:26343862
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

JOURNAL
MEDLINE
PUBMED

99279253
10349636

REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374
11042159

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AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Harai, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
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Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
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Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., De Bonaldo, M. F., Brownstein, M. J., Bult, C.,
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Marchionni, L., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P.,
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

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11217851

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The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2994)

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kojima, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Matsura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Submitted (16-JUL-2001)

REFERENCE
AUTHORS

Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

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putative"

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BASE COUNT

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ORIGIN

Alignment Scores:
Pred. No.: 4,07e-124 Length: 2994
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AK053911 (1-2994)

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Db 368 GTGAGCTCCGCGAGTGTGTGACGATGGAACATCTCAATGTCAGATTGTATGAGACC 427
Qy 21 CysLeuAsnProValCysLeuValMetGluTyAlaGluGlySerLeuTyAsnVal 40
Db 428 TGCCTGAATCCAGTATGCTCTGTGATGGAATATGACAGAGGGGGCTCATTTGATAATGTG 487
Qy 41 LeuHisGlyAlaGluProLeuProTyTyTyThrAlaAlaHisAlaMetSerTrpCysLeu 60
Db 488 CTGCATGTGTCTGAACCATTCCTCTACTACATCTCTCTCATGCGATGAGTGTGTGTTA 547
Qy 61 GlnCysSerGlnGlyValAlaTyLeuHisSerMetGlnProIysAlaLeuIleHisArg 80
Db 548 CAGTGTTCACAGGAGTGCTTACTGACAGCATGACGAGCCAAAGCGCTGATTCACAGG 607
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Db      848  GCTTTCAGAAATCATGTGGGCTGTTTCAATATGCACCTCGACACCACTGATCAAAATTTA 907
Qy      181  ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
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Qy      201  SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db      968  TCAATGGAGGAAATTTGAAATAATAATGACTCACTTGATGCGGTACTTCCAGGAGCGAT 1027
Qy      221  GluProLeuGlnTyrProCysGln 228
Db      1028  GAGCCGTACAGTATCTCTTGTCAG 1051

RESULT 2
BUS11353
LOCUS
DEFINITION
  AGENCOURT 10128981 NIH_MGC_134 Mus musculus cDNA clone
  IMAGE:6506145 5', mRNA sequence.
ACCESSION
  BUS11353
VERSION
  BUS11353.1 GI:22817586
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-k@mail.nih.gov
  Tissue Procurement: Dr. David Rowe
  cDNA Library Preparation: Invitrogen Corp
  DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.llnl.gov
  Plate: LLAM14068 row: c column: 10
  High quality sequence stop: 733.
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  ORIGIN

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Pred. No.:
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Percent Similarity: 1246.00 Matches: 227
Best Local Similarity: 99.56% Conservative: 0
Query Match: 99.56% Mismatches: 1
DB: 13 Indels: 0
Gaps: 0
US-09-830-144-2_COPY_76_303 (1-228) x BUS11353 (1-1221)
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Qy      61  GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80
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Qy      101  PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
Db      448  TTTGGTACAGCTTGTGACATCCAAACACACATGACCAATAATAAAGGAGTGTCTGTGG 507
Qy      121  MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
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Qy      141  GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
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Qy      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
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Db      748  TTCATGGAGAAATTTGGAATAATATGACTCACTTGTATGCGGTACTTCCAGGAGCGGAT 807
Qy      221  GluProLeuGlnTyrProCysGln 228
Db      808  GAGCCATTACAGTATCTCTTGTCAG 831

RESULT 3
AK046565
LOCUS
DEFINITION
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  protein kinase kinase kinase 7, full insert sequence.
ACCESSION
  AK046565
VERSION
  AK046565.1 GI:26091589
KEYWORDS
  HTC; CAP trapper.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE

```

AUTHORS

TITLE High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

99279253
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20493374
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishigaki, T., Harada, A.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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11076861

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staab, J., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hall, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ringo, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohetsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

21085660
11217851

5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2976)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, I., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

COMMENT

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

1. 2976

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/clone="B430101B05"

/sex="male"

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/dev_stage="4 days neonate"

124. 1862

/note="mitogen activated protein kinase kinase 7
(MGI:1346877, GB|D76446, evidence: BLASTN, 99%,
match=2403)
putative"

2963. 2968

/note="putative"

2976

/note="putative"

850 a 851 c 743 g 732 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 2,17e-122 Length: 2976

Score: 1236.00 Matches: 226

Percent Similarity: 99.12% Conservative: 0

Best Local Similarity: 99.12% Mismatches: 2

Query Match: 98.72% Indels: 0

DB: 11 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x AK046565 (1-2976)

Qy 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyVala 20

Db 348 GTGGAGCTCGGCGAGTTGTCCAGCTGTGAACCTCTTAACATTGTCAAGTTGTATGGAGCC 407

Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40

Db 408 TGCCCTGAATCCAGTATGCTGTGTATGGGATATGAGAGGGGGGCTCATTTGTAATGTG 467

Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60

Db 468 CTGCATGCTGCTGACCATTTGCCTTACTACATCTCTGCTCATGCATGCATGCTGTTA 527

Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80

Db 528 CAGTGTTCCTCAAGAGTGGCTTACCTGCACAGCATGCAGCCCAAGGCTCATTCACAGG 587

Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100

Db 588 GACCTCAAGCTCCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647

Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120

Db 648 TTTGGTACAGCTTGTGACATCCAAACACACATGACCAATAATAAAGGAGTGTCTCTGG 707

Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140

Db 708 ATGGCGCATGAAGTATTTGAAGGTAGCAATTTACAGTGAAGAGTGTGTCTTTCAGTGG 767

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QY 141 GlyllelleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
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QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
DB 828 GCTTTTCAAGATCATGTGGCTCTTCATAATGGCACTCGACACCACTGATCAAAATTTA 887
QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
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QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
DB 948 TCAATAGGAGGAATGTGAAATAATGACTCACTTGTGCGGTACTTCCAGGACGGAT 1007
QY 221 GluProLeuGlnTyrProCysGln 228
DB 1008 GAGCGTTACAGTATCCTTGTGCAG 1031

RESULT 4
BI696710 739 bp mRNA linear EST 18-SEP-2001
LOCUS 603347214F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5374971 5',
DEFINITION mRNA sequence.
ACCESSION BI696710
VERSION BI696710.1 GI:15659339
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM11954 row: k column: 04
High quality sequence stop: 717.
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            /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
            Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
BASE COUNT 195 a 169 c 188 g 187 t
ORIGIN

Alignment Scores:
Pred. No.: 7,35e-116 Length: 739
Score: 1167.00 Matches: 220
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 1
Query Match: 93.21% Indels: 3
DB: 12 Gaps: 0

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US-09-830-144-2_COPY_76_303 (1-228) x BI696710 (1-739)
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DB 3 CGTGTGAACCATCTTAACATTCAGTTGTACGGAGCCTGCCTGAATCCAGTATGCTT 62
QY 28 ValMetGluTyrAlaGluGlySerLeuTyrAsnValLeuHisGlyAlaGluProLeu 47
DB 63 GTGATGGAATATGCAGAGGGGGCTCATTTATATATGCTGTCATGTTGTGACCATG 122
QY 48 ProTyrThrAlaAlaHisAlaMetSerTrpCysLeuGlnCysSerGlnGly-ValAl 67
DB 123 CTTACTACATGCTGCTCATGCCATGAGCTGGTGTTCAGTGTTCACAGGTAGTGC 182
QY 67 atYrLeuHisSerMetGlnProLysAlaLeuIleHisArgAspLeuLysProAsnLe 87
DB 183 TTACCTGCACAGCATGCAGCCCAAGCGCTGATTCACAGGGACCTCAAGCCTCCAACT 242
QY 87 uLeuLeuValAlaGlyGlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp 107
DB 243 GCTGCTGGTTGCAGAGGGACAGTTCTAAAAATCTGCGATTTTGGTACAGCTTGTG 302
QY 107 eGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrpMetAlaProGluValPhe 127
DB 303 CCAACACACATGATGACCAATAATAAGGGAGTGTCTTGGATGGCGCTGAAGTGT 362
QY 127 uGlySerAsnTyrSerGluLysCysAspValPheSerTrpGlyIleIleLeuTyr 147
DB 363 AGGTAGCAATTACAGTGAAGAGTGTGATCTTCAGCTGGGGTATTATCCTCTGGAA 422
QY 147 lIleThrArgArgLysProPheAspGluIleGlyGlyProAlaPheArgIleMetT 167
DB 423 GATAACACGCGGAAACCTTCGATGATGATCGGTGGCCAGCTTTCAGATCATGTGG 482
QY 167 aValHisAsnGlyThrArgProProLeuIleLysAsnLeuProLysProIleGlu 187
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QY 187 uMetThrArgCys-TrpSerLysAspProSerGlnArgProSerMetGluGluVal 207
DB 543 GATGACACGCTGTGTGTCTAAGACCCATCTCAGGC-CCTTCAATGGAGGAATTG 601
QY 207 ystleMetThrHisLeuMetArgTyrPheProGlyAlaAspGluProLeuGlnTyr 227
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QY 227 ysgln 228
DB 662 GTCAG 666

BX364931 1201 bp mRNA linear EST 05-MAY-2003
BX364931 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CS0D1032YB01 5-PRIME, mRNA sequence.
BX364931
ACCESSION BX364931
VERSION BX364931.1 GI:30376863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3613.r For

```

more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSIAI008ZH01QP1&cluster=3613.r>. Contact :
 Feng liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSIAI008ZH01QP1.
 Location/Qualifiers

FEATURES
 source
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 /note="First strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT6 vector. Library was normalized."
 BASE COUNT 290 a 253 c 320 g 299 t 39 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,58e-108 Length: 1201
 Score: 1099.00 Matches: 213
 Percent Similarity: 95.95% Conservative: 0
 Best Local Similarity: 95.95% Mismatches: 9
 Query Match: 87.78% Indels: 3
 DB: 13 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BX364931 (1-1201)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 20
 DB 446 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATGTAAGCTTTATGAGGCC 505
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluClyGlySerLeuTyrAsnVal 40
 DB 506 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATAATGTG 565
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
 DB 566 CTGCATGGTGTGAACCATTCGCCATATATCTGCTGCCACGCAATGAGTGTGTGTTA 625
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 80
 DB 626 CAGTGTTCACAGAGAGTGTATCTTCACAGCATGCAACCCAAAGCGCTAAATTCACAGG 685
 QY 81 AspLeuIysProProAsnLeuLeuValAlaGlyGlyThrValLeuIleCysAsp 100
 DB 686 GACCTGAACACCAACCACTTACTCTGCTGTCMGGGGGACAGTCTTAAATAATTTGTGAT 745
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTyr 120
 DB 746 TTTGGTACAGCTGTGACATTCACACACACATGACCAATAACAGGGGAGTGTCTGTGG 805
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTyr 140
 DB 806 ATGGCACTGAAGTTTGAAGGTAGTAAATTCACAGTGAATAATGCTGCTTCAGCTGG 865
 QY 141 GlyIleLeuLeuTyrGluValIleThrArgGlySerProPheAspGluIleGlyClyPro 160
 DB 866 GGTATTATCTTTCGGAGTGTATACCGCTCGGAACCCCTTTGATGAGATTTGGTGCCCA 925
 QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleGlyAsnLeu 180
 DB 926 GCTTTCGGAACATGTGGCTGTTCATAATGTACTCGACACCACTGATATAAAATTTA 985
 QY 181 ProIysProIleGluSerLeuMetThrArgCysTyrSerIysAspProSerGluArgPro 200
 DB 986 CCTAAGCCCAATGAGAGCGCTGATGACTCGTGTGTGCTTAAGATCCTTCCAGCG-CCY 1044
 QY 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220

Db 1045 TCAATGGAGGAATTGTGAAAAATAATGTCMC-TTGTATGGCGGACTTTCM-GGGAGAGAT 1102

QY 221 GluPro 222
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 Db 1103 GAGCCW 1108

RESULT 6

LOCUS EM426610
 DEFINITION BM426610 604 bp mRNA linear EST 30-JAN-2002
 pgf2n.pk004.d15 Normalized Chicken Abdominal Fat Library (pgf2n)
 Gallus gallus cDNA clone pgf2n.pk004.d15 5' similar to
 emb|CAB87605.1 (AL121964) dU154G14.1.4 [mitogen-activated protein
 kinase kinase kinase 7 (TGF-beta activated kinase 1d (TAK1))] (Homo
 sapiens), mRNA sequence.

ACCESSION BM426610
 VERSION BM426610.1 GI:18431087
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 604)

REFERENCE
 AUTHORS Cogburn,L.A., Morgan,R. and Burnside,J.
 TITLE ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal
 Genome Project
 JOURNAL Unpublished
 COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
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 w16,lyr)"
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 (pgf2n)"
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 (across strains); Single pass sequencing from 5'-end"
 BASE COUNT 167 a 125 c 140 g 167 t 5 others
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Alignment Scores:
 Pred. No.: 2.17e-105 Length: 604
 Score: 1069.00 Matches: 194
 Percent Similarity: 98.99% Conservative: 2
 Best Local Similarity: 97.98% Mismatches: 0
 Query Match: 85.38% Indels: 0
 DB: 12 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BM426610 (1-604)

QY 30 GluTyrAlaGluGlyGlySerLeuTyrAsnValLeuHisGlyAlaGluProLeuProTyr 49
 DB 2 GAGTATGCTGAAGGAGGTCTCTGTACATGTGTGTGATGTGTGACCTTCGCTCAT 61

QY 50 TyrThrAlaAlaHisAlaMetSerTyrCysLeuGlnCysSerGlnGlyValAlaTyrLeu 69
 DB 62 TATACTGCTGCACACGCAATGAGTTGGTTTACAGTGTTCACAGGAGTGGCATATCTT 121

QY 70 HisSerMetGlnProIysAlaLeuIleHisArgAspLeuIysProProAsnLeuLeu 89

KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
Gasterosteus aculeatus (three spined stickleback)	Gasterosteus aculeatus	1	Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J., and Myers, R.M.	Expressed sequence tags from <i>Gasterosteus aculeatus</i>	Unpublished	Contact: Kingsley, DM HHMI and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA Tel: 650 725 5954 Fax: 650 725 7739 Email: kingsley@cmsgm.stanford.edu Plate: 93 High quality sequence stop: 796.	
FEATURES	source	1..1157	Location/Qualifiers	/organism="Gasterosteus aculeatus"	/mol_type="mRNA"	/strain="Salinas river, CA"	
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		/clone_lib="SHGC-CDA"	/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI (5' adaptor); Site 2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs were inserted in to the ZAP express vector undirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."	267 a	354 c	322 g	214 t
BASE COUNT	ORIGIN	Alignment Scores:	4.43e-100	Length:	1157		
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		Score:	93.72%	Conservative:	16		
		Best Local Similarity:	86.55%	Mismatches:	14		
		Query Match:	81.79%	Indels:	2		
		DB:	14	Gaps:	0		
US-09-830-144-2_COPY_76_303 (1-228) x CD508913 (1-1157)							
QY	1	ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla	20				
Db	226	GTGAGCTCCGCCAGCTGTCGGGTGAATCACCCCAATATTTGAAGCTGTATGGCTCG	285				
QY	21	CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal	40				
Db	286	TGTGCAACCCAGCTGCTGCTATGAGTATGCAGTCCGCTCTCTGTATAACCTC	345				
QY	41	LeuHisGlyAlaGluProLeuProTyrTyrThrAlaHisAlaMetSerTyrCysLeu	60				
Db	346	CTGCACAGTGGCGACCCCGCCACTACACGGCGTCCACGCCCATGAGCTGTGCTG	405				
QY	61	GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuHisArg	80				

directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

BASE COUNT 253 a 243 c 298 g 266 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2,85e-99 Length: 1062
Score: 1016.00 Matches: 203
Percent Similarity: 94.52% Conservative: 4
Best Local Similarity: 92.69% Mismatches: 5
Query Match: 81.15% Indels: 7
DB: 12 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BM554120 (1-1062)

QY 1 ValGluLeuArgGlnLeuSerArgValAenHisProAsnIleVallysLeuTyrGlyAla 20
DB GTAGAGCTTCGCGACATTATCCGCTGTGAACCATCTAATATTGTAAGCTTTATGGAGCC 467
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
DB TGCTTGAAATCCAGTGCTTGTGTGTAATATGCTGAAGGGGGCTCTTTATTAATGTG 527
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
DB CTGCATGTGTGTGAACCATTCCTATATATCTGCTGCCACGCAATGAGTTGGTGTGTTA 587
QY 61 GlnCysSerGlnGlyValAlaTyrIleHisSerMetGlnProLysAlaLeuIleHisArg 80
DB CAGTGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 647
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
DB GACCTGGAACCAACCAACTTACTCTGCTGTCAGGGGGAGCAGTTCTAAATAATTGTGAT 707
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuLysGlySerAlaAlaTrp 120
DB TTGCTGACAGCTGTGACATTCAGACACATGACCAATACCAAGGGGGAGTGTGCTGTG 767
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
DB ATGGCACTTGAAGTGTGAGGTAGTAATATACAGTGAAATAATGTGACGCTTCAGCTGG 827
QY 141 GlyIleIleLeuTrpGluValIleThrArgArg-LysProPheAspGluIleGly-P 160
DB GGTATATATCTTTGGGAAGTGATACCGCTGCGAAACCCCTTTGATGAGATGGTGGGCC 887
QY 160 roAlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeu-IleLysAsn 179
DB CAGCTTTCGAATCATGTGGCTGGTCATATATGATCTGACCACTGTATATAAAAAAT 947
QY 180 LeuProLysProIleGlu-SerLeuMetThr-ArgCysTrpSerLysAspPro-SerGln 198
DB TTACCTAGGCCCATTTGAAAGCCTGATGACTCCNTGNTTGGGTAAAGATCTTTCCAG 1007
QY 199 ArgProSerMetGlu-GluIleVallysIleMetThrHisLeu 212
DB CGCCCTTTATGGAGGAAATGTTGTAATAATATGACTCACTG 1050

RESULT 10
LOCUS BU104161
DEFINITION 603005894F1 CSEQCHL01 Gallus gallus linear EST 25-NOV-2002
sequence.
ACCESSION BU104161
VERSION BU104161.1 GI:25304988
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
1 (bases 1 to 750)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

TITLE JOURNAL
MEDLINE PUBMED
COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source

1..750
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST23K24"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSEQCHL01"
/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites [5'ggcgcgtgcagcccgatccgaaacaaag] [5'aattcttttggatccggctgcagc]"
BASE COUNT 222 a 146 c 181 g 201 t
ORIGIN

Alignment Scores:

Pred. No.: 1.47e-97 Length: 750
Score: 998.00 Matches: 194
Percent Similarity: 97.52% Conservative: 3
Best Local Similarity: 96.04% Mismatches: 4
Query Match: 79.71% Indels: 3
DB: 13 Gaps: 1

US-09-830-144-2_COPY_76_303 (1-228) x BU104161 (1-750)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleVallysLeuTyrGlyAla 20
DB GTAGAGCTTCGACCACTGTCAAGTAACCATCTAATATTGTAAGTTATATGGAGCC 208
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
DB T--CTAAACCCAGTGCTTGTGATGGATGCTGGAAGGAGGTTCTCTGTACAATGTG 266
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
DB CTGCATGTGTGCTGAACCTCTGCTCATATATCTGTCGACACGCAATGATGTGGTGTGTTA 326
QY 61 GlnCysSerGlnGlyValAlaTyrIleHisSerMetGlnProLysAlaLeuIleHisArg 80
DB CAGTGTGTCCCAAGAGTGGCATATCTTCACAGTATGAAACCAAGCCCTAATTCACAGA 386
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
DB GACCTGGAACCAACCAAAATTTGCTCTTGTGTAGTGGGGGACAGTTCTTAAAGATCTGTGAT 446

Thu Dec 4 17:00:24 2003

```

QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
Db 447 TTGTGTCAGCCTGTGATATTCAAAACACACATGACCAACAATAAGGGAAGTCTCTGG 506
QY 121 MetAlaProGluValPheGluCysSerAsnTrpSerGluLysCysAspValPheSerTrp 140
Db 507 ATGGCACCTGAAGTTTTCGAAGGTAGCAATACAGTGAAATGATGACGTTTCAGTTGG 566
QY 141 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 567 GGTATATCTCTGGAGGTATACCCGCTAGAAACCTTTTGATGAGATTGGTGCTCA 626
QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 627 GCTTCCGCAATAATGGGCGAGTTCAATAGTGTACTCCACCACTGATCAAAACTTA 686
QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
Db 687 CCTAAACCAATTGAGAG-TTAATGACCGCTGTGTCCAGATCTCTACA---AGACCT 742
QY 201 SerMet 202
Db 743 TCCATG 748

RESULT 11
BJ073883
LOCUS
DEFINITION
  BJ073883 NIBB Mochii normalized Xenopus tailbud library Xenopus
  laevis cDNA clone XL010n05 5', mRNA sequence.
ACCESSION
  BJ073883
VERSION
  BJ073883.1 GI:17504072
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
  Xenopodinae; Xenopus.
  1 (bases 1 to 646)
REFERENCE
  Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Unpublished
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@gene.nig.ac.jp.
  Location/Qualifiers
  1..646
  /organism="Xenopus laevis"
  /mol_type="mRNA"
  /db_xref="taxon:8355"
  /clone="XL010n05"
  /tissue_type="whole embryo"
  /dev_stage="stage 25"
  /clone_lib="NIBB Mochii normalized Xenopus tailbud
  library"
  BASE COUNT 190 a 132 c 143 g 181 t
ORIGIN

Alignment Scores:
Pred. No.: 3..83e-96 Length: 646
Score: 984.00 Matches: 182
Percent Similarity: 97.3% Conservative: 3
Best Local Similarity: 95.79% Mismatches: 5
Query Match: 78.59% Indels: 1
DB: 12 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BJ073883 (1-646)
QY 39 AsnValLeuHisGlyAlaGluProLeuProTyrTrpThrAlaAlaHisAlaMetSerTrp 58

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Db 4 AATGTTTTCATGAGCTGAACCTTTGCTTTACAT-ACTGCTGCCATGCAATAGATTGG 62
QY 59 CysLeuGlnCysSerGlnGlyValAlaTrpLeuHisSerMetGlnProLysAlaLeuIle 78
63 TGTTTACAAATGTGCCAAGGAGTTGCAATATTTACATAGCATGAGCCAAAGGCTGTGATT 122
QY 79 HisArgAspLeuLysProAsnLeuLeuValAlaGlyGlyThrValLeuLysIle 98
123 CACAGGACCTCAACACCAACCTTTGTTGCTGTAGCTGGAGGCACCTGTTCTTAAGATT 182
QY 99 CysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAla 118
183 TGTGACTTTGTTGACACGCTGTGATATTTCAGACTCATGACTATATAACAAAGAGAGTGA 242
QY 119 AlaTrpMetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPhe 138
243 GCATGGATGGCTCCAGAGTTTTCGGAAGTAAATAACCCGAGAAACCTTTTCGATGAAATTGGT 302
QY 139 SerTrpGlyIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGly 158
303 AGTTGGGCAATTATCTTTGGGAAGTAAATAACCCGAGAAACCTTTTCGATGAAATTGGT 362
QY 159 GlyProAlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuLys 178
363 GTGCCAGCGTTCCGTATAATGTGGGCTGTTCAATGGTACTGGGCCACCAITTAATAA 422
QY 179 AsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGln 198
423 AATTTGCTTCAAGCTTATGAAAGCTTAATGACTCGCTGTGCTCCAAAGATCCCCCAA 482
QY 199 ArgProSerMetGluGluIleValIleMetThrHisLeuMetArgTrpPheProGly 218
483 AGACCTTCAATGAGGAGATTGTCAAGATAATCACACATCTAAAGCAGTATTTTCTCTGA 542
QY 219 AlaAspGluProLeuGlnTrpProCysGln 228
543 GCACAGCTTCTTCTTACATGATCTCTGTGTCAG 572
Db

RESULT 12
BJ062988
LOCUS
DEFINITION
  BJ062988 NIBB Mochii normalized Xenopus tailbud library Xenopus
  laevis cDNA clone XL069m17 5', mRNA sequence.
ACCESSION
  BJ062988
VERSION
  BJ062988.1 GI:17470746
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
  Xenopodinae; Xenopus.
  1 (bases 1 to 688)
REFERENCE
  Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Unpublished
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@gene.nig.ac.jp.
  Location/Qualifiers
  1..688
  /organism="Xenopus laevis"
  /mol_type="mRNA"
  /db_xref="taxon:8355"
  /clone="XL069m17"
  /tissue_type="whole embryo"
  /dev_stage="stage 25"
  /clone_lib="NIBB Mochii normalized Xenopus tailbud
  library"
  BASE COUNT 190 a 132 c 143 g 181 t
ORIGIN

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BASE COUNT 206 a 139 c 154 g 188 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 6 95e-96 Length: 688
Score: 982.00 Matches: 177
Percent Similarity: 97.83% Conservative: 3
Best Local Similarity: 96.20% Mismatches: 4
Query Match: 78.43% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BJ062988 (1-688)

QY 45 GluProLeuProTyrThrAlaAlaHisAlaMetSerTyrCysLeuGlnCysSerGln 64
DB 22 GAACCTTTGCCCTTACTATCTACTGCTGCCCATGCAATGAGTTGGTTTCAATGTGCCCAA 81
QY 65 GlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArgAspLeuLysPro 84
DB 82 GGAGTTGCATATTACATAGCATGAAGCCAAAGGCTCTGATTCACAGGACCTCAACCA 141
QY 85 ProAsnLeuLeuValAlaGlyThrValLeuLysIleCysAspPheGlyThrAla 104
DB 142 CCAAACTTTGCTGCTAGTGGAGGACCTGTTCTTAAGATTGTGACTTTGGTACAGCC 201
QY 105 CysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlu 124
DB 202 TGTGATATTTCAGACTCACATGACTTAATAACAAAGAGTGCAGCATGATGCTCCAGAA 261
QY 125 ValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyrGlyIleLeu 144
DB 262 GTTTTGAAGTAGCACTACAGCGAAATGTGACGTGTTTAGTTGGGCATTATTCTT 321
QY 145 TrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyProAlaPheArgile 164
DB 322 TGGGAAGTAATAACCCGAGAAACCTTTCCATGAAATTTGGTGCCAGCGTTCGTATA 381
QY 165 MetTrpAlaValHisAsnGlyThrArgProProLeuLysAsnLeuProLysProIle 184
DB 382 ATGTGGCTGTTCACATGTTACTCGGCCACCATTAATAAAATTTGCCCTAAGCCTATT 441
QY 185 GluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgProSerMetGluGlu 204
DB 442 GAAAGCTTAATAGCTCGCTGCTGCTCAAAAGATCCCCCACAAGACCTTCAATGGAGAG 501
QY 205 IleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAspGluProLeuGln 224
DB 502 ATGTCAAGATATGACACATCTAAAGCAGTATTTCTCTGGAGCAGACGTTTCTCTTACAG 561
QY 225 TyrProCysGln 228
DB 562 TATCCTTGTTCAG 573

RESULT 13

BJ074867
LOCUS
DEFINITION BJ074867 NIBB Mochii mRNA linear EST 11-DEC-2001
ACCESSION laevis cDNA clone XL071110 5', mRNA sequence.
VERSION BJ074867
KEYWORDS EST, GI:17505056

SOURCE

Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 696)

REFERENCE

AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.

TITLE

Expressed genes in X. laevis embryo

JOURNAL

Unpublished

COMMENT

Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source
1..696
Location/Qualifiers
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL071110"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

BASE COUNT 210 a 142 c 155 g 188 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 7 07e-96 Length: 696
Score: 982.00 Matches: 177
Percent Similarity: 97.83% Conservative: 3
Best Local Similarity: 96.20% Mismatches: 4
Query Match: 78.43% Indels: 0
DB: 12 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x BJ074867 (1-696)

QY 45 GluProLeuProTyrThrAlaAlaHisAlaMetSerTyrCysLeuGlnCysSerGln 64
DB 22 GAACCTTTGCCCTTACTATCTACTGCTGCCCATGCAATGAGTTGGTTTCAATGTGCCCAA 81
QY 65 GlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuHisArgAspLeuLysPro 84
DB 82 GGAGTTGCATATTACATAGCATGAAGCCAAAGGCTCTGATTCACAGGACCTCAACCA 141
QY 85 ProAsnLeuLeuValAlaGlyThrValLeuLysIleCysAspPheGlyThrAla 104
DB 142 CCAAACTTTGCTGCTAGTGGAGGACCTGTTCTTAAGATTGTGACTTTGGTACAGCC 201
QY 105 CysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlu 124
DB 202 TGTGATATTTCAGACTCACATGACTTAATAACAAAGAGTGCAGCATGATGCTCCAGAA 261
QY 125 ValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyrGlyIleLeu 144
DB 262 GTTTTGAAGTAGCACTACAGCGAAATGTGACGTGTTTAGTTGGGCATTATTCTT 321
QY 145 TrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyProAlaPheArgile 164
DB 322 TGGGAAGTAATAACCCGAGAAACCTTTCCATGAAATTTGGTGCCAGCGTTCGTATA 381
QY 165 MetTrpAlaValHisAsnGlyThrArgProProLeuLysAsnLeuProLysProIle 184
DB 382 ATGTGGCTGTTCACATGTTACTCGGCCACCATTAATAAAATTTGCCCTAAGCCTATT 441
QY 185 GluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgProSerMetGluGlu 204
DB 442 GAAAGCTTAATAGCTCGCTGCTGCTCAAAAGATCCCCCACAAGACCTTCAATGGAGAG 501
QY 205 IleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAspGluProLeuGln 224
DB 502 ATGTCAAGATATGACACATCTAAAGCAGTATTTCTCTGGAGCAGACGTTTCTCTTACAG 561
QY 225 TyrProCysGln 228
DB 562 TATCCTTGTTCAG 573

RESULT 14

CB112561
LOCUS
DEFINITION K-EST0154393 L6ChoCKO Homo sapiens cDNA clone L6ChoCKO-4-G09 5',
linear EST 28-JAN-2003

61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuLeuHisArg 80
 251 CAGTGTTCCTCCCAAGGAGTGGCTTAATCTTACAGCATGCAACCAAGCGCTAATTCACAGG 310
 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
 311 GACCTGAAACACCAAACTTACTGCTGTGTCAGGGGGACAGTCTTCTAAAAATTTGTGAT 370
 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120
 371 TTTGTGACAGCTGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTCTGTCTGG 430
 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140
 431 ATGGCACCTGAAGTTTGAAGGTAGTAAATACAGTGAAGAAATGACGCTCTTCAGCTGG 490
 141 GlyIleLeuLeuTrpGluValIleThrArgArgLysProPheAsnGluLeuGlyGlyPro 160
 491 GGTATTATTCTTTGGGAGTGTAAAGCGCTCGGAAACCTTTGATGAGATTGGTGCCCA 550
 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeu 176
 551 GCTTTCGAATCATGTGGGCTGTTCATATGTTACTGACCACTG 598

RESULT 15
 BF780358 910 bp mRNA linear EST 12-JAN-2001
 LOCUS 602103276F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4221379
 DEFINITION 5', mRNA sequence.
 ACCESSION BF780358
 VERSION BF780358.1 GI:12085481
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 910)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9806 row: h column: 20
 High quality sequence stop: 664.
 Location/Qualifiers
 1..910
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4221379"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Kid14"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library. |"
 BASE COUNT 247 a 209 c 246 g 207 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1..92 Length: 910
 Score: 953.50 Matches: 194
 Percent Similarity: 92.86% Conservative: 1
 Best Local Similarity: 92.38% Mismatches: 6

mRNA sequence.
 CB112561 GI:27938368
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 4 row: G column: 09
 High quality sequence stop: 600.
 Location/Qualifiers
 1..600
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L6ChoCK0-4-G09"
 /sex="M"
 /cell_line="Cho-CK"
 /lab_host="Top10p"
 /clone_lib="L6ChoCK0"
 /note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10p by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."
 BASE COUNT 164 a 113 c 154 g 169 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3..03e-94 Length: 600
 Score: 966.00 Matches: 176
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 77.16% Indels: 0
 DB: 14 Gaps: 0
 US-09-830-144-2_COPY_76_303 (1-228) x CB112561 (1-600)
 QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAla 20
 DB 71 GTAGAGCTTCGGCAGTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGCC 130
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
 DB 131 TGTTCGAATCCAGTGTCTGTGTGTGAATATGCTGAAGGGGGCTCTTTATATATG 190
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60
 DB 191 CTGATGGTGGTCTGAACCAITGGCCATATTATCTGCTGCCACCGCATGAGTTGGTGT 250

Query Match:	76.16%	Indels:	12
DB:	10	Gaps:	1
US-09-830-144-2_COPY_76_303 (1-228) x BF780358 (1-910)			
QY	28	ValMetGluTyrAlaGluGlySer-Leu-----TyrAsnVa	40
DB	4	GTGATGGAATATGCAGAGGGGGCTCATGTATAATGTTTGTGTGCTTCTCTTACAGT	63
QY	40	lLeuHsGlyAlaGluProLeuProTyrTyrThrAlaAlaHsAlaMetSerTrpCysIle	60
DB	64	GCTGCATGGTGTGAACCATTCCTTACTACACTGCTGCTCATGCCCATCAGCTGGTGT	123
QY	60	uGlnCysSerGlnGlyValAlaTyrLeuHsSerMetGlnProLysAlaLeuIleHisAr	80
DB	124	ACAGTGTTCCTCCAAAGAGTGGCTTACTGTGCACAGCATGCACCCAAAGCCGTGATTCACAG	183
QY	80	qASpLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAs	100
DB	184	GGACCTCAAGCCTCAAACTTGTCTGGTTGCAGAGGGACAGTCTTAAAAATCTGCCA	243
QY	100	pPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTr	120
DB	244	TTTTGGTACAGCTTGTCATCCCAACACACATGACCAATAATAAGGAGAGTGTGCTGTG	303
QY	120	pMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTr	140
DB	304	GATGCGCGCTCAAGTGTTTGAAGGTAGCAATACAGTGAAGAAGTGTGATGTCCTCAGCTG	363
QY	140	pGlyIleIleLeuTrpGluValIle-ThrArgArgLysProPheAspGluIleGlyLp	160
DB	364	GGGTATTATCTCTGGGAAGTGATAAACACACCGGAACCCCTTCGATGAGATCGGTGCC	423
QY	160	roAlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnL	180
DB	424	CAGCTTTCAGAATCATGTGGCTCTTCATAATGGCACTCGACCCATCATGATCAAAAAAT	483
QY	180	euProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgp	200
DB	484	TACCTAAGCCCATTTAGAGAGCTTGATGCACGCTG-TGGTCTAAGGACCCCATCTCAGCG-C	541
QY	200	roSerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaA	220
DB	542	CTTCAATGGAGGAAATTGTGAAATAATGACTCACTTGTATCGGTACTTCCAGAGCGG	601
QY	220	spGluProLeuGlnTyrProCysGln	228
DB	602	ATGAGCA-TTACAGTATACTTGTTCAG	626

Search completed: December 4, 2003, 12:42:49
Job time : 2906.3 secs

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SQ SEQUENCE 579 AA; 64227 MW; 97CBF6F3C9E283BE CRC64;
Query Match 100.0%; Score 1252; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.5e-110;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEAGGSLYNVLHGAELPPYTTAAHMSWCL 60
Db 76 VELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEAGGSLYNVLHGAELPPYTTAAHMSWCL 135
QY 61 QCSQGVAYLHSMOPKALIHRLDLPNLLVAGTVLKI CDFTACDIQTHMTNKGSAW 120
Db 136 QCSQGVAYLHSMOPKALIHRLDLPNLLVAGTVLKI CDFTACDIQTHMTNKGSAW 195
QY 121 MAPEVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
Db 196 MAPEVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 PKPIESLMTRCWSKDPQRSQPSMEBIVKIMTHLMRYFFGADEPLQYPCQ 228
Db 256 PKPIESLMTRCWSKDPQRSQPSMEBIVKIMTHLMRYFFGADEPLQYPCQ 303

RESULT 2
M3K7 HUMAN STANDARD; PRT; 606 AA.
ID M3K7 DROME STANDARD; PRT; 393 AA.
AC P83104;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative mitogen-activated protein kinase kinase 7
DE (EC 2.7.1.-)
GN TAK1L.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
PIR; JC5955; JCS955.

Query Match 100.0%; Score 1252; DB 1; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.6e-110;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEAGGSLYNVLHGAELPPYTTAAHMSWCL 60
Db 76 VELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEAGGSLYNVLHGAELPPYTTAAHMSWCL 135
QY 61 QCSQGVAYLHSMOPKALIHRLDLPNLLVAGTVLKI CDFTACDIQTHMTNKGSAW 120
Db 136 QCSQGVAYLHSMOPKALIHRLDLPNLLVAGTVLKI CDFTACDIQTHMTNKGSAW 195
QY 121 MAPEVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 180
Db 196 MAPEVEFGSNYSKCDVFSWGIIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL 255
QY 181 PKPIESLMTRCWSKDPQRSQPSMEBIVKIMTHLMRYFFGADEPLQYPCQ 228
Db 256 PKPIESLMTRCWSKDPQRSQPSMEBIVKIMTHLMRYFFGADEPLQYPCQ 303

RESULT 3
M3K7 DROME STANDARD; PRT; 393 AA.
ID M3K7 DROME STANDARD; PRT; 393 AA.
AC P83104;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative mitogen-activated protein kinase kinase 7
DE (EC 2.7.1.-)
GN TAK1L.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
PIR; JC5955; JCS955.
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA The genome sequence of *Drosophila melanogaster*.;
RA Science 287:2185-2195 (2000).
RA [2]
RA
RA CONCEPTUAL TRANSLATION.
RA Manning G., Sudarsanam S., Plowman G.;
RA "Prediction of novel protein kinases from the *Drosophila* genome
RA project and EST sequences";
RA Unpublished observations (AUG-2001).
CC -!- FUNCTION: Can phosphorylate and activate yet undefined MAPKs.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE003732; ; NOT ANNOTATED_CDS.
DR FlyBase; FBgn046689; Tak1l.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW Tyrosine-protein kinase; ATP-binding.
FT DOMAIN 11 266 PROTEIN KINASE.
FT NP_BIND 17 25 ATP (By similarity).
FT BINDING 38 38 ATP (By similarity).
FT ACT_SITE 133 133 BY SIMILARITY.
SQ SEQUENCE 393 AA; 45238 MW; 43370C98490F0384 CRC64;
Query Match 34.8%; Score 435.5; DB 1; Length 393;
Best Local Similarity 39.2%; Pred. No. 1.3e-33;
Matches 91; Conservative 50; Mismatches 80; Indels 11; Gaps 6;

QY 2 EURQSRVNNHPIVKLYGACLN--PVLVMEYAEGSLYNVLHGAEPLFYTTAAHMSWC 59
DB 54 EITHLSEIDHENVIRIGRASNGKDYLLMEYLEEGSLHNYLGGDKWE-YTVEQAVRMA 112
QY 60 LOSQGVAVLHSMQPKALHRLDKPNNLLVAGGVILKICDRGTACDIQTHMTNNGSAA 119
DB 113 LQCAKALAYLHSLD-RPIVHRDIKQNNMLLYNQCHEDKICDFGLATDMNNKTDMQGTLR 171
QY 120 WMAPEVFECSNYSEKCDVFSWGIILWEIVTRKRPDEIGCP--APRIMWAVHNGTRPPL- 176
DB 172 YNAPEAIRKHLKYATKCDVYFGLMLWELMTROLPYSHLENFNSQVAIMKAISSGEKLPME 231
QY 177 --IKNLPKPIESIMTRCWSKQSPSMEIEIKVIMTHLMRYFPFGADEPLQYP 226
DB 232 AVRSDCPEGIKQLMECCMDINPEKPSMKEIEKFLGE--QYESGTDDEDFIKP 281

RESULT 4
M3KA_HUMAN
ID M3KA_HUMAN STANDARD; PRT; 954 AA.
AC Q02779; Q12761; Q14871;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
DE (Mixed lineage kinase 2) (Protein kinase MST).
GN MAP3K10 OR MLK2 OR MST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96128179; PubMed=8536694;
RA Dorow D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
RA Sutherland G.R., Simpson R.J.;
RT "Complete nucleotide sequence, expression, and chromosomal
RT localisation of human mixed-lineage kinase 2";
RL Eur. J. Biochem. 234:492-500(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95249256; PubMed=7731697;
RA Katoh M., Hirai M., Sugimura T., Terada M.;
RT "Cloning and characterization of MST, a novel (putative)
RT serine/threonine kinase with SH3 domain.";
RL Oncogene 10:1447-1451(1995).
RN [3]
RP SEQUENCE OF 244-480 FROM N.A.
RC TISSUE=Colon epithelium;
RX MEDLINE=93238756; PubMed=8477742;
RA Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;
RT "Identification of a new family of human epithelial protein kinases
RT containing two leucine/isoleucine-zipper domains.";
RL Eur. J. Biochem. 213:701-710(1993).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X90846; CAA62351.1; -;
DR EMBL; Z48615; CAA88531.1; -;

OC PIR; S68178; S68178.
OC HSP; P11362; 1FGK.
OC Genew; HGNC:6849; MAP3K10.
OC MIM; 600137; -
OC GO; GO:0006917; P-induction of apoptosis; TAS.
OC GO; GO:0007254; P-JNK cascade; TAS.
OC GO; GO:0007165; P-signal transduction; TAS.
OC InterPro; IPR000719; Prot kinase.
OC InterPro; IPR002290; Ser Thr_pkinase.
OC InterPro; IPR001452; SH3.
OC InterPro; IPR001245; Tyr_pkinase.
OC Pfam; PF00069; pkinase; 1.
OC PRINTS; PF00018; SH3; 1.
OC PRINTS; PF00452; SH3DOMAIN.
OC PRINTS; PR00109; TYRKINASE.
OC ProDom; PD000001; Prot kinase; 1.
OC ProDom; PD000066; SH3; 1.
OC SMART; SM00326; SH3; 1.
OC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
OC PROSITE; PS00108; PROTEIN KINASE ST; 1.
OC PROSITE; PS00011; PROTEIN KINASE_DOW; 1.
OC PROSITE; PS00002; SH3; 1.
KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW ATP-binding; SH3 domain.
FT DOMAIN 2 5 POLY-GLU.
FT DOMAIN 16 81 SH3.
FT DOMAIN 98 360 PROTEIN KINASE.
FT NP BIND 104 112 ATP (BY SIMILARITY).
FT BINDING 125 125 ATP (BY SIMILARITY).
FT ACT_SITE 222 222 BY SIMILARITY.
FT DOMAIN 384 402 LEUCINE-ZIPPER 1 (BY SIMILARITY).
FT DOMAIN 419 440 LEUCINE-ZIPPER 2 (BY SIMILARITY).
FT DOMAIN 449 463 ARG/LYS-RICH (BASIC).
FT CONFLICT 462 464 SRL -> AV (IN REF. 2).
FT CONFLICT 465 480 LKLRGGSHSLPSGF -> AQAAGRQPHOPALWL (IN REF. 3).
FT CONFLICT 471 471 G -> S (IN REF. 2).
FT CONFLICT 807 807 G -> R (IN REF. 2).
FT CONFLICT 818 818 V -> A (IN REF. 2).
SQ SEQUENCE 954 AA; 103623 MW; 538F4AAA559B0ABA CRC64;

Query Match 31.3%; Score 392.5; DB 1; Length 954;
Best Local Similarity 40.6%; Pred. No. 4e-29; Indels 17; Gaps 6;
Matches 88; Conservative 35; Mismatches 77;

QY 2 ELRQLSRVNHPIVVKLYGACINP--VCLVMEYAEAGSLYVHLHGAELPYPYTAHAHMSWC 59
Db 145 EARLFGALOHENITIALRGACINPPLHCLVMEYAGGALSRYLAGRRVPHV---LVNWA 200
QY 60 LQCSQGVAYLHSMOPKALIHRLDLPNLLV-----AGTVLKICDFGTACD-IQTHM 111
Db 201 VQVARGMNYLNDAPVPIIHRDLKSNILILEAIENHNLAFTVLKIDTFGLAREWHKTK 260
QY 112 TNNKGSAAWAPVEYEGSNYSKCDVFSWGIIILWEVITRRRPFDEIGGPAFRIMWAV-HN 170
Db 261 MSAAGTYAWMAPEVIRLSFGSSDWSVGLVLLWELLTGEVYREI--DALAVAGVAMN 318
QY 171 GTRPLIKNLPKPIESLMTRCWSKDPSPQSPMEIEIVK 207
Db 319 KLTLPSTCTPEPPARLEECWDPPHGRDPFGSILK 355

RESULT 5
M3K9 HUMAN STANDARD; PRT; 394 AA.
AC P80192;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase 9 (EC 2.7.1.-) (Mixed lineage kinase 1) (Fragment).
DE MAP3K9 OR MLK1 OR PRKX1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OC [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Colon epithelium;
RX MEDLINE=93238756; PubMed=8477742;
RA Dorow D.S., Devereux L., Dietzsch B., de Kretser T.,
RT "Identification of a new family of human epithelial protein kinases
containing two leucine/isoleucine-zipper domains.";
RL Eur. J. Biochem. 213:701-710(1993).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF
COLONIC, BREAST AND OESOPHAGEAL ORIGIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
DR PIR; S32467; J00229.
DR HSP; P12931; 1FMK.
DR Genew; HGNC:6861; MAP3K9.
DR MIM; 600136; -
DR GO; GO:0005524; F:ATP binding activity; NAS.
DR GO; GO:0004708; F:MAP kinase activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TYKKG; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOW; 1.
KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW ATP-binding.
FT NON TER 1 1 PROTEIN KINASE.
FT DOMAIN 3 271 ATP (BY SIMILARITY).
FT NP BIND 9 17 ATP (BY SIMILARITY).
FT BINDING 30 30 BY SIMILARITY.
FT ACT_SITE 127 127 LEUCINE-ZIPPER 1 (BY SIMILARITY).
FT DOMAIN 289 310 LEUCINE-ZIPPER 2 (BY SIMILARITY).
FT DOMAIN 324 345 ARG/LYS-RICH (BASIC).
FT DOMAIN 354 368 ARG/LYS-RICH (BASIC).
SQ SEQUENCE 394 AA; 44975 MW; DBE40B7D31047FD8 CRC64;

Query Match 29.0%; Score 363.5; DB 1; Length 394;
Best Local Similarity 37.7%; Pred. No. 7.8e-27;
Matches 83; Conservative 36; Mismatches 84; Indels 17; Gaps 6;

QY 2 ELRQLSRVNHPIVVKLYGACINP--VCLVMEYAEAGSLYVHLHGAELPYPYTAHAHMSWC 59
Db 50 EAKLFAMLKHPNITIALRGVCLKEPNCLVMEFARGGPNRVLSKRIIPDI---LVNWA 105
QY 60 LQCSQGVAYLHSMOPKALIHRLDLPNLLV-----AGTVLKICDFGTACD-IQTHM 111
Db 106 VQIARGMNYLHDEAVPIIHRDLKSNILILQKVENGSLNKLKIDTFGLAREWHKTK 165
QY 112 TNNKGSAAWAPVEYEGSNYSKCDVFSWGIIILWEVITRRRPFDEIGGPAFRIMWAV-HN 170
Db 166 MSAAGTYAWMAPEVIRASMFSGSDWSVGLVLLWELLTGEVYREI--LRVAVGAMN 223
QY 171 GTRPLIKNLPKPIESLMTRCWSKDPSPQSPMEIEIVKIMT 210
Db 224 KLALPISTCTPEPPAKLMEDCWNPDHRSRPSFTNILDQLT 263

RESULT 6
M3K9 RAT STANDARD; PRT; 888 AA.
AC Q63796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)

Qy 177 IKNLKPFTSLMTRCWSKDPQRSMBEIVKIMTHL 212
 Db 365 PSSCPDGFKILLRQCWNKPRNRPSPRQ---ILLHL 397

RESULT 7

M3KC_HUMAN	STANDARD;	PRT;	859 AA.
ID	M3KC_HUMAN	STANDARD;	PRT;
AC	Q12852;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37) (leucine-zipper protein kinase) (ZPK).		
GN	MAP3K12 OR ZPK.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis; Carcinoma;		
RX	MEDLINE=94311945; PubMed=8037767;		
RT	Reddy U.R.; Pleasure D.;		
RT	"Cloning of a novel putative protein kinase having a leucine zipper domain from human brain."		
RL	Biochem. Biophys. Res. Commun. 202:613-620(1994).		
CC	!- FUNCTION: May be an activator of the JNK/SAPK pathway.		
CC	Phosphorylates beta-casein, histone 1 and myelin basic protein <i>in vitro</i> .		
CC	!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	!- COFACTOR: Magnesium.		
CC	!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By similarity).		
CC	!- TISSUE SPECIFICITY: Highly expressed in brain and kidney.		
CC	!- PTM: Auto-phosphorylated on Ser/Thr. Phosphorylated in cytosol under basal conditions and dephosphorylated when membrane-associated (By similarity).		
CC	!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE SUBFAMILY.		
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CC	EMBL; U07358; AAA67343.1; -.		
DR	HSSP; P12931; 1FMK.		
DR	Genew; HGNC:6851; MAP3K12.		
DR	MIM; 600447; -.		
DR	GO; GO:0005737; C:cytoplasm; TAS.		
DR	GO; GO:0005886; C:plasma membrane; TAS.		
DR	GO; GO:0007254; P:JNK cascade; TAS.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_Thr_kinase.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	Pfam; PF00069; pkinase; 1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Magnesium; Membrane.		
XW	DOMAIN 125 366 PROTEIN_KINASE.		
FT	NP_BIND 131 139 ATP (BY SIMILARITY).		
FT	BLINDING 152 152 ATP (BY SIMILARITY).		
FT	ACT_SITE 236 236 BY SIMILARITY.		
FT	DOMAIN 665 668 POLY-PRO.		
FT	DOMAIN 720 725 POLY-GLU.		

under basal conditions and dephosphorylated when membrane-associated.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE SUBFAMILY.

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EMBL; U14636; AA57280.1; --
EMBL; U23789; AAB17123.1; --
PIR; A55318; A55318.
HSP; P12931; 1FMK.
MGD; MGI:134681; Mep3kl2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Magnesium; Membrane.
FT DOMAIN 18 399 PROTEIN KINASE
FT NP_BIND 164 172 ATP (BY SIMILARITY).
FT BINDING 185 185 BY SIMILARITY.
FT ACT_SITE 269 269 POLY-GLY.
FT DOMAIN 56 62 POLY-PRO.
FT DOMAIN 668 671 POLY-PRO.
FT DOMAIN 698 701 POLY-GLU.
FT DOMAIN 753 758 K->A: NO CATALYTIC ACTIVITY.
FT MUTAGEN 185 185 E->A: NO CHANGE.
FT MUTAGEN 192 192 V->A (IN REF. 2).
FT CONFLICT 18 18 KL->V (IN REF. 2).
FT CONFLICT 28 29 S->T (IN REF. 2).
FT CONFLICT 382 382 EQ->D (IN REF. 2).
FT CONFLICT 494 495 N->D (IN REF. 2).
FT CONFLICT 517 517 E->G (IN REF. 2).
FT CONFLICT 794 794 E
SQ SEQUENCE 888 AA; 96083 MW; CFECDID34F889ABB CRC64;

Query Match 28.2%; Score 353.5; DB 1; Length 888;
Best Local Similarity 34.7%; Pred. No. 1.7e-25;
Matches 75; Conservative 43; Mismatches 81; Indels 17; Gaps 8

QY 2 ELRQLSRVNHVNIKLYGACLN--VCLVMEYAEAGSLYNVLHGAEPLPYTTAAHMSWC 59
Db 194 DIKHLRKLKHPNIITFGVCTQAPCYCILMEFCAQGLYEVLRAGRPV--TPSLVDWS 250
QY 60 LQCSOGVAYLHSMQPKALIHRLDKPNNLLVAGTVLKICDPGTACDIQTMTNNK--GS 117
Db 251 MGIAGMNYLHLK---LIHRDLKSPN-MLITYDDVVKISDFGTSKLSKTSKMSFAGT 306
QY 118 AAMWAEVPEGSNYSEKDVFSWGIIIVETTRKPFDEIGGPAFRIMWAV-HNCTRPL 176
Db 307 VAMWAEVIRNEPVSEKVDIWSFGVWELLTGEIPYKDVSSA--IIWVGNSLHLFPV 364
QY 177 IKNLKPIESLMTRCWSKDPSPQSFMEIEIVKIMTHL 212
Db 365 PSSCPDGFKILLRQCNWSPKRNPSFRQ---ILLHL 397

RESULT 9
KV2 DICI
ID_KV2 DICI STANDARD; PRT; 410 AA.
AC P18161;
DT 01-NOV-1990 (Rel. 16, Created)

DR ProDom: PD000001; Prot kinase; 1.
 DR SMART; SM0220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 65 69 POLY-GLY.
 FT DOMAIN 135 141 POLY-GLY.
 FT DOMAIN 551 809 PROTEIN KINASE.
 FT NP BIND 557 565 ATP (BY SIMILARITY).
 FT BINDING 578 578 ATP (BY SIMILARITY).
 FT ACT SITE 676 676 E-K; IN CTIR-4; EXHIBITS ETHYLENE-
 FT MUTAGEN 596 596 TREATED PHENOTYPE.
 FT MUTAGEN 694 694 D-S; IN CTIR-1; EXHIBITS ETHYLENE-
 FT TREATED PHENOTYPE.
 SQ SEQUENCE 821 AA; 90306 MW; 29223DCDCC15BC CRC64;
 Query Match 25.8%; Score 323; DB 1; Length 821;
 Best Local Similarity 33.9%; Pred. No. 1.2e-22;
 Matches 74; Conservative 45; Mismatches 91; Indels 8; Gaps 6;
 QY 2 ELRLSRVHNPIVLYGACLP--VCLVMEYAEGLSVNVLHGAEPLPYTAAHAWSC 59
 Db EVAIMKELRHPIVLFMGAVTQPNLSIVTEYLSRGLYRLHKGAREQLDERRRLSMA 655
 QY 60 LQCSQGVAYLHQPVALIHRDLKPPNLLVAGGVVLKIDFG-TACDIOTHTNNK--G 116
 Db 656 YDVAKGMYLHNRNP-PIVHRDLKSPNLLVDRKYTV-KVCDPGLSRKASTFLSSKSAAG 713
 QY 117 SAAMVAPEVSGNSYKCVFSGVGIILWEIVTRKPFDFIGGPAFRIMWAVHNGTRPPL 176
 Db 714 TPWMAPEVURDEPSNEKSDYVSGVILWELATLQDPWGNL-NPAQVVAAGVFKCKLEI 772
 QY 177 IKNLKPESIMTRCWSKDFSPSMBEIVKIMTHLMR 214
 Db 773 PRNLNPQVAALIEGCWINEPWKRFSEFATIMDLRLPLIK 810
 RESULT 11
 RET MOUSE STANDARD; PRT; 1115 AA.
 AC P35546;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase receptor ret precursor
 DE (EC 2.7.1.112) (C-ret).
 GN RET.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93205390; PubMed=8455936;
 RA Iwamoto T., Iantguchi M., Asai N., Ohkusu K., Nakashima I.,
 RA Takahashi M.;
 RT "cDNA cloning of mouse ret proto-oncogene and its sequence similarity
 RT to the cadherin superfamily.";
 RL Oncogene 8:1087-1091(1993).
 RN [2]
 RP INTERACTION WITH DOK2; DOK4 AND DOK5, PHOSPHORYLATION, AND MUTAGENESIS
 RP OF TYR-1063.
 RX MEDLINE=211363571; PubMed=11470823;
 RA Grimm J., Sachs M., Britsch S., Di Cesare S., Schwarz-Romond T.,
 RA Alitalo K., Birchmeier W.;
 RT "Novel p62dok family members, dok-4 and dok-5, are substrates of the
 RT c-ret receptor tyrosine kinase and mediate neuronal
 RT differentiation.";
 RL J. Cell Biol. 154:345-354(2001).
 CC -!- FUNCTION: Probable receptor with tyrosine-protein kinase activity;
 CC important for development.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Phosphorylated form interacts with the PBT domain of
 CC DOK2, DOK4 and DOK5.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in peripheral nerve cells and
 CC hematopoietic cells.
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: Contains 1 cadherin domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; X67812; CAA48013.1; -.
 CC PIR; I48735; S29926.
 CC HSP; P11362; IFGI.
 CC MGD; MGI:97902; Ret.
 CC GO; GO:0001657; P:retic bud development; IMP.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000719; Prot kinase.
 CC InterPro; IPR001245; Tyr.pkinase.
 CC Pfam; PF00028; cadherin; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PRD0109; TYRKINASE.
 CC ProDom; PD000001; Prot kinase; 1.
 CC SMART; SM00112; CA; 1.
 CC SMART; SM00219; TyKC; 1.
 CC PROSITE; PS0268; CADHERIN 2; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC Transferrase; Tyrosine-protein kinase; ATP-binding; Proto-oncogene;
 CC Transmembrane; Phosphorylation; Glycoprotein; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 1115 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
 FT RECEPTOR RET.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT CADHERIN.
 FT PROTEIN KINASE.
 FT ATP (BY SIMILARITY).
 FT BINDING 759 759 ATP (BY SIMILARITY).
 FT BY SIMILARITY.
 FT ACT SITE 875 875 PHOSPHORYLATION.
 FT MOD RES 1063 1063 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 1063 1063 Y->F: ABOLISHES INTERACTION WITH DOK
 FT PROTEINS.
 SQ SEQUENCE 1115 AA; 123728 MW; 4D75576095C7D2C8 CRC64;
 Query Match 24.6%; Score 307.5; DB 1; Length 1115;
 Best Local Similarity 32.1%; Pred. No. 4.8e-21;
 Matches 79; Conservative 44; Mismatches 78; Indels 45; Gaps 9;
 QY 2 ELRLSRVHNPIVLYGACLP--NPVCLVMEYAEGLSVNVLHGAEPL-PYY----- 50
 CC -!- FUNCTION: Probable receptor with tyrosine-protein kinase activity;
 CC important for development.

Db 776 BFNLLKQVNHVHVIKLYGACSGPGLLLIVVEYAKYSLRGLRDLRDKKIGPAYVGGSRN 835

QY 51 -----TAAHMSWCLQCSQGVAYLHSMQPKALHRLDKPNNLLVAGGVTLKI 98

Db 836 SSSLDHPDRLVTGLDLSFAWQISGMQVLAEMK---LVHRLAARN-ILVAEGRKMKI 891

QY 99 CDFGTACDI---QTHMNNKG--SAAWMAPEVFEKSGSEKCDVFSWGIILWEVITRRKP 153

Db 892 SDFGLSRDVEEDSYVKKSGKGRIPVXWMAIESLFDHIYTTQSDVWFGVLLWEIVT--- 947

QY 154 FDEIGG-----PAPRIMVAVHNGTTPPLIKNLPKPIESLMTFCWKSQSPRSMEEIVK 207

Db 948 ---LGNPVPGPPIPERLFLNLLKTGHRMRPDNCSEMYRLMLQCWKQEPDKRPVFADISK 1004

QY 208 INTHLM 213

Db 1005 DLEKWM 1010

RESULT 12

RET HUMAN

AC P07949; STANDARD; PRT; 1114 AA.

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Proto-oncogene tyrosine-protein kinase receptor ret precursor

DE (EC 2.7.1.112) (C-ret).

GN RET.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE OF 1-280 FROM N.A.

RX MEDLINE=89282215; PubMed=2660074;

RA Takahashi M.;

RT "Isolation of ret proto-oncogene cDNA with an amino-terminal signal

RT sequence.";

RL Oncogene 4:805-806(1989).

RN [2]

RP SEQUENCE OF 255-1114 FROM N.A.

RX MEDLINE=90272230; PubMed=3078962;

RA Takahashi M., Buma Y., Iwamoto T., Inaguma Y., Ikeda H., Hiai H.;

RT "Cloning and expression of the ret proto-oncogene encoding a tyrosine

RT kinase with two potential transmembrane domains.";

RL Oncogene 3:571-578(1988).

RN [3]

RP SEQUENCE OF 598-1063 FROM N.A.

RX MEDLINE=87257826; PubMed=3037315;

RA Takahashi M., Cooper G.M.;

RT "ret transforming gene encodes a fusion protein homologous to

RT tyrosine kinases.";

RL Mol. Cell. Biol. 7:1378-1385(1987).

RN [4]

RP TROSPINE AUTOPHOSPHORYLATION, AND MUTAGENESIS OF TYR-1015 AND

RP TYR-1062.

RX MEDLINE=20513733; PubMed=11061555;

RA Salvatore D., Barone M.V., Salvatore G., Melillo R.M., Chiappetta G.,

RA Mineo A., Fenzi G., Vecchio G., Fusco A., Santoro M.;

RT "Tyrosines 1015 and 1062 are in vivo autophosphorylation sites in ret

RT and ret-derived oncoproteins.";

RL J. clin. Endocrinol. Metab. 85:3898-3907(2000).

RN [5]

RP REVIEW ON HSCR VARIANTS

RX MEDLINE=98023959; PubMed=9359036;

RA Hofstra R.M.W., Osinga J., Buys C.H.C.M.;

RT "Mutations in Hirschsprung disease: when does a mutation contribute to

RT the phenotype.";

RL Eur. J. Hum. Genet. 5:180-185(1997).

RN [6]

RP REVIEW ON VARIANTS

RX MEDLINE=97220587; PubMed=9067749;

RA

RA Eng C., Mulligan L.M.;

RT "Mutations of the RET proto-oncogene in the multiple endocrine

RT neoplasia type 2 syndromes, related sporadic tumours, and

RT Hirschsprung disease.";

RL Hum. Mutat. 9:97-109(1997).

RN [7]

RP VARIANTS MEN2A/FMTC TRP-611; SER-618; ARG-620; TYR-620 AND ARG-634.

RX MEDLINE=93372843; PubMed=8103403;

RA Donis-Keller H., Dou S., Chi D., Carlson K.M., Toshima K.,

RA Laitmore T.C., Howe J.R., Moley J.F., Goodfellow P., Wells S.A. Jr.;

RT "Mutations in the RET proto-oncogene are associated with MEN 2A and

RT FMTC.";

RL Hum. Mol. Genet. 2:851-856(1993).

RN [8]

RP VARIANTS MEN2A GLY-618; 632-ASP-VAL-ARG-634; GLY-634; PHE-634; TYR-634

RP AND SER-634.

RX MEDLINE=93275414; PubMed=8099202;

RA Mulligan L.M., Kwok J.B.J., Healey C.S., Elsdon M.J., Eng C.,

RA Gardner E., Love D.R., Mole S.E., Moore J.K., Papi L., Ponder M.A.,

RA Telenius H., Tunncliffe A., Ponder B.A.J.;

RT "Germ-line mutations of the RET proto-oncogene in multiple endocrine

RT neoplasia type 2A.";

RL Nature 363:458-460(1993).

RN [9]

RP VARIANTS HSCR PRO-40; LEU-399; GLN-762; PRO-765; GLN-897; GLY-972 AND

RP LEU-973.

RX MEDLINE=95219414; PubMed=7704557;

RA Yin L., Barone V., Seri M., Bolino A., Boccardi R., Ceccherini I.,

RA Pasini B., Tocco T., Lerone M., Cywes S., Moore S.,

RA Vandervinden J.-M., Abramowicz M.J., Kristoffersson U., Larsson L.T.,

RA Hamel B.C.J., Silengo M., Martucciello G., Romeo G.;

RT "Heterogeneity and low detection rate of RET mutations in Hirschsprung

RT disease.";

RL Eur. J. Hum. Genet. 2:272-280(1994).

RN [10]

RP VARIANT MEN2B THR-918.

RX MEDLINE=94272459; PubMed=7911697;

RA Eng C., Smith D.P., Mulligan L.M., Nagai M.A., Healey C.S.,

RA Ponder M.A., Gardner E., Scheumann G.F., Jackson C.E., Tunncliffe A.,

RA Ponder B.A.J.;

RT "Point mutation within the tyrosine kinase domain of the RET

RT proto-oncogene in multiple endocrine neoplasia type 2B and related

RT sporadic tumours.";

RL Hum. Mol. Genet. 3:237-241(1994).

RN [11]

RP VARIANTS MEN2A/FMTC ARG-618; SER-618; PHE-620; ARG-620; PHE-634;

RP GLY-634 AND TYR-634.

RX MEDLINE=94348513; PubMed=7915165;

RA Xue F., Yu H., Maurer L.H., Memoli V.A., Nutile-Mcmenemy N.,

RA Schuster M.K., Browden D.W., Mao J.-I., Noll W.W.;

RT "Germline RET mutations in MEN 2A and FMTC and their detection by

RT simple DNA diagnostic tests.";

RL Hum. Mol. Genet. 3:635-638(1994).

RN [12]

RP VARIANTS FMTC/MEN2A TYR-609; ARG-618; SER-618 AND SER-620.

RX MEDLINE=95152521; PubMed=7849720;

RA Blaugrund J.E., Johns M.M. Jr., Eby Y.J., Ball D.W., Baylin S.B.,

RA Hruban R.H., Sidransky D.;

RT "RET proto-oncogene mutations in inherited and sporadic medullary

RT thyroid cancer.";

RL Hum. Mol. Genet. 3:1895-1897(1994).

RN [13]

RP VARIANTS FMTC, AND VARIANTS MEN2A.

RX MEDLINE=95179108; PubMed=7874109;

RA Schuffenecker I., Billaud M., Calender A., Chambe B., Ginot N.,

RA Calmettes C., Modigliani E., Lenoir G.M.;

RT "RET proto-oncogene mutations in French MEN 2A and FMTC families.";

RL Hum. Mol. Genet. 3:1939-1943(1994).

RN [14]

RP VARIANT HSCR TRP-609, VARIANT HSCR/MEN2A ARG-618, AND VARIANT

RP HSCR/FMTC ARG-620.

RX MEDLINE=95187155; PubMed=7881414;

RA Mulligan L.M., Eng C., Attie T., Lyonnet S., Marsh D.J., Hyland V.J.,

RT Hirschsprung disease.";
 RL Hum. Mol. Genet. 4:1381-1386(1995).
 Query Match 24.3%; Score 304.5; DB 1; Length 1114;
 Best Local Similarity 32.1%; Pred. No. 9.3e-21;
 Matches 79; Conservative 44; Mismatches 78; Indels 45; Gaps 9;
 QY 2 ELRQLSRVNHPIVILYGLACL--NPVCLVMEYAEAGSLYNVLHGAEPL-PYY----- 50
 Db 775 EFNVLQVNHPIVILYGLACSDGGLLLIVEYAKYGLRGFLRSKRKVGPLYGSGGSRN 834
 QY 51 -----TAAHAMSWCLOCSGVAYLHSMQPKALHRLDKPNNLLVAGGTVLKI 98
 Db 835 SSSLDHPDERALTMGDLISFAWQISQMOYLAEMK--LVHRDLAARN-ILVAEGRKKKI 890
 QY 99 CDFTGACDI---QTHMTNKG--SAAWMAPEVEGSGNYSKCDVFSWGIILWEIVTRRK 153
 Db 891 SDFGLSRDVEEDSYKRSQGRIPVKMAIESLFDHIYTTQSDVSWFGLLWEIVT--- 946
 QY 154 FDEIGG-----PAFRIMVAVHNGTRPPLIKNPKIESLMTWCWKDPQSRSMIEIVK 207
 Db 947 ---LGGNYPGIPPERLNLKTGHRMERPDNCSEMYRLMLQCKQEPDKRPVFADISK 1003
 QY 208 IMTHLM 213
 Db 1004 DLEKMM 1009
 RESULT 13
 TEC MOUSE STANDARD; PRT; 630 AA.
 ID TEC MOUSE AC P24604: Q9RLM9; Q9WVN1; Q9WVN2; Q9WVN3;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase Tec (EC 2.7.1.112).
 GN TEC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=93149603; PubMed=7678927;
 RA Mano H., Mano K., Tang B., Koehler M., Yi T., Gilbert D.J.,
 RA Jenkins N.A., Copeland N.G., Ihle J.N.;
 RA "Expression of a novel form of Tec kinase in hematopoietic cells and
 RT mapping of the gene to chromosome 5 near Kit.";
 RL Oncogene 8:417-424(1993).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5 AND 6).
 RP STRAIN=129; PubMed=10343129;
 RC MEDLINE=99276475; PubMed=10343129;
 RX Merkel A.L., Atmosukarto I.I.C., Stevens K., Rathjen P.D.,
 RA Booker G.W.;
 RA "Splice variants of the mouse Tec gene are differentially expressed in
 RT vivo.";
 RL Cytogenet. Cell Genet. 84:132-139(1999).
 RN [3]
 RN SEQUENCE OF 82-630 FROM N.A. (ISOFORM 2).
 RP STRAIN=BALB/c; TISSUE=Liver;
 RC MEDLINE=91133729; PubMed=2284097;
 RX Mano H., Ishikawa F., Nishida J., Hirai H., Takaku F.;
 RA "A novel protein-tyrosine kinase, tec, is preferentially expressed in
 RT liver.";
 RL Oncogene 5:1781-1786(1990).
 RN [4]
 RN SEQUENCE OF 485-553 FROM N.A.
 RP MEDLINE=90152381; PubMed=2482828;
 RX Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
 RA "The application of the polymerase chain reaction to cloning members
 RT of the protein tyrosine kinase family.";
 RL Gene 85:67-74(1989).

RA Robinson B.G., Frilling A., Verellen-Dumoulin C., Safar A.,
 RA Venter D.J., Munnich A., Ponder B.A.J.;
 RT "Diverse phenotypes associated with exon 10 mutations of the RET
 RT proto-oncogene.";
 RL Hum. Mol. Genet. 3:2163-2167(1994).
 RN [15]
 RP VARIANT MEN2B THR-918.
 RX MEDLINE=94159102; PubMed=7906866;
 RA Hofstra R.M.W., Landsvater R.M., Ceccherini I., Stulp R.P.,
 RA Stelwagen T., Luo Y., Pasini B., Hoepfner J.W.M., van Amstel H.K.P.,
 RA Romeo G., Lips C.J.M., Buys C.H.C.M.;
 RT "A mutation in the RET proto-oncogene associated with multiple
 RT endocrine neoplasia type 2B and sporadic medullary thyroid
 RT carcinoma.";
 RL Nature 367:375-376(1994).
 RN [16]
 RN VARIANTS HSCR PRO-765; GLN-897 AND GLY-972.
 RP MEDLINE=94159103; PubMed=8114938;
 RA Romeo G., Ronchetto P., Luo Y., Barone V., Seri M., Ceccherini I.,
 RA Pasini B., Bocciaardi R., Lerone M., Kaariainen H., Martucciello G.;
 RT "Point mutations affecting the tyrosine kinase domain of the RET
 RT proto-oncogene in Hirschsprung's disease.";
 RL Nature 367:377-378(1994).
 RN [17]
 RN VARIANTS HSCR LEU-32; LEU-64; GLN-330 AND LEU-393.
 RP MEDLINE=94159104; PubMed=8114939;
 RA Ederly P., Lyonnet S., Mulligan L.M., Pelet A., Dow E., Abel L.,
 RA Holder S., Nihoul-Fekete C., Ponder B.A.J., Munnich A.;
 RT "Mutations of the RET proto-oncogene in Hirschsprung's disease.";
 RL Nature 367:378-380(1994).
 RN [18]
 RN VARIANT MEN2B THR-918.
 RX MEDLINE=94151373; PubMed=7906417;
 RA Carlson K.M., Dou S., Chi D., Scavarda N., Toshima K., Jackson C.E.,
 RA Wells S.A., Jr., Goodfellow P.J., Donis-Keller H.;
 RT "Single missense mutation in the tyrosine kinase catalytic domain of
 RT the RET proto-oncogene is associated with multiple endocrine neoplasia
 RT type 2B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1579-1583(1994).
 RN [19]
 RN VARIANTS MTC; FVTC; MEN2A AND MEN2B.
 RP MEDLINE=96223053; PubMed=8625130;
 RA Komminoth P., Kunz E.K., Matias-Guiu X., Hiort O., Christiansen G.,
 RA Colomer A., Roth J., Heitz P.U.;
 RT "Analysis of RET proto-oncogene point mutations distinguishes heritable
 RT from nonheritable medullary thyroid carcinomas.";
 RL Cancer 76:479-489(1995).
 RN [20]
 RN VARIANTS MEN2A SER-618; SER-620; ARG-634 AND TYR-634.
 RP MEDLINE=95163936; PubMed=7860065;
 RA Takiguchi-Shirahama S., Koyama K., Miyauchi A., Wakasugi T., Oishi S.,
 RA Takami H., Hikiiji K., Nakamura Y.;
 RT "Germline mutations of the RET proto-oncogene in eight Japanese
 RT patients with multiple endocrine neoplasia type 2A (MEN2A).";
 RL Hum. Genet. 95:187-190(1995).
 RN [21]
 RN VARIANTS HSCR LEU-20; SER-93; GLN-330; TYR-609 AND ARG-620, AND
 RP VARIANT CYS-982.
 RC TISSUE=Blood;
 RX MEDLINE=95360000; PubMed=7633441;
 RA Angrist M., Bolk S., Thiel B., Puffenberger E.G., Hofstra R.M.W.,
 RA Buys C.H.C.M., Cass D.T., Chakravarti A.;
 RT "Mutation analysis of the RET receptor tyrosine kinase in Hirschsprung
 RT disease.";
 RL Hum. Mol. Genet. 4:821-830(1995).
 RN [22]
 RN VARIANTS HSCR.
 RP TISSUE=Leukocyte;
 RX MEDLINE=96090258; PubMed=7581377;
 RA Attie T., Pelet A., Ederly P., Eng C., Mulligan L.M., Amiel J.,
 RA Boutrand L., Beldjord C., Nihoul-Fekete C., Munnich A., Ponder B.A.J.,
 RA Lyonnet S.;
 RT "Diversity of RET proto-oncogene mutations in familial and sporadic

Thu Dec 4 17:00:24 2003

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FT CONFLICT 34 34 P -> T (IN REF. 2).
FT CONFLICT 535 535 V -> E (IN REF. 4).
FT CONFLICT 550 550 FGLV -> YGIP (IN REF. 4).
FT CONFLICT 590 590 T -> S (IN REF. 2).
FT CONFLICT 611 611 L -> F (IN REF. 2 AND 3).
FT CONFLICT 630 630 AA; 73426 MW; 26240E90D46D2 CRC64;
SQ SEQUENCE 630 AA; 73426 MW; 26240E90D46D2 CRC64;

Query Match 24.1%; Score 301.5; DB 1; Length 630;
Best Local Similarity 32.4%; Pred. No. 9.2e-21;
Matches 71; Conservative 44; Mismatches 89; Indels 15; Gaps 7;

QY 2 ELRQLSRVNHPIVLYGACL--NPVCLVMEYAEGLSVNVLHGAEPPLPYTAAHAMSG 59
Db 412 EAKVMMKLTPLKVLQVLYGVCCTQKPIYIVTFEMERGCLLNFLRQ--GHFSRDVLLSVC 469
QY 60 LQCSQGVAYLHSMOPKALIHRLKPPNLLVAGGTVLKICDFGTA----CDIQTHMTNNK 115
Db 470 QDVCEGMEYL---ERNSEFIHRDLAARNCLVNEAG-VVKVSDFGMARVLDQVTSSSGAK 525
QY 116 GSAAMMAPEVEGNSYSEKDFVSGIILWEVITR-RKPFDEIGGPAFRIMWAVHNGTRP 174
Db 526 FPKWCPPEVENYSRFSKSDVMSFGVLWMEIFTEGRMPFEK--NTNVEVVTMTVRGHL 583
QY 175 PLINKLPKPIESLMTRCWSKDPSPSRMERIVKIMTHLM 213
Db 584 HRPKLTATKLYEVMRCWQRPGRPSLEDLRTIDELV 622

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RESULT 14

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ID - TEC HUMAN STANDARD; PRT; 631 AA.
AC P42680;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase Tec (EC 2.7.1.112).
GN TEC OR P8CTK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95019807; PubMed=79341162;
RA Sato K., Mano H., Ariyama T., Inazawa J., Yazaki Y., Hirai H.;
RT "Molecular cloning and analysis of the human Tec protein-tyrosine
RL Leukemia 8:1663-1672(1994).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: HEMATOPOIETIC CELL LINES INCLUDING MYELOID,
CC B-, AND T-CELL LINESAGES.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TEC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/TECID75.html".
CC
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CC -----
CC EMBL; D29767; BAA06171.1; -
CC PIR; I56997; I56997.

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DR HSSP; Q06187; IBS5.
DR Genew; HGNC:11719; TEC.
DR MIM; 600583; -.
DR GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. . .; TAS.
DR GO; GO:0008468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007243; P:protein kinase cascade; TAS.
DR InterPro; IPR001562; BTK.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00779; BTK; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00402; TECBTKDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00107; BTK; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; Phosphorylation.
FT DOMAIN 4 111 PH.
FT DOMAIN 179 239 SH2.
FT DOMAIN 247 345 SH2.
FT DOMAIN 370 623 PROTEIN KINASE.
FT NP_BIND 376 384 ATP (BY SIMILARITY).
FT BINDING 398 398 ATP (BY SIMILARITY).
FT ACT_SITE 489 489 BY SIMILARITY.
FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 631 AA; 73629 MW; A55DECAF991A9022 CRC64;

Query Match 24.1%; Score 301.5; DB 1; Length 631;
Best Local Similarity 32.9%; Pred. No. 9.2e-21;
Matches 73; Conservative 42; Mismatches 86; Indels 21; Gaps 9;

QY 2 ELRQLSRVNHPIVLYGACL--NPVCLVMEYAEGLSVNVLHGAEPPLPYTAAHAMSG 59
Db 413 EAKVMMKLTPLKVLQVLYGVCCTQKPIYIVTFEMERGCLLNFLRQ--GHFSRDVLLSVC 470
QY 60 LQCSQGVAYLHSMOPKALIHRLKPPNLLVAGGTVLKICDFGTA----CDIQTHMTNNK 115
Db 471 QDVCEGMEYL---ERNSEFIHRDLAARNCLVSEAG-VVKVSDFGMARVLDQVTSSSGAK 526
QY 116 GSAAMMAPEVEGNSYSEKDFVSGIILWEVITR-RKPFDEIGGPAFRIMWAVHNGTR- 173
Db 527 FPKWCPPEVENYSRFSKSDVMSFGVLWMEVFTGRMPFEKTYN--YEVVTMTVRGHL 584
QY 174 --PLINKLPKPIESLMTRCWSKDPSPSRMERIVKIMTHLM 213
Db 585 YQPKLASNY---YVEVMRCWQKPEGRPSFEDLRTIDELV 623

RESULT 15
ID - TEC HUMAN STANDARD; PRT; 625 AA.
AC Q03526;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase ITK/TSK (EC 2.7.1.112) (T-cell-specific
GN kinase) (II-2-inducible T-cell kinase) (Kinase EMT) (Kinase TLK).
DE ITK OR TSK OR EMT OR TLK.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=93087493; PubMed=1280821;
RA Siliciano J.D., Morrow T.A., Desiderio S.V.;
RT "Itk, a T-cell-specific tyrosine kinase gene inducible by interleukin
RL 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11194-11198(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=93113848; PubMed=8421704;
RA Heyeck S.D., Berg L.J.;
RT "Developmental regulation of a murine T-cell-specific tyrosine kinase
RL gene, Tsk.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:669-673(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/J; TISSUE=Mast cells;
RX MEDLINE=93236578; PubMed=8476425;
RA Yamada N., Kawakami Y., Kimura H., Fukamachi H., Baier G.,
RA Altman A., Kato T., Ingaki Y., Kawakami T.;
RT "Structure and expression of novel protein-tyrosine kinases, Emb and
RL Emt, in hematopoietic cells.";
RL Biochem. Biophys. Res. Commun. 192:231-240(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA Ogata M., Sawada M., Fujiwara H., Hamaoka T.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 160-236.
RX MEDLINE=97138229; PubMed=8985255;
RA Andreotti A.H., Bunnell S.C., Feng S., Berg L.J., Schreiber S.L.;
RT "Regulatory intramolecular association in a tyrosine kinase of the
RL Tec family.";
RL Nature 385:93-97(1997).
RN [6]
RP CHARACTERIZATION
RX MEDLINE=95023908; PubMed=7524075;
RA August A., Gibson S., Kawakami Y., Kawakami T., Mills G.B., Dupont B.;
RT "CD28 is associated with and induces the immediate tyrosine
RT phosphorylation and activation of the Tec family kinase ITK/EMT in
RL the human Jurkat leukemic T-cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9347-9351(1994).
RN [7]
RP CHARACTERIZATION
RX MEDLINE=9708950; PubMed=8943565;
RA King P.D., Sadra A., Han A., Liu X.-R., Sunder-Plassmann R.,
RA Reinherz E.L., Dupont B.;
RT "CD2 signaling in T cells involves tyrosine phosphorylation and
RT activation of the Tec family kinase, EMT/ITK/TSK.";
RL Int. Immunol. 8:1707-1714(1996).
RN [8]
RP CHARACTERIZATION
RX MEDLINE=20040393; PubMed=10570289;
RA Ching K.A., Kawakami Y., Kawakami T., Tsoukas C.D.;
RT "Emt/Itk associates with activated TCR complexes: role of the
RT pleckstrin homology domain.";
RL J. Immunol. 163:6006-6013(1999).
CC -!- FUNCTION: MAY PLAY A ROLE IN T-CELL DEVELOPMENT, POTENTIALLY IN
CC THYMIC SELECTION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: LIGATION OF CD2, TCR OR CD28 INDUCES ACTIVATION AND

CC TYROSINE PHOSPHORYLATION OF ITK.
CC -!- SUBCELLULAR LOCATION: LOCALIZES TO CELL SURFACE RECEPTORS IN THE
CC PLASMA MEMBRANE AFTER STIMULATION WITH RESPECTIVE RECEPTORS (TCR,
CC CD28, CD2) IN T-CELLS.
CC -!- TISSUE SPECIFICITY: IS DETECTED IN THE THYMUS, LYMPH NODE AND VERY
CC FAINTLY IN THE SPLEEN, BUT IS NOT DETECTED IN THE LIVER, LUNG,
CC KIDNEY, HEART, BRAIN, INTESTINE OR TESTIS. EXPRESSED IN T-
CC LYMPHOCYTES AND MAST CELLS. IT MAY ALSO BE EXPRESSED IN NATURAL
CC KILLER CELLS.
CC -!- DEVELOPMENTAL STAGE: IS PRESENT IN THE FETAL THYMUS AS EARLY AS
CC DAY 14 OF GESTATION. THE LEVELS ARE 5- TO 10-FOLD HIGHER IN
CC THYMOCYTES THAN IN PERIPHERAL T CELLS, AND INCREASE IN THE THYMUS
CC DURING DEVELOPMENT FROM NEONATE TO ADULT.
CC -!- INDUCTION: By interleukin-2.
CC -!- DOMAIN: THE PH DOMAIN MEDIATES TARGETING OF ITK/TSK AND IS
CC INDISPENSIBLE FOR THE ACTIVATION THROUGH TCR/CD3.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TEC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L00619; AAA39337.1; -;
CC EMBL: L05631; AAA40518.1; -;
CC EMBL: L10628; -; NOT ANNOTATED_CDS.
CC EMBL: D14042; BAA03129.1; -;
CC PIR: A43030; A43030.
CC PDB: 1AWJ; 14-JAN-98.
CC PDB: 1LUK; 27-NOV-02.
CC PDB: 1LUM; 27-NOV-02.
CC PDB: 1LUN; 27-NOV-02.
CC MGD: MGI:96621; Itk.
CC InterPro: IPR001562; BTK.
CC InterPro: IPR001849; PH.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00779; BTK; 1.
CC Pfam: PF00169; PH; 1.
CC Pfam: PF00069; Pkinase; 1.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF00018; SH3; 1.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00402; TECBTKDOMAIN.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC ProDom: PD000093; SH2; 1.
CC ProDom: PD000066; SH3; 1.
CC SMART: SM00107; BTK; 1.
CC SMART: SM00233; PH; 1.
CC SMART: SM00252; SH2; 1.
CC SMART: SM00326; SH3; 1.
CC SMART: SM00219; Tyrc; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00109; PROTEIN KINASE TYR; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS50001; SH2; 1.
CC PROSITE: PS50002; SH3; 1.
CC PROSITE: PS50003; PH_DOMAIN; 1.
CC TRANSFERASE; Tyrosine-protein kinase; Phosphorylation;
CC ATP-binding; SH2 domain; SH3 domain; 3D-structure.
CC DOMAIN 4 117 PH.
CC DOMAIN 177 237 SH3.
CC DOMAIN 245 343 SH2.
CC FT

Thu Dec 4 17:00:24 2003

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FT DOMAIN 368 620 PROTEIN KINASE.
FT NP BIND 374 382 ATP (BY SIMILARITY).
FT BINDING 396 396 ATP (BY SIMILARITY).
FT ACT SITE 487 487 BY SIMILARITY.
FT MOD RES 517 517 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 82 87 MISSING (IN REF. 2, 3 AND 4).
FT CONFLICT 535 535 F -> S (IN REF. 3).
FT CONFLICT 540 540 Y -> C (IN REF. 3).
FT STRAND 188 188
FT STRAND 193 194
FT TURN 198 198
FT STRAND 209 210
FT TURN 214 214
FT STRAND 228 228
FT TURN 230 231
SQ SEQUENCE 625 AA; 72291 MW; F7A4A18A8A1AADD C RC64;

Query Match 23.9%; Score 299.5; DB 1; Length 625;
Best Local Similarity 32.1%; Pred. No. 1.4e-20;
Matches 72; Conservative 37; Mismatches 88; Indels 27; Gaps 9;

QY 2 ELRQLSRVNPNTVTKLYGACLN--PVCLVMEYAEAGGSLYNVLHGAEPLPYTTAAHAMSWC 59
Db 411 EAEVMMKLSHPKLVQLYGVCLQEAPICLVFEFMEHGCLSDYLRSGRCL--FAAETLLGMC 468
QY 60 LQCSQGVAYLHSMQPKALIHRLDKPPNLLLVAGGTVLKICDFG----TACDIQTHMTNKK 115
Db 469 LDVCEGWAYL--EKACVHIRDLAARN-CLVGENQVIKVSDFGMTRFVLDQYTSSTGTK 524
QY 116 GSAAMMAPEVFECSNYSEKCDVFSWGILLWEVITRRK-PFEIGGPAFRINWAVHNGTRP 174
Db 525 FPKWASPEVFSFSYSSKSDVWSFGVLMWEVSEGKIPYENRNS--EVVEDISTGFR- 581
QY 175 PLIKNLEKP-----IESLMTRCWSDPSQSPSMEIIVKIMTHL 212
Db 582 -----LYKPRIASCHVIQIMNHCWKKEPDEPPFSQLSLAEI 620

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Search completed: December 4, 2003, 09:30:48
Job time : 23.3378 secs

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OM protein - protein search, using sw model

Run on: December 22, 2004, 13:58:54 ; Search time 90.2825 Seconds
(without alignments)
1997.604 Million cell updates/sec

Title: US-09-830-144-4

Perfect score: 2580

Sequence: 1 MAQRSLQSEQPSWTDD.....AEFYRLWSVDHGGSVVTAP 504

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2580	100.0	504	13	US-10-123-427-2
2	2580	100.0	504	13	US-10-156-895-2
3	2580	100.0	504	14	US-10-384-743-2
4	2580	100.0	504	17	US-10-820-583A-10
5	2580	100.0	517	13	US-10-156-895-11
6	2580	100.0	517	14	US-10-384-743-11
7	2577	99.9	513	13	US-10-156-895-43
8	2577	99.9	513	14	US-10-384-743-43
9	2575	99.8	504	13	US-10-123-427-6
10	409	15.9	84	9	US-09-925-300-1270
11	391	15.2	180	17	US-10-425-115-264407
12	365	14.1	70	9	US-09-864-761-34065
13	261	10.1	51	9	US-09-864-761-34067

14	249.5	9.7	252	15	US-10-072-012-854	Sequence 854, App
15	244.5	9.5	260	15	US-10-072-012-853	Sequence 853, App
16	218	8.4	338	9	US-09-801-267-5	Sequence 5, Appli
17	218	8.4	338	14	US-10-170-789-36	Sequence 36, Appl
18	208	8.1	338	15	US-10-424-599-226401	Sequence 226401,
19	208	8.1	338	15	US-10-424-599-226412	Sequence 226412,
20	206	8.0	432	15	US-10-425-114-59312	Sequence 59312, A
21	205	7.9	274	9	US-09-860-351-4	Sequence 4, Appli
22	205	7.9	300	9	US-09-801-267-4	Sequence 4, Appli
23	205	7.9	300	14	US-10-170-789-35	Sequence 35, Appl
24	203.5	7.9	284	16	US-10-437-963-151472	Sequence 151472,
25	202	7.8	370	17	US-10-425-115-314480	Sequence 314480,
26	202	7.8	416	15	US-10-425-114-72766	Sequence 72766, A
27	201	7.8	312	15	US-10-424-599-219880	Sequence 219880,
28	200.5	7.8	354	17	US-10-425-115-189784	Sequence 189784,
29	198	7.7	290	17	US-10-425-115-288785	Sequence 288785,
30	198	7.7	311	15	US-10-425-114-42276	Sequence 42276, A
31	198	7.7	311	15	US-10-425-114-53347	Sequence 53347, A
32	198	7.7	311	15	US-10-425-114-67199	Sequence 67199, A
33	197.5	7.7	327	16	US-10-437-963-125417	Sequence 125417,
34	197.5	7.7	356	15	US-10-425-114-39847	Sequence 39847, A
35	197.5	7.7	423	15	US-10-425-114-49889	Sequence 49889, A
36	196.5	7.6	356	15	US-10-424-599-208454	Sequence 208454,
37	194.5	7.5	363	15	US-10-424-599-251587	Sequence 251587,
38	194.5	7.5	384	15	US-10-425-114-55810	Sequence 55810, A
39	194	7.5	290	16	US-10-437-963-167104	Sequence 167104,
40	193	7.5	362	16	US-10-437-963-144908	Sequence 144908,
41	192	7.4	285	15	US-10-424-599-206342	Sequence 206342,
42	191.5	7.4	284	17	US-10-425-115-298390	Sequence 298390,
43	191.5	7.4	314	15	US-10-424-599-219869	Sequence 219869,
44	191.5	7.4	321	15	US-10-425-114-58854	Sequence 58854, A
45	191	7.4	284	16	US-10-767-701-45122	Sequence 45122, A

ALIGNMENTS

RESULT 1
US-10-123-427-2
; Sequence 2, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; INVENTOR: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/123,427
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.

```

: PRIOR FILING DATE: 1997-10-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 504
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-158-895-2

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Query Match	100.0%;	Score 2580;	DB 13;	Length 504;
Best Local Similarity	100.0%;	Pred No. 4.5e-200;		
Matches 504;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAAQRRLQSEQPSWTDLPLCLHSLGVGSASNRYSADGKGTSHHPEDSWLKFREN	60	
Db	1	MAAQRRLQSEQPSWTDLPLCLHSLGVGSASNRYSADGKGTSHHPEDSWLKFREN	60	
Qy	61	NCFLYGVFNFGDGNRVNFTNFAOBLSEALLGQLNAEHAADVRRVLLQAFDVVERSEFLS	120	
Db	61	NCFLYGVFNFGDGNRVNFTNFAOBLSEALLGQLNAEHAADVRRVLLQAFDVVERSEFLS	120	
Qy	121	IDDLAELAKASIQSLQPGVPOHQLPOYQKILERLKTLEIREISGGAMAVVALLNNKLYV	180	
Db	121	IDDLAELAKASIQSLQPGVPOHQLPOYQKILERLKTLEIREISGGAMAVVALLNNKLYV	180	
Qy	181	ANVGNTNRALLCKSVTDGLQVTLNVNVDHTTENEDELFRLSQLGLDAGKIKQVGIICQEST	240	
Db	181	ANVGNTNRALLCKSVTDGLQVTLNVNVDHTTENEDELFRLSQLGLDAGKIKQVGIICQEST	240	
Qy	241	RRIGDYKVYGYTDDLLLSAAKSPITIAEPIHGAQPLDGVGTGFLVMSEGLYKALEAAH	300	
Db	241	RRIGDYKVYGYTDDLLLSAAKSPITIAEPIHGAQPLDGVGTGFLVMSEGLYKALEAAH	300	
Qy	301	GFGQANQBIAMIDTEFAKQTSLDVAQAQVVDVRKRIHSDTFASGGERARFCPRHEDMTL	360	
Db	301	GFGQANQBIAMIDTEFAKQTSLDVAQAQVVDVRKRIHSDTFASGGERARFCPRHEDMTL	360	
Qy	361	LVNRFGYPLGMSQPTSPAPAGGRVYPVSVYSSAQSTSKTSVTLSLVMPSSQGVNMG	420	
Db	361	LVNRFGYPLGMSQPTSPAPAGGRVYPVSVYSSAQSTSKTSVTLSLVMPSSQGVNMG	420	
Qy	421	AHSASTLDEAFTLTNQSPITLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPQGEDGRVPP	480	
Db	421	AHSASTLDEAFTLTNQSPITLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPQGEDGRVPP	480	
Qy	481	YVDPAEFYRLMSVDHGEOQSVVTAP	504	
Db	481	YVDPAEFYRLMSVDHGEOQSVVTAP	504	

RESULT 3
US-10-384-743-2
Sequence 2, Application US/10384743
Publication No. US20030162228A1
GENERAL INFORMATION:
APPLICANT: OHO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/10/384,743
CURRENT FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US/09/529,279
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/290188
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 504
TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-384-743-2

Query Match      100.0%; Score 2580; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.5e-200;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60

QY 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120

QY 121 IDALAELKASLOSQPLPGVPOHQPPOYQKILRLKTLERISGGAMAVAVLLNNKLYV 180
Db 121 IDALAELKASLOSQPLPGVPOHQPPOYQKILRLKTLERISGGAMAVAVLLNNKLYV 180

QY 181 ANVGTNRALLCKSVTDGLQVTLNVDHTTENEDELFRSLQGLDAGKIKQVGIICGQEST 240
Db 181 ANVGTNRALLCKSVTDGLQVTLNVDHTTENEDELFRSLQGLDAGKIKQVGIICGQEST 240

QY 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPEIHAQAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPEIHAQAQPLDGVTFGLVLMSEGLYKALEAAH 300

QY 301 GPGQANOEIAAMIDTEFAKOTSLDVAQAQVVDVVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANOEIAAMIDTEFAKOTSLDVAQAQVVDVVKRIHSDTFASGGERARFCPRHEDMTL 360

QY 361 LVNFGYPLGEMSOPTSPAPAGRVYPVSVYSSAQSTSKTSVTLSLWMPGQGMVNG 420
Db 361 LVNFGYPLGEMSOPTSPAPAGRVYPVSVYSSAQSTSKTSVTLSLWMPGQGMVNG 420

QY 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

QY 481 YVDFAEFYRLWSVDHGEOQSVVTAP 504
Db 481 YVDFAEFYRLWSVDHGEOQSVVTAP 504

RESULT 4
US-10-820-583A-10
; Sequence 10, Application US/10820583A
; Publication No. US20040242461A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Michael
; APPLICANT: Oh, Hidemasa
; TITLE OF INVENTION: Modulators of Telomere Stability
; FILE REFERENCE: HO-02673US1
; CURRENT APPLICATION NUMBER: US/10/820,583A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/461,095
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 504
; TYPE: PRT
; ORGANISM: HUMAN
US-10-820-583A-10

Query Match      100.0%; Score 2580; DB 17; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.5e-200;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60

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QY 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120

QY 121 IDALAELKASLOSQPLPGVPOHQPPOYQKILRLKTLERISGGAMAVAVLLNNKLYV 180
Db 121 IDALAELKASLOSQPLPGVPOHQPPOYQKILRLKTLERISGGAMAVAVLLNNKLYV 180

QY 181 ANVGTNRALLCKSVTDGLQVTLNVDHTTENEDELFRSLQGLDAGKIKQVGIICGQEST 240
Db 181 ANVGTNRALLCKSVTDGLQVTLNVDHTTENEDELFRSLQGLDAGKIKQVGIICGQEST 240

QY 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPEIHAQAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPEIHAQAQPLDGVTFGLVLMSEGLYKALEAAH 300

QY 301 GPGQANOEIAAMIDTEFAKOTSLDVAQAQVVDVVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANOEIAAMIDTEFAKOTSLDVAQAQVVDVVKRIHSDTFASGGERARFCPRHEDMTL 360

QY 361 LVNFGYPLGEMSOPTSPAPAGRVYPVSVYSSAQSTSKTSVTLSLWMPGQGMVNG 420
Db 361 LVNFGYPLGEMSOPTSPAPAGRVYPVSVYSSAQSTSKTSVTLSLWMPGQGMVNG 420

QY 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

QY 481 YVDFAEFYRLWSVDHGEOQSVVTAP 504
Db 481 YVDFAEFYRLWSVDHGEOQSVVTAP 504

RESULT 5
US-10-158-895-11
; Sequence 11, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-11

Query Match      100.0%; Score 2580; DB 13; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.6e-200;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60

QY 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLQLNAEHAEDVRRVLLQAFDIVERSFLES 120

QY 121 IDALAELKASLOSQPLPGVPOHQPPOYQKILRLKTLERISGGAMAVAVLLNNKLYV 180

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Db 121 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 180
QY 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
Db 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
QY 241 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 241 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
QY 301 GPGQANQIEAAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQIEAAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
QY 361 LVRNFGYPLGEMSQTPSPAPAAGGRVVPVSPYSSAOSTSKTSVTLSLWMP SQOMVNG 420
Db 361 LVRNFGYPLGEMSQTPSPAPAAGGRVVPVSPYSSAOSTSKTSVTLSLWMP SQOMVNG 420
QY 421 AHSASTLDEATPTLNQSPPTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLNQSPPTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
QY 481 YVDFAEFYRLMSVDHGEQSVVTPAP 504
Db 481 YVDFAEFYRLMSVDHGEQSVVTPAP 504

RESULT 7
US-10-158-895-43
; Sequence 43, Application US/10158895
; Publication No. US2002015624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Query Match 99.9%; Score 2577; DB 13; Length 513;
Best Local Similarity 99.8%; Pred. No. 8e-200;
Matches 503; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQRSLQSQEQPSTDDPLCHLSGVGSANRSYSADGKGTESHPPEDSMKFRSEN 60
Db 10 MAQRSLQSQEQPSTDDPLCHLSGVGSANRSYSADGKGTESHPPEDSMKFRSEN 69
QY 61 NCFLYGVFNGYDGNRVNFAQRLSABLLIGQLNAEHAEDVRVLLQAFDVVERSPLES 120
Db 70 NCFLYGVFNGYDGNRVNFAQRLSABLLIGQLNAEHAEDVRVLLQAFDVVERSPLES 129
QY 121 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 180
Db 130 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 189
QY 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
Db 190 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 249
QY 241 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 250 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 309
QY 301 GPGQANQIEAAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
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Db 121 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 180
QY 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
Db 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
QY 241 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 241 RRIIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
QY 301 GPGQANQIEAAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQIEAAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
QY 361 LVRNFGYPLGEMSQTPSPAPAAGGRVVPVSPYSSAOSTSKTSVTLSLWMP SQOMVNG 420
Db 361 LVRNFGYPLGEMSQTPSPAPAAGGRVVPVSPYSSAOSTSKTSVTLSLWMP SQOMVNG 420
QY 421 AHSASTLDEATPTLNQSPPTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLNQSPPTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
QY 481 YVDFAEFYRLMSVDHGEQSVVTPAP 504
Db 481 YVDFAEFYRLMSVDHGEQSVVTPAP 504

RESULT 6
US-10-384-743-11
; Sequence 11, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-11

Query Match 100.0%; Score 2580; DB 14; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.6e-200;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQRSLQSQEQPSTDDPLCHLSGVGSANRSYSADGKGTESHPPEDSMKFRSEN 60
Db 1 MAQRSLQSQEQPSTDDPLCHLSGVGSANRSYSADGKGTESHPPEDSMKFRSEN 60
QY 61 NCFLYGVFNGYDGNRVNFAQRLSABLLIGQLNAEHAEDVRVLLQAFDVVERSPLES 120
Db 61 NCFLYGVFNGYDGNRVNFAQRLSABLLIGQLNAEHAEDVRVLLQAFDVVERSPLES 120
QY 121 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 180
Db 121 IDDALEKASLQSQLPQGVPOHLPPOYQKILERIKTLERISGGAMAVAVLNNKLYV 180
QY 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
Db 181 ANVTNRALLCKSTVDGLQVTLNVDHTTENEDELFRLSQLGLDAGKIKQVGIICGQEST 240
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Db 310 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTEASGGERARFCPRHEDMTL 369
QY 361 LVNFGYPLGMSQPTSPAPAGGRVYVPVSYSSAQSTSKTSVTLSLVMPSQGQWNG 420
Db 370 LVNFGYPLGMSQPTSPAPAGGRVYVPVSYSSAQSTSKTSVTLSLVMPSQGQWNG 429
QY 421 AHSASTLDEATPTLTNQSPTLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGSDGRVPE 480
Db 430 AHSASTLDEATPTLTNQSPTLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGSDGRVPE 489
QY 481 YVDFAEFYRLWSVDHGEQSVVVTAP 504
Db 490 YVDFAEFYRLWSVDHGEQSVVVTAP 513
RESULT 8
US-10-384-743-43
; Sequence 43, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; PRIOR FILING DATE: 2003-03-11
; PRIOR FILING DATE: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-43

Query Match 99.9%; Score 2577; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 8e-200;
Matches 503; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQRSLQSQEQSWTDDPLCHLSGVGSASNRYSADGKGTEGSHHPEDSWLKFRSEN 60
Db 10 MAQRSLQSQEQSWTDDPLCHLSGVGSASNRYSADGKGTEGSHHPEDSWLKFRSEN 69
QY 61 NCFLYGVFNQYDGNRVNFTNFAQRLSAEALLGQNAEHAEDVRRVLLQAFDVVERSFLES 120
Db 70 NCFLYGVFNQYDGNRVNFTNFAQRLSAEALLGQNAEHAEDVRRVLLQAFDVVERSFLES 129
QY 121 IDDAEAKASLSQSQPEGVQHPQYQKILRLKTLEREISGGAMAVVAVLNNKLYV 180
Db 130 IDDAEAKASLSQSQPEGVQHPQYQKILRLKTLEREISGGAMAVVAVLNNKLYV 189
QY 181 ANVTGNRALLCKSTVDGLQVTLQNVDTHTTENEDELFRSLQGLDAGKIKQVGIICQEST 240
Db 190 ANVTGNRALLCKSTVDGLQVTLQNVDTHTTENEDELFRSLQGLDAGKIKQVGIICQEST 249
QY 241 RRGIDYKVKYGYTDIDLSAASKPIIARPEITHGAQPLDGVTFGLVLMSEGLYKALEAH 300
Db 250 RRGIDYKVKYGYTDIDLSAASKPIIARPEITHGAQPLDGVTFGLVLMSEGLYKALEAH 309
QY 301 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTEASGGERARFCPRHEDMTL 360
Db 310 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTEASGGERARFCPRHEDMTL 369
QY 361 LVNFGYPLGMSQPTSPAPAGGRVYVPVSYSSAQSTSKTSVTLSLVMPSQGQWNG 420
Db 370 LVNFGYPLGMSQPTSPAPAGGRVYVPVSYSSAQSTSKTSVTLSLVMPSQGQWNG 429

QY 421 AHSASTLDEATPTLTNQSPTLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGSDGRVPE 480
Db 430 AHSASTLDEATPTLTNQSPTLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGSDGRVPE 489
QY 481 YVDFAEFYRLWSVDHGEQSVVVTAP 504
Db 490 YVDFAEFYRLWSVDHGEQSVVVTAP 513
RESULT 9
US-10-123-427-6
; Sequence 6, Application US/10123427
; Publication No. US20020119525A1
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiko
; NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/123,427
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-123-427-6

Query Match 99.8%; Score 2575; DB 13; Length 504;
Best Local Similarity 99.8%; Pred. No. 1.1e-199;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQRSLQSQEQSWTDDPLCHLSGVGSASNRYSADGKGTEGSHHPEDSWLKFRSEN 60
Db 1 MAQRSLQSQEQSWTDDPLCHLSGVGSASNRYSADGKGTEGSHHPEDSWLKFRSEN 60
QY 61 NCFLYGVFNQYDGNRVNFTNFAQRLSAEALLGQNAEHAEDVRRVLLQAFDVVERSFLES 120
Db 61 NCFLYGVFNQYDGNRVNFTNFAQRLSAEALLGQNAEHAEDVRRVLLQAFDVVERSFLES 120
QY 121 IDDAEAKASLSQSQPEGVQHPQYQKILRLKTLEREISGGAMAVVAVLNNKLYV 180

Db 121 IDDAAEKASLQSLPEGVPOHLPPOYQKILERLKLTEREISGAMAVAVLNNKLIY 180
Qy 181 ANVTNRAALLCKSVTDGLQVTLQVNDHTTENEDELFRLSQLDAGKIKQVGIICGQEST 240
Db 181 ANVTNRAALLCKSVTDGLQVTLQVNDHTTENEDELFRLSQLDAGKIKQVGIICGQEST 240
Qy 241 RRIIGDYKVKYGYTDIDLLSAAKSPITIAEPIHGAQPLDGVTFVLVMSGLYKALEAAH 300
Db 241 RRIIGDYKVKYGYTDIDLLSAAKSPITIAEPIHGAQPLDGVTFVLVMSGLYKALEAAH 300
Qy 301 GPGQANQEIAMIDTEFAKQTSLSDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQEIAMIDTEFAKQTSLSDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
Qy 361 LVRNFGYPLGEMSQTPSPAPAAAGRVVPVSPYSSAQSTKSTVTLVLVMPSCQMVNG 420
Db 361 LVRNFGYPLGEMSQTPSPAPAAAGRVVPVSPYSSAQSTKSTVTLVLVMPSCQMVNG 420
Qy 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPPTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVEP 480
Qy 481 YVDFAEFYRLKSVVDHGQSVVTAP 504
Db 481 YVDFAEFYRLKSVVDHGQSVVTAP 504

RESULT 10
US-09-925-300-1270
; Sequence 1270, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1270
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1270

Query Match 15.9%; Score 409; DB 9; Length 84;
Best Local Similarity 97.5%; Pred. No. 2.3e-25;
Matches 78; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 425 STLDEATPTLTNQSPPTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVEPYVDF 484
Db 5 ATLDEATPTLTNQSPPTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVEPYVDF 64
Qy 485 AEFYRLKSVVDHGQSVVTAP 504
Db 65 AEFYRLKSVVDHGQSVVTAP 84

RESULT 11
US-10-425-115-264407
; Sequence 264407, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 264407
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_172752C.1.pep
US-10-425-115-264407
Query Match 15.2%; Score 391; DB 17; Length 180;
Best Local Similarity 57.2%; Pred. No. 2.1e-23;
Matches 87; Conservative 10; Mismatches 31; Indels 24; Gaps 3;
Qy 258 LSAAKSPITIAEPIHGAQPLDGVTFVLVMSGLYKALEAAHGGQANQEIAMIDTEF 317
Db 25 LSKTSLAPIIV-----YVKISSPKVLQRLIKSRGKSOAKHLNVQWVAADK 69
Qy 318 AKQ-----TSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTLVRNFGYPLG 370
Db 70 LAQCPELDFVILDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTLLVRNFGYPLG 129
Qy 371 EMSQTPSPAPAAAGRVVPVSPYSSAQSTK 402
Db 130 EMSQTPSPAP--GGRVVPVSPYSSAQSTR 159
RESULT 12
US-09-864-761-34065
; Sequence 34065, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34065
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z83845.14
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: BE746542.1, EVALUE 5.00e-35
; OTHER INFORMATION: SWISSPROT HIT: Q15750, EVALUE 4.00e-36
US-09-864-761-34065

Query Match 14.1%; Score 365; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 MIDTEFAKTSIDAVAQAQVVDVKRTHSTFASGGERARFCPRHEDMTLLVRNFGYPLGE 371
Db 1 MIDTEFAKTSIDAVAQAQVVDVKRTHSTFASGGERARFCPRHEDMTLLVRNFGYPLGE 60

QY 372 MSQPTSPAP 381
Db 61 MSQPTSPAP 70

RESULT 13
US-09-864-761-34067
; Sequence 34067, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34067
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z83845.14
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
; OTHER INFORMATION: SWISSPROT HIT: Q15750, EVALUE 7.00e-24
; OTHER INFORMATION: EST HUMAN HIT: AL118967.1, EVALUE 9.00e-23
US-09-864-761-34067

Query Match 10.1%; Score 261; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 SENNCFLYGVFNGYDGNRVTFNFAORLSAELLGOLNABHAADVRRVLQ 108
Db 1 SENNCFLYGVFNGYDGNRVTFNFAORLSAELLGOLNABHAADVRRVLQ 51

RESULT 14
US-10-072-012-854
; Sequence 854, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zertusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
```

Wed Dec 22 14:29:07 2004

		Sequence 853, Application US/10072012	
		Publication No. US20040033493A1	
		GENERAL INFORMATION:	
		APPLICANT: Tchernev, Velizar	
		APPLICANT: Spytek, Kimberly	
		APPLICANT: Zerhusen, Bryan	
		APPLICANT: Patturajan, Meera	
		APPLICANT: Shimkets, Richard	
		APPLICANT: Li, Li	
		APPLICANT: Gangolli, Esha	
		APPLICANT: Padigaru, Muralidhara	
		APPLICANT: Anderson, David W.	
		APPLICANT: Rastelli, Luca	
		APPLICANT: Miller, Charles E.	
		APPLICANT: Gerlach, Valerie	
		APPLICANT: Taupier Jr, Raymond J.	
		APPLICANT: Gusev, Vladimir Y.	
		APPLICANT: Colman, Steven D.	
		APPLICANT: Wolenc, Adam R.	
		APPLICANT: Pena, Carol E. A	
		APPLICANT: Furtak, Katarzyna	
		APPLICANT: Groesse, William M.	
		APPLICANT: Alsbrook II, John P.	
		APPLICANT: Lepley, Denise M.	
		APPLICANT: Rieger, Daniel K.	
		APPLICANT: Burgess, Catherine E.	
		TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same	
		FILE REFERENCE: 21402-258	
		CURRENT APPLICATION NUMBER: US/10/072,012	
		CURRENT FILING DATE: 2002-01-31	
		PRIOR APPLICATION NUMBER: 60/265,102	
		PRIOR FILING DATE: 2001-01-30	
		PRIOR APPLICATION NUMBER: 60/265,514	
		PRIOR FILING DATE: 2001-01-31	
		PRIOR APPLICATION NUMBER: 60/265,517	
		PRIOR FILING DATE: 2001-01-31	
		PRIOR APPLICATION NUMBER: 60/265,412	
		PRIOR FILING DATE: 2001-01-31	
		PRIOR APPLICATION NUMBER: 60/265,395	
		PRIOR FILING DATE: 2001-01-31	
		PRIOR APPLICATION NUMBER: 60/266,406	
		PRIOR FILING DATE: 2001-02-02	
		PRIOR APPLICATION NUMBER: 60/266,767	
		PRIOR FILING DATE: 2001-02-05	
		PRIOR APPLICATION NUMBER: 60/267,057	
		PRIOR FILING DATE: 2001-02-07	
		PRIOR APPLICATION NUMBER: 60/266,975	
		PRIOR FILING DATE: 2001-02-07	
		PRIOR APPLICATION NUMBER: 60/267,459	
		PRIOR FILING DATE: 2001-02-08	
		Remaining Prior Application data removed - See File Wrapper or PALM.	
		NUMBER OF SEQ ID NOS: 1391	
		SOFTWARE: PatentIn Ver. 2.1	
		SEQ ID NO 853	
		LENGTH: 260	
		TYPE: PRT	
		ORGANISM: Artificial Sequence	
		FEATURE:	
		OTHER INFORMATION: Description of Artificial Sequence:	
		OTHER INFORMATION: Serine/threonine phosphatases, family 2C,	
		OTHER INFORMATION: catalytic domain	
		US-10-072-012-853	
		Query Match 9.5%; Score 244.5; DB 15; Length 260;	
		Best Local Similarity 27.9%; Pred. No. 2.6e-11;	
		Matches 81; Conservative 59; Mismatches 77; Indels 73; Gaps 14;	
		QY 48 PPEDSWL---KFRSENNCFLYGVNGYDGNRVTFVAQRLSAEILLGQLNAEHAADVRR 104	
		Db 23 PMEDAHVITPDLSDGSDSGGFGFVDFDGGGSEAAKFLSKNL-PRILABEL----- 70	
		QY 105 VLIQAFDVVERSFLESIDDAEAKASLQSLPEGVPQHLPPQYOKILERLKTLEITSG 164	
		RESULT 15	
		US-10-072-012-853	

Db	71	-----IKDKDEDEDVEDAL-RKAFRLTD-----BEILBELESLEDQRS-	107
QY	165	GAMAVVAVLLNNKLYVANVGTNRALLCKSTVDGLQVTLNVVDHTTENEDELFRLSQLG--	222
Db	108	GTAVVVALIRGNKLYVANVGDSRAVLCRNG---KAVQLTEDHKPSNEDERERIREAGGF	163
QY	223	LDAGKIKQVGIICQESTRRIGDYKVYGYTDIDLLSAKSKPIIARPEIHGAQPLDGVT	282
Db	164	VSNGRVN--GVLA--LSRALGDFFLX-----PYVIAEPDVTVE-LTEKD	203
QY	283	GFLVLMSEGLYKALEAAHGPQANQETAAAMIDTEFAKQTSLDVAQAQAVD	332
Db	204	DFLILASDGLWDVL-----SNQEVVDIVRKHLKSGGPQEA-AKKLID	244

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OM protein - protein search, using sw model

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(without alignments)
1330.044 Million cell updates/sec

Title: US-09-830-144-2

Perfect score: 3014

Sequence: 1 MSTASAASSSSSSAGEMIE.....QCKKQLEVIRSQQKRGQTS 579

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3014	100.0	579	4	US-10-158-895-4
3	3014	100.0	590	4	US-09-529-279-15
4	3014	100.0	590	4	US-10-158-895-15
5	481	16.0	455	3	US-09-221-235-5
6	481	16.0	455	3	US-09-221-928-5
7	481	16.0	455	3	US-09-221-527-5
8	481	16.0	455	3	US-09-221-236-5
9	481	16.0	455	3	US-09-221-416-5
10	481	16.0	455	3	US-09-221-245-5
11	481	16.0	455	3	US-09-163-115-5
12	481	16.0	455	3	US-09-221-528-5
13	481	16.0	455	3	US-09-593-553-5
14	481	16.0	455	3	US-09-221-237-5
15	481	16.0	455	3	US-09-399-588-2
16	481	16.0	455	4	US-09-757-982-5
17	461.5	15.3	1036	4	US-10-014-882-2
18	418.5	13.9	394	4	US-09-345-473E-19
19	418	13.9	835	3	US-09-291-839-2
20	418	13.9	835	4	US-09-458-457-2
21	418	13.9	835	4	US-09-947-199A-2
22	416	13.8	328	4	US-09-345-473E-18
23	414	13.7	835	4	US-09-458-457-8
24	414	13.7	835	4	US-09-947-199A-8
25	412	13.7	668	1	US-08-205-018-2
26	412	13.7	859	1	US-08-395-580-2
27	412	13.7	859	5	PCT-US95-02792-2

ALIGNMENTS

RESULT 1

US-09-529-279-4

; Sequence 4, Application US/09529279

; Patent No. 6451617

; GENERAL INFORMATION:

; APPLICANT: ONO, KOICHIRO

; APPLICANT: OHTOMO, TOSHIHIKO

; APPLICANT: TSUCHIYA, MASAYUKI

; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

; FILE REFERENCE: 053466/0278

; CURRENT APPLICATION NUMBER: US/09529,279

; CURRENT FILING DATE: 2000-04-11

; PRIOR APPLICATION NUMBER: PCT/JP98/04796

; PRIOR FILING DATE: 1998-10-22

; PRIOR APPLICATION NUMBER: JP 9/290188

; PRIOR FILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-529-279-4

Query Match	100.0%;	Score	3014;	DB	4;	Length	579;
Best Local Similarity	100.0%;	Pred. No.	3.6e-222;	Mismatches	0;	Indels	0;
Matches	579;	Conservative	0;	Gaps	0;		
QY	1	MSTASAASSSSSSAGEMIEAPSOVLNFEEDYKIEIEVEEVVGRGAFVGVCKAKRAKDV	60				
Db	1	MSTASAASSSSSSSSAGEMIEAPSOVLNFEEDYKIEIEVEEVVGRGAFVGVCKAKRAKDV	60				
QY	61	AIKQIESERKAFIVELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEGLSYNLVHGAE	120				
Db	61	AIKQIESERKAFIVELRQLSRVNHNPVIVKLYGACLNPCVCLVMEYAEGLSYNLVHGAE	120				
QY	121	PLPYTTAAHMSWCLQCSQGVAYLHSPKALIHRLDKPPNLLVAGGTVLKICDFGTAC	180				
Db	121	PLPYTTAAHMSWCLQCSQGVAYLHSPKALIHRLDKPPNLLVAGGTVLKICDFGTAC	180				
QY	181	DIQTHMTNNKGAAMAPAEVEFGSNYSKCDVFSWGIILWEVITRRKPFDEIGGPAPRIM	240				
Db	181	DIQTHMTNNKGAAMAPAEVEFGSNYSKCDVFSWGIILWEVITRRKPFDEIGGPAPRIM	240				
QY	241	WAVNGTRPPLIKNLKPPIESLMTRCWSKDSQPSMBEIVKIMTHLMRYFPFGADEPQY	300				
Db	241	WAVNGTRPPLIKNLKPPIESLMTRCWSKDSQPSMBEIVKIMTHLMRYFPFGADEPQY	300				
QY	301	PCOYSDGQSNATSTGSMFMDIASNTNSKSDTNWEQVPATNDTIKRLESKLLKNQAKQ	360				

Db	301	PCQVSDRGQNSATS	TGSGFDIA	TNTN	SGNSTN	MEQVP	ATND	TI	KRL	ESK	LLK	NQAK	QKQ	360							
Qy	361	SESGLSLGASHGSGSVESL	PPTSEGRKMS	AD	MS	SE	IE	AR	IA	AT	TG	NG	QPRRR	IQDL	TVTG	420					
Db	361	SESGLSLGASHGSGSVESL	PPTSEGRKMS	AD	MS	SE	IE	AR	IA	AT	TG	NG	QPRRR	IQDL	TVTG	420					
Qy	421	TEPGVSSRSRSPSVRM	TTTTGGTSEKPTR	SH	PT	PD	DS	TD	TG	NS	D	SG	NS	I	P	MAX	IL	DHQL	480		
Db	421	TEPGVSSRSRSPSVRM	TTTTGGTSEKPTR	SH	PT	PD	DS	TD	TG	NS	D	SG	NS	I	P	MAX	IL	DHQL	480		
Qy	481	QPLAPCNSKESMA	VFEGHC	KMAQ	YVM	KV	OT	EI	ALL	QK	QBL	VA	EL	D	O	K	D	Q	QNT	SRL	540
Db	481	QPLAPCNSKESMA	VFEGHC	KMAQ	YVM	KV	OT	EI	ALL	QK	QBL	VA	EL	D	O	K	D	Q	QNT	SRL	540
Qy	541	VOEHKKLLDENKSL	STYYQ	CKK	QK	LE	V	IR	S	O	O	K	R	G	T	S	579				
Db	541	VOEHKKLLDENKSL	STYYQ	CKK	QK	LE	V	IR	S	O	O	K	R	G	T	S	579				

RESULT 2
US-10-158-895-4
; Sequence 4, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

361	Qy	SEGRLSIGASHGSSVESLPTPTSGEKWMSADMSIEARIAANTTNGQPPRRRSIQDLTVTG	421
361	Db	SEGRLSIGASHGSSVESLPTPTSGEKWMSADMSIEARIAANTTNGQPPRRRSIQDLTVTG	420
421	Qy	TEPQGVSSRSSPSVRMITTTSGPTSEKPTRSHMPDSDTDTNGSDNSIPMAYLTLDHQL	480
421	Db	TEPQGVSSRSSPSVRMITTTSGPTSEKPTRSHMPDSDTDTNGSDNSIPMAYLTLDHQL	480
481	Qy	QPLAPCNSKESMAVFQHCWKMAQYMKVQTEIALLQRKQELVAELDDQDKQOOTSRL	540
481	Db	QPLAPCNSKESMAVFQHCWKMAQYMKVQTEIALLQRKQELVAELDDQDKQOOTSRL	540
541	Qy	VOEHKLLDENKSLSTYYQCKKOLEVIRSQOQKRGTS	579
541	Db	VOEHKLLDENKSLSTYYQCKKOLEVIRSQOQKRGTS	579

RESULT 3
 US-09-529-279-15
 ; Sequence 15, Application US/09529279
 ; Patent No. 6451617
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/09/529,279
 ; CURRENT FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 590
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-279-15

Query Match	100.0%;	Score	3014;	DB	4;	Length	590;
Best Local Similarity	100.0%;	Prod.	No.	3.7e-22;			
Matches	579;	Conservative	0;	Mismatches	22;	Indels	0;
Gaps	0;						
Qy	1	MSTASAASSSSSSSAGEMIEAPSOVLNFEEDIYKEIEVEEVVGRGAFGVCKAKRAKD	60				
Db	1	MSTASAASSSSSSSAGEMIEAPSOVLNFEEDIYKEIEVEEVVGRGAFGVCKAKRAKD	60				
Qy	61	AIKQIESSEKAFIVEIURQLSRVNHPNIVKLYGACLNPCVLVMEIYAGGSLYNVLHGAE	120				
Db	61	AIKQIESSEKAFIVEIURQLSRVNHPNIVKLYGACLNPCVLVMEIYAGGSLYNVLHGAE	120				
Qy	121	PLPYVYTAHAHMSWCIQCQSGVAYLHSMOPKALIHRLDKPPNLLLVAGGTVLKICDFGTAC	180				
Db	121	PLPYVYTAHAHMSWCIQCQSGVAYLHSMOPKALIHRLDKPPNLLLVAGGTVLKICDFGTAC	180				
Qy	181	DIQTHMTNKNKGSAAWPAEVEFEGSNYSKCDVFSWGIIILWEVITRRKPDEIGGPAFRIM	240				
Db	181	DIQTHMTNKNKGSAAWPAEVEFEGSNYSKCDVFSWGIIILWEVITRRKPDEIGGPAFRIM	240				
Qy	241	WAVHNGTPPLIKNLPKDIESLMTFCWSKDSQPSRSMEEIVKIMTHLMRYFFPGADEPQY	300				
Db	241	WAVHNGTPPLIKNLPKDIESLMTFCWSKDSQPSRSMEEIVKIMTHLMRYFFPGADEPQY	300				
Qy	301	PCQYSDGQSNATSSTGSGFMDIASNTNKSNDTNMEQVPAINDTIKRLSKLLKNQAKQ	360				
Db	301	PCQYSDGQSNATSSTGSGFMDIASNTNKSNDTNMEQVPAINDTIKRLSKLLKNQAKQ	360				
Qy	361	SESGLKLSLGASHGSSVESLPPSTSEGRKMSADMSSEIARIAATNTGNGQPRRSIQDITVTG	420				
Db	361	SESGLKLSLGASHGSSVESLPPSTSEGRKMSADMSSEIARIAATNTGNGQPRRSIQDITVTG	420				

QY 421 TEPGVSSSSSSPSVRMITTSPTSEKPTRSHPTDDSTDTNGSDNSIPMAYLTLDHQL 480
Db 421 TEPGVSSSSSSPSVRMITTSPTSEKPTRSHPTDDSTDTNGSDNSIPMAYLTLDHQL 480
QY 481 QPLAPCNSKESMAVFEQHCMAQYMKVQTEIALLQKQELVAELDDQDEKQOQNTSRL 540
Db 481 QPLAPCNSKESMAVFEQHCMAQYMKVQTEIALLQKQELVAELDDQDEKQOQNTSRL 540
QY 541 VQEHKKLLDENKSLSTYYQCKKQLEVIRSQOQKROGTS 579
Db 541 VQEHKKLLDENKSLSTYYQCKKQLEVIRSQOQKROGTS 579

RESULT 4

US-10-158-895-15
; Sequence 15, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Query Match 100.0%; Score 3014; DB 4; Length 590;
Best Local Similarity 100.0%; Pred. No. 3,7e-222;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTAASASSSSSSAGEMEATPSQVLNFEIDYKEIIEVEEVGRCGAFVGVCKAKRAXDV 60
Db 1 MSTAASASSSSSSAGEMEATPSQVLNFEIDYKEIIEVEEVGRCGAFVGVCKAKRAXDV 60
QY 61 AIKQIESESERKAFIVELFQLSRVNHNPVIVKLYGACLPVCLVMEYAEAGSLYVNLHGAE 120
Db 61 AIKQIESESERKAFIVELFQLSRVNHNPVIVKLYGACLPVCLVMEYAEAGSLYVNLHGAE 120
QY 121 PLPYVYTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTAC 180
Db 121 PLPYVYTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTAC 180
QY 181 DIQHTMTNNKGAAMAPVFEVGSNYSEKCDVFSMGILLWEVITRRKPPDETGGAFRIM 240
Db 181 DIQHTMTNNKGAAMAPVFEVGSNYSEKCDVFSMGILLWEVITRRKPPDETGGAFRIM 240
QY 241 WAVHNGTRPPLKNIKPPIESLMTRCWSDPQSPSMEEIVKIMTHLMRYFFGADEPLQY 300
Db 241 WAVHNGTRPPLKNIKPPIESLMTRCWSDPQSPSMEEIVKIMTHLMRYFFGADEPLQY 300
QY 301 PCQYDEGOSNATSGSFMQIASTNTSNKSDTNMEQVPAINDTKRLSKLLKNQAKQO 360
Db 301 PCQYDEGOSNATSGSFMQIASTNTSNKSDTNMEQVPAINDTKRLSKLLKNQAKQO 360
QY 361 SESGRLSLGASHGSSVESLPPTSEKGRMSADMSIEARIAATTGNGQPRRSIQDLTVTG 420
Db 361 SESGRLSLGASHGSSVESLPPTSEKGRMSADMSIEARIAATTGNGQPRRSIQDLTVTG 420
QY 421 TEPGVSSSSSSPSVRMITTSPTSEKPTRSHPTDDSTDTNGSDNSIPMAYLTLDHQL 480

Db 421 TEPGVSSSSSSPSVRMITTSPTSEKPTRSHPTDDSTDTNGSDNSIPMAYLTLDHQL 480
QY 481 QPLAPCNSKESMAVFEQHCMAQYMKVQTEIALLQKQELVAELDDQDEKQOQNTSRL 540
Db 481 QPLAPCNSKESMAVFEQHCMAQYMKVQTEIALLQKQELVAELDDQDEKQOQNTSRL 540
QY 541 VQEHKKLLDENKSLSTYYQCKKQLEVIRSQOQKROGTS 579
Db 541 VQEHKKLLDENKSLSTYYQCKKQLEVIRSQOQKROGTS 579

RESULT 5

US-09-221-235-5
; Sequence 5, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-235-5

Query Match 16.0%; Score 481; DB 3; Length 455;
Best Local Similarity 30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative 81; Mismatches 151; Indels 70; Gaps 18;
QY 27 NFEEDYKEIIEVEEVGRCGAFVGVCKAKW-RAKQVIAK---QIESESERKAFIVELRQL 81
Db 7 SFVQIKFDLQPFENGCGGSGVSVRAKVISQDKEVAVKLLKIEKEAE-----IL 57
QY 82 SRVNHNPVIVKLYGACLP--VCLVMEYAEAGSLYVNLHG--AEPLPYTAAHAMSWCLQC 137
Db 58 SVLSHRNIIQFVGLVLEPNYGVIVTEYASLSLYDYINSRSEEM---DMDHMTWATDV 114
QY 138 SQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKI CDPGTACDIQHTMTNNK--GSAAM 195
Db 115 AKGMHYLHMEAPVKVTHRLDKSRNVVIAADG-VLKICDFG-ASRPHNHTTHMSLVGTFW 172
QY 196 MAPEVFEGSNYSEKCDVFSMGILLWEVITRRKPPDEIGGPAFRIMW-AVHNGTRPPLKN 254
Db 173 MAPEVIOQLPVSCTCTSYGVVLWEMLTREVPFKLEG--LQVAVLVVEKNERLTIPS 230
QY 255 LPKPIESLMTRCWSDPQSPSMEEIVKIMTHLMRYFFGADEPLQYPCQYSDGOSNSAT 314
Db 231 CPRSFAELLHQWEADAKRPSFKIISL-----ESVSDNT- 267
QY 315 STGSFMQIASTNTSNKSDTNMEQVPAINDTKRLSKLLKNQAKQCSGRLSL---GAS 371
Db 268 ---SLPDKCNPSLHNKAERWCE-IEATLERLKLRLDSFKQELKERRLKQWEQKLT 323
QY 372 HGSSVESLPPTS-----EGKMSADMSIEARIAATT--GNGQPRRSIQDLTVTG 421
Db 324 QOSNTPLLLPAAARMSSESYFESKTESNAEMSCQITATSNNGEGHGMNPSLQAMLMGF 383
QY 422 EPGQVSSSSSSPSV 435
Db 384 --GDIFSNNKAGAV 395

RESULT 6

US-09-221-928-5
; Sequence 5, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:

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RESULT 7
US-09-221-527-5
; Sequence 5, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MN1-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-527-5
Query Match 16.0%; Score 481; DB 3; Length 455;

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Best Local Similarity   30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative      81; Mismatches 151; Indels    70; Gaps    18;

QY      27 NFEIDYKEIEVEVVGAGFVGVCKAKW--RAKDVAIK---QIESESERKAFIVELRQL 81
Db      7 SFVIQKFDLQFFENGCGGSGFGSVYRAKWI SQDEKAVAVKKLLKIEKEA-----IL 57

QY      82 SRVNHPNIVKLYGACLNLP--VCLVMVEYAEGLSYNVLHG--AEPLPYTYAAHMSWCLOC 137
Db      58 SVLSHRNIIOFYGVILEPPNYGI VTEVASLGSLDYINSRSEBEM--DMDHIMTWATDV 114

QY      138 SQGVAYIHSMPKALIHRLDKPKNLLLVAGGTVLKICDFGTACDIQTHMTNNK--GSAAW 195
Db      115 AKGMHYLHMEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLVGTFPW 172

QY      196 MAPEVFEGSNYSBKCDVFSWGIIILWEVITRRKPDEFDIGGPAPFRIMW-AVHNGTRPPLIKN 254
Db      173 MAPEVIOQLPVSTFCDTYSYGVVWMLTREVDPFKLEG--LQVALMVEKNERLTIPSS 230

QY      255 LPKPIESLMTRCWSKOPSRPSMBEIVKIETHLMRYFPFGADEPLOYPQCVSDGGQSNSAT 314
Db      231 CPRSF AEILLHQCEWADA KRPSPKQIISIL-----BSMSNDT- 267

QY      315 STGSFMDIASTNTSINKSDTMWEQVPATNDTIKLESKLLKNQAQQOSESGRLSL---GAS 371
Db      268 ---SLPDKCNFSFLHNKAWEKCE-IETATLERLKLRLDLSPKEQELKERERLRKNWEOKLT 323

QY      372 HGSSVESLPTPS-----EGKRMSADMSETEARIAATT-GNGOPRRRSIQDLTVTGT 421
Db      324 EQNTPTLLLPLAARMSEESYFESKTESNAEMSQCITATNSGEHGGMNFSLQAMLMGF 383

QY      422 EPGQVSRSRSSPSV 435
Db      384 --GDIFSMNKAGAV 395

RESULT 8
US-09-221-236-5
; Sequence 5, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MMI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-236-5

Query Match          16.0%; Score 481; DB 3; Length 455;
Best Local Similarity 30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative      81; Mismatches 151; Indels    70; Gaps    18;

QY      27 NFEIDYKEIEVEVVGAGFVGVCKAKW--RAKDVAIK---QIESESERKAFIVELRQL 81
Db      7 SFVIQKFDLQFFENGCGGSGFGSVYRAKWI SQDEKAVAVKKLLKIEKEA-----IL 57

QY      82 SRVNHPNIVKLYGACLNLP--VCLVMVEYAEGLSYNVLHG--AEPLPYTYAAHMSWCLOC 137
Db      58 SVLSHRNIIOFYGVILEPPNYGI VTEVASLGSLDYINSRSEBEM--DMDHIMTWATDV 114

QY      138 SQGVAYIHSMPKALIHRLDKPKNLLLVAGGTVLKICDFGTACDIQTHMTNNK--GSAAW 195
Db      115 AKGMHYLHMEAPVKVIHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLVGTFPW 172

QY      196 MAPEVFEGSNYSBKCDVFSWGIIILWEVITRRKPDEFDIGGPAPFRIMW-AVHNGTRPPLIKN 254

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US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Accog, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-415-5

Query Match      16.0%; Score 481; DB 3; Length 455;
Best Local Similarity 30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative 81; Mismatches 151; Indels 70; Gaps 18;

QY 27 NFEIDYKEIEVEEVGAGFVCKAKW--RAKDVAIK--QIESEERKAFIVELQOL 81
DQ 7 SFVQIKFDLQFFENCNGGSGFVSVRKAWISQDEKAVKLLKIEKAE-----IL 57

QY 82 SRVNHNTVKLYGACLN--VCLNMEYAEAGSLYNVLHG--AEPLPYTAHAMSWCLQC 137
DQ 58 SVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLDYINSRSEEM---DMDHIMTWATDV 114

QY 138 SQGVAYLHSMOPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNK--GSAAW 195
DQ 115 AKGMHYLHMEAPVKVIHRDLKSRNVVIAADG-VLKICDFG-ASRFHNETHMSLVGTFPW 172

QY 196 MAPEVFEGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAPRIMW-AVHNGTRPPLKN 254
DQ 173 MAPEVIQSLPVSETCDTYSYGVLMWMLTREVPFKGLEG--LQVAWLVEKNERLTIPSS 230

QY 255 LPKPIESLMTRCWSKDPQSRPSMBEIVKIMTHLMRYFPFGADEPLQYPCQYSDGOSNAT 314
DQ 231 CPRSPAEHLHCWEADAKRPSFKQIISIL-----ESMSNDT- 267

QY 315 STGSFMDIASNTNKNSTNNMEQVPATNDTKRLSKLLKNQAKQOSGRLSL---GAS 371
DQ 268 ---SLPDKCNFLHNAEWRCE-IEATLERLKKLERDLSFKEQELKERERRLKNWEQKLT 323

QY 372 HGSSVESLPPTS-----EGKMSADMSEIARIAATT-GNGOPRRRSIQDLTVTGT 421
DQ 324 EQSNTPLLPLAARMSSESYFESKTESNSAEMSCQITATNGEGHGMNPSIQAMLMGF 383

QY 422 EPGQVSSRSSPSV 435
DQ 384 --GDFSMNKAGAV 395

RESULT 13
US-09-593-553-5
; Sequence 5, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-553-5

Query Match      16.0%; Score 481; DB 3; Length 455;
Best Local Similarity 30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative 81; Mismatches 151; Indels 70; Gaps 18;

QY 27 NFEIDYKEIEVEEVGAGFVCKAKW--RAKDVAIK--QIESEERKAFIVELQOL 81
DQ 7 SFVQIKFDLQFFENCNGGSGFVSVRKAWISQDEKAVKLLKIEKAE-----IL 57

QY 82 SRVNHNTVKLYGACLN--VCLNMEYAEAGSLYNVLHG--AEPLPYTAHAMSWCLQC 137
DQ 58 SVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLDYINSRSEEM---DMDHIMTWATDV 114

QY 138 SQGVAYLHSMOPKALIHRLDKPPNLLVAGGTVLKICDFGTACDIQTHTMNNK--GSAAW 195
DQ 115 AKGMHYLHMEAPVKVIHRDLKSRNVVIAADG-VLKICDFG-ASRFHNETHMSLVGTFPW 172

QY 196 MAPEVFEGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAPRIMW-AVHNGTRPPLKN 254
DQ 173 MAPEVIQSLPVSETCDTYSYGVLMWMLTREVPFKGLEG--LQVAWLVEKNERLTIPSS 230

QY 255 LPKPIESLMTRCWSKDPQSRPSMBEIVKIMTHLMRYFPFGADEPLQYPCQYSDGOSNAT 314
DQ 231 CPRSPAEHLHCWEADAKRPSFKQIISIL-----ESMSNDT- 267

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DQ 268 ---SLPDKCNFLHNAEWRCE-IEATLERLKKLERDLSFKEQELKERERRLKNWEQKLT 323

QY 372 HGSSVESLPPTS-----EGKMSADMSEIARIAATT-GNGOPRRRSIQDLTVTGT 421
DQ 324 EQSNTPLLPLAARMSSESYFESKTESNSAEMSCQITATNGEGHGMNPSIQAMLMGF 383

QY 422 EPGQVSSRSSPSV 435
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US-09-221-528-5
; Sequence 5, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-528-5

Query Match      16.0%; Score 481; DB 3; Length 455;
Best Local Similarity 30.4%; Pred. No. 1.1e-28;
Matches 132; Conservative 81; Mismatches 151; Indels 70; Gaps 18;

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QY 82 SRVNHNTVKLYGACLN--VCLNMEYAEAGSLYNVLHG--AEPLPYTAHAMSWCLQC 137
DQ 58 SVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLDYINSRSEEM---DMDHIMTWATDV 114
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Db 384 --GDFSMNKAGAV 395

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RESULT 14

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US-09-221-237-5
; Sequence 5, Application US/09221237
; Patent No. 6214597
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,237
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-237-5

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Search completed: December 22, 2004, 13:59:57
Job time : 30.8698 secs

RESULT 15

US-09-399-588-2 ; Sequence 2, Application US/09399588
; Patent No. 6511825
; GENERAL INFORMATION:

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2004, 13:58:54 ; Search time 103.717 Seconds
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1997.604 Million cell updates/sec

Title: US-09-830-144-2

Perfect score: 3014

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Gapop 10.0 , Gapext 0.5

Searched: 1599859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1599859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3014	100.0	579	13	US-10-158-895-4
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3	3014	100.0	590	13	US-10-158-895-4
4	3014	100.0	590	14	US-10-158-895-4
5	2488.5	82.6	518	14	US-10-283-023-2
6	2488.5	82.6	518	15	US-10-283-023-2
7	1781	59.1	336	16	US-10-386-414-13
8	502	16.7	953	14	US-10-664-421-135
9	502	16.7	953	15	US-10-369-022-56
10	493.5	16.4	954	15	US-10-042-865-98
11	493.5	16.4	954	15	US-10-042-865-97
12	482.5	16.0	330	16	US-10-263-929-187
13	482	16.0	473	15	US-10-664-421-136
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					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 2, Appl
					Sequence 13, Appl
					Sequence 135, Appl
					Sequence 56, Appl
					Sequence 98, Appl
					Sequence 97, Appl
					Sequence 187, Appl
					Sequence 136, Appl
					Sequence 837, Appl

14 481 16.0 455 9 US-09-757-982-5
15 481 16.0 455 14 US-10-094-749-3477
16 481 16.0 455 15 US-10-352-674A-2
17 462.5 15.3 1066 15 US-10-042-865-95
18 462.5 15.3 1096 15 US-10-210-130-130
19 462.5 15.3 1118 15 US-10-112-944-359
20 462 15.3 1021 15 US-10-451-168-87
21 461.5 15.3 719 15 US-10-182-243-55
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24 461.5 15.3 1036 14 US-10-354-358-24
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31 459.5 15.2 847 15 US-10-263-929-188
32 459.5 15.2 847 15 US-10-380-235-2
33 456.5 15.1 800 16 US-10-408-765A-1101
34 456.5 15.1 800 17 US-10-737-450-66
35 456.5 15.1 1036 16 US-10-408-765A-2675
36 456 15.1 948 13 US-10-087-192-1869
37 455 15.1 312 16 US-10-664-421-137
38 454 15.1 964 15 US-10-210-130-32
39 451.5 15.0 1097 14 US-10-288-798-12
40 451.5 15.0 1097 15 US-10-362-892-12
41 451 15.0 1046 15 US-10-258-106-9
42 450.5 14.9 1002 15 US-10-263-929-193
43 445.5 14.8 376 15 US-10-424-599-271998
44 444.5 14.7 1024 15 US-10-042-865-16
45 439.5 14.6 422 16 US-10-437-963-132604

ALIGNMENTS

RESULT 1
US-10-158-895-4
; Sequence 4, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JF98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

Query Match 100.0%; Score 3014; DB 13; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.6e-193;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MSTAASASSSSSSSAGEMIEAPSOVLNFEEDYKEIEVEEVVGRGAFGWCKAKWRAKDV 60
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Db 61 AIKQIESERKAFIVELRQLSRVNHNPVVKLYGACLPVCLVMEYAEAGGSLYNVLHGAE 120
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Db 181 DIQTHMTNNKGAAMAPVEFEGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIM 240
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Db 361 SESGRSLGASHGSSVESLPPTSEGRKMSADMSIEARIAATTGNGOPRRRSIQDLTVTG 420
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RESULT 2

US-10-384-743-4
; Sequence 4, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-4

Query Match 100.0%; Score 3014; DB 14; Length 579;
Best Local Similarity 100.0%; Pred. No. 3,6e-193;
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Db 361 SESGRSLGASHGSSVESLPPTSEGRKMSADMSIEARIAATTGNGOPRRRSIQDLTVTG 420
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RESULT 3

US-10-158-895-15
; Sequence 15, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Query Match 100.0%; Score 3014; DB 13; Length 590;
Best Local Similarity 100.0%; Pred. No. 3,7e-193;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ; Sequence 15, Application US/10384743
 ; Publication No. US20030162228A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ONO, KOICHIRO
 ; APPLICANT: OHTOMO, TOSHIHIKO
 ; APPLICANT: TSUCHIYA, MASAYUKI
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
 ; FILE REFERENCE: 053466/0278
 ; CURRENT APPLICATION NUMBER: US/10/384,743
 ; CURRENT FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US/09/529,279
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: JP 9/290188
 ; PRIOR FILING DATE: 1997-10-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 590
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-384-743-15

Query Match 100.0%; Score 3014; DB 14; Length 590;
 Best Local Similarity 100.0%; Pred. No. 3.7e-193;
 Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 301 PCQYDEGQSNATSGSFMDIASNTSNKSDTNMEQVPAATNDTIKRLSKLLKNQAKQ 360
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RESULT 5
 US-10-283-023-2
 ; Sequence 2, Application US/10283023
 ; Publication No. US20030091573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Garroll, Joseph M.
 ; TITLE OF INVENTION: Methods and compositions for the
 ; diagnosis and treatment of hematological disorders using
 ; FILE REFERENCE: 16319
 ; CURRENT APPLICATION NUMBER: US/10/283,023
 ; CURRENT FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 60/335,044
 ; PRIOR FILING DATE: 2001-10-31
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-283-023-2

Query Match 82.6%; Score 2488.5; DB 14; Length 518;
 Best Local Similarity 93.8%; Pred. No. 4.4e-158;
 Matches 481; Conservative 0; Mismatches 5; Indels 27; Gaps 1;

QY 1 MSTAAGSSSSSSSAGEMIEAPSOVLNFEEDYKIEVEEVVGRGAFGVCKAKWRAKDV 60
 Db 1 MSTAAGSSSSSSSAGEMIEAPSOVLNFEEDYKIEVEEVVGRGAFGVCKAKWRAKDV 60

QY 61 AIKQIESSEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLWMEYAEAGSSLYNVLHGA 120
 Db 61 AIKQIESSEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLWMEYAEAGSSLYNVLHGA 120

QY 121 PLPYTAAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTAC 180
 Db 121 PLPYTAAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFGTAC 180

QY 181 DIQHTMTNNKGSAAWMAPEVFEKSNYSEKCDVFSWGIILLWEVITRRKPPDEIGGPAFRIM 240
 Db 181 DIQHTMTNNKGSAAWMAPEVFEKSNYSEKCDVFSWGIILLWEVITRRKPPDEIGGPAFRIM 240
 QY 241 WAVHNGTRPPLIKNLPKPIESLMTWCWSDPSQPSMEEIVKIMTHLMRYFFGADPELOY 300
 Db 241 WAVHNGTRPPLIKNLPKPIESLMTWCWSDPSQPSMEEIVKIMTHLMRYFFGADPELOY 300

Db 241 WAVHNGTRPPLIKNLKPESLMTRCWSKDPQSPQSMEEIVKIMTHLMRYPPGADEPLOY 300
Qy 301 PCQYSDGQNSATSTGSMFMDIASNTSNKSDTNMEQVPAATNDTIKRLESKLLKNQAKQ 360
Db 301 PCQYSDGQNSATSTGSMFMDIASNTSNKSDTNMEQVPAATNDTIKRLESKLLKNQAKQ 360
Qy 361 SESGRSLGASHGSSVESLPTSTSEGRKMSADMSEIEARIAATT----- 403
Db 361 SESGRSLGASHGSSVESLPTSTSEGRKMSADMSEIEARIAATTAYSKPKRHRKTASFGN 420
Qy 404 -----GNGOPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTSSEKPTRSH 453
Db 421 ILDVPEIVISGNGOPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTSSEKPTRSH 480
Qy 454 WTPDDSTDTNGSDNSIPMAYILTDHQLQPLAPC 486
Db 481 WTPDDSTDTNGSDNSIPMAYILTDHQLQARTSC 513

RESULT 6

US-10-386-414-13
; Sequence 13, Application US/10386414
; Publication No. US2004006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16313,
; FILE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0210MNTM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-386-414-13

Query Match 82.6%; Score 2488.5; DB 15; Length 518;
Best Local Similarity 93.8%; Pred. No. 4.4e-158;
Matches 481; Conservative 0; Mismatches 5; Indels 27; Gaps 1;

Qy 1 MSTAASASSSSSSSAGEMIEAPSVLNFEEDYKIEIEVEEVVGRGAFGVCKAKRAKDV 60
Db 1 MSTAASASSSSSSSAGEMIEAPSVLNFEEDYKIEIEVEEVVGRGAFGVCKAKRAKDV 60

Qy 61 AIKOIESESEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLMVEYABGGSILYNVLHGAE 120
Db 61 AIKOIESESEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLMVEYABGGSILYNVLHGAE 120
Qy 121 PLPYTTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGTGLKICDFGTAC 180
Db 121 PLPYTTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGTGLKICDFGTAC 180
Qy 181 DIQTHMTNNKGAAMPAPEVPEGSNYSEKCDVFWNGIILMEVITRRKPFDDIGGPAFRIM 240
Db 181 DIQTHMTNNKGAAMPAPEVPEGSNYSEKCDVFWNGIILMEVITRRKPFDDIGGPAFRIM 240
Qy 241 WAVHNGTRPPLIKNLKPESLMTRCWSKDPQSPQSMEEIVKIMTHLMRYPPGADEPLOY 300
Db 241 WAVHNGTRPPLIKNLKPESLMTRCWSKDPQSPQSMEEIVKIMTHLMRYPPGADEPLOY 300
Qy 301 PCQYSDGQNSATSTGSMFMDIASNTSNKSDTNMEQVPAATNDTIKRLESKLLKNQAKQ 360
Db 301 PCQYSDGQNSATSTGSMFMDIASNTSNKSDTNMEQVPAATNDTIKRLESKLLKNQAKQ 360
Qy 361 SESGRSLGASHGSSVESLPTSTSEGRKMSADMSEIEARIAATT----- 403
Db 361 SESGRSLGASHGSSVESLPTSTSEGRKMSADMSEIEARIAATTAYSKPKRHRKTASFGN 420
Qy 404 -----GNGOPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTSSEKPTRSH 453
Db 421 ILDVPEIVISGNGOPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTSSEKPTRSH 480
Qy 454 WTPDDSTDTNGSDNSIPMAYILTDHQLQPLAPC 486
Db 481 WTPDDSTDTNGSDNSIPMAYILTDHQLQARTSC 513

RESULT 7

US-10-664-421-135
; Sequence 135, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ASHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 135
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-664-421-135

Query Match 59.1%; Score 1781; DB 16; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.4e-111;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAASASSSSSSSAGEMIEAPSVLNFEEDYKIEIEVEEVVGRGAFGVCKAKRAKDV 60
Db 1 MSTAASASSSSSSSAGEMIEAPSVLNFEEDYKIEIEVEEVVGRGAFGVCKAKRAKDV 60

Qy 61 AIKOIESESEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLMVEYABGGSILYNVLHGAE 120
Db 61 AIKOIESESEKAFIVELRQLSRVNHNPVVKLYGACLNPCVLMVEYABGGSILYNVLHGAE 120
Qy 121 PLPYTTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPPNLLVAGTGLKICDFGTAC 180

```

Db 121 PLYPTAAHMSWCQCQGVAYLHSMQPKALIHRLDKPPNLLLVAGGVVLKICDFGTAC 180
QY 181 DIQHTMTNKGSAAMWAEVFEVGSNSYSEKCDVFSWGIILWEVITRRKPPDEIGGPAFRIM 240
Db 181 DIQHTMTNKGSAAMWAEVFEVGSNSYSEKCDVFSWGIILWEVITRRKPPDEIGGPAFRIM 240
QY 241 WAVHNGTAPPLIKNPKPIESIMTRCWSKDPQRSQPSMEEIVKIMTHLMRYFFGADPELQY 300
Db 241 WAVHNGTAPPLIKNPKPIESIMTRCWSKDPQRSQPSMEEIVKIMTHLMRYFFGADPELQY 300
QY 301 PCQYSDGQNSATSGFMDIASNTSNKSDTNME 336
Db 301 PCQYSDGQNSATSGFMDIASNTSNKSDTNME 336

RESULT 8
US-10-369-022-56
; Sequence 56, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNMIM
; CURRENT APPLICATION NUMBER: US/10369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/387,536
; PRIOR FILING DATE: 2002-06-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-022-56

Query Match 16.7%; Score 502; DB 14; Length 953;
Best Local Similarity 29.3%; Pred. No. 7.2e-25;
Matches 147; Conservative 78; Mismatches 194; Indels 82; Gaps 15;

QY 21 APSQVNLFEIDYKEIEVEVVRGAFGVVCKWRAKDAVAKQISESESRKAFIV---- 76
Db 83 APAGQLQPOEIPFHELQIEITGVGGFGKVKYRALMRVEEVAVKAAARLDPEKDPAVTAEQV 142
QY 77 --ELQLSRVNHPNTVKLYGACLN--VCLVMVEAGGSLYNVLHGABPLPYVYTAHAAMS 132
Db 143 CQEARLFGALQHPNIIALRGACLNPHULCLVWEYARGGALSRLAGRRVPPHV----LVN 198

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QY 133 WCLQSCQGVAYLHSMQPKALIHRLDKPPNLLLV-----AGGTVLKICDFGTACD-IQT 184
Db 139 WAVQVARGMNYLHNDAPVPIIHRDLKSNILILEAIENHNLAADTVLKITDFGLAREWHKT 258
QY 185 HMTNKNKSAAMWAEVFEVGSNSYSEKCDVFSWGIILWEVITRRKPPDEIGGPAFRIMWAV- 243
Db 259 TQMSAAGTYAMWAEVIRLSLFSKSDVMSFGVLLWELLTGEVVPYREI--DALAVAYGVA 316
QY 244 HNGTAPPLIKNPKPIESIMTRCWSKDPQRSQPSMEEIVKIMTHLMRYFFGADPELQYPCQ 303
Db 317 MNKLTLPSTCPEPFARLLEECWDPDGHRPFDGSLKRLLEVIEQ-----SALQMPLE 371
QY 304 YSDGQNSATSGFMDIASNTSNKSDTNMEQVPAT-----NDTIRLESKLLKNQ- 356
Db 372 SFHSLQEDWKLEIQHMFDDLRTKELRSREBELRAAQEQRFQEEQLRRRQELAEREM 431
QY 357 -----AKQOSESGRSLGASHGSSVESLP-----PTS 383
Db 432 DIVERELHLLMCQLSQEKPRVKRKNFRAVLKUREGSSHLSLPSGFEHKITVQASPTL 491
QY 384 EGRKMSADMSEIEARIAATNGQPPRRRSIQDLTVTGTGPGQVSSRSRSPSVRMITTSGP 443
Db 492 D-KRKSGDASPPASPSII-----PRLRAIR--LTPVDCGSGSSSGSGSGGTWSRGCP 542
QY 444 TSEK-----PTRSHPWTPDDSD 459
Db 543 PKKEELVGGKKKGRTWGPSSST 563

RESULT 9
US-10-042-865-98
; Sequence 98, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10

```

```
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-98

Query Match      16.7%; Score 502; DB 15; Length 953;
Best Local Similarity 29.3%; Pred. No. 7.2e-25;
Matches 147; Conservative 78; Mismatches 194; Indels 82; Gaps 15;

QY 21 APSQVLFEEIDYKEIEVEEVGGAFCVCKAKWRAKQVAIKQIESERKAFIV--- 76
Db 83 APAGLQLPQELPFHELOLEELIGVGKGVTRALWRGEEVAVKARLDPEKDPVTAEOV 142
QY 77 --ELRQLSRVNHNPVIVKLYGACLPN--VCLVMEYAEAGSLYNVLHGAEPLPYTTAAHAMS 132
Db 143 CQEARLFGALQHPNIIALRGACLPNPHLCLVMEYARGGALSRLVLAGRRVPHV---LVN 198
QY 133 WCLQCSQGVAYLHSMQKALIHRLDKPPNLLV-----AGGTVLKICDFTGACD-IQT 184
Db 199 WAVQVARGMNYLHNDAPVPIIHRDLKSNIIILAEIENHNLDVTLKTDGFLAREWHT 258
QY 185 HMTNKGSAAMWAVEFEGSNYSKCDVFSNGIILWEVITRRKPFDEIGGPAFRIMWAV- 243
Db 259 TKMSAAGTYAMWAVEVIRLSFSKSSDVMSFGVLLWELLTGEVYREI--DALAVAYGVA 316
QY 244 HNGTRPPLIKNLKPPIESLMTRCKSKDPSRPSMEEIVKIMTHLMRYPPGADPELQYPCQ 303
Db 317 MNKLTLPSTCPEPPFARLLDEECWDPDHGRDPFGSILKRLVIEQ-----SALFQMLE 371
QY 304 YSDGQNSATSGSFMIDASTNTSNKSDTNWQVPAT-----NDITKRLSKLLKNQ- 356
Db 372 SFHSLQEDWKLEIQHMFDDLRKTKEKLSREBELLRAAQEQRFQELRRREQELAREM 431
QY 357 -----AKQSSGRLSLGASHGSSVESLP-----PTS 383
Db 432 DIVERBELHLLMCQLSQEKPRVKRKKGNKRAVLKLRGSSHSILSPSGFEHKITVQASPTL 491
QY 384 EGKMSADMSEIARIAATTGNGOFRRRSIQDLTVTGTGEPGQVSSRSSSPSVRMITTSGP 443
Db 492 D-KRKGSDGASPPASPSII-----PRLRAIR--LTPVDCGSSGSSGSGGTSWRRGP 542
QY 444 TSEK-----PTRSHPTPDDS 459
Db 543 PKBELVGGKKKGRTWGPST 563

RESULT 10
US-10-042-865-97
; Sequence 97, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
```

```
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 954
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-97

Query Match      16.4%; Score 493.5; DB 15; Length 954;
Best Local Similarity 28.9%; Pred. No. 2.7e-24;
Matches 145; Conservative 82; Mismatches 192; Indels 83; Gaps 16;

QY 21 APSQVLFEEIDYKEIEVEEVGGAFCVCKAKWRAKQVAIKQIESERKAFIV--- 76
Db 83 APAGLQLPQELPFHELOLEELIGVGKGVTRALWRGEEVAVKARLDPEKDPVTAEOV 142
QY 77 --ELRQLSRVNHNPVIVKLYGACLPN--VCLVMEYAEAGSLYNVLHGAEPLPYTTAAHAMS 132
Db 143 CQEARLFGALQHPNIIALRGACLPNPHLCLVMEYARGGALSRLVLAGRRVPHV---LVN 198
QY 133 WCLQCSQGVAYLHSMQKALIHRLDKPPNLLV-----AGGTVLKICDFTGACD-IQT 184
Db 199 WAVQVARGMNYLHNDAPVPIIHRDLKSNIIILAEIENHNLDVTLKTDGFLAREWHT 258
QY 185 HMTNKGSAAMWAVEFEGSNYSKCDVFSNGIILWEVITRRKPFDEIGGPAFRIMWAV- 243
Db 259 TKMSAAGTYAMWAVEVIRLSFSKSSDVMSFGVLLWELLTGEVYREI--DALAVAYGVA 316
QY 244 HNGTRPPLIKNLKPPIESLMTRCKSKDPSRPSMEEIVKIMTHL-----MRYFPGA 294
Db 317 MNKLTLPSTCPEPPFARLLDEECWDPDHGRDPFGSILKRLVIEQSALEFQMPLESFHS 376
QY 295 DEPLOYPCQY-----SDEGQNSATSGSF-----MDTAST 325
Db 377 QEDWKLEIQHMFDDLRKTKEKLSREBELLRAAQEQRFQELRRREQELAREMDI--- 433
QY 326 NTSNKSNTNMEQVPATNDITKRLSKLLKNQAKQSSG---RLSLGASHGSSVESLPPT 382
Db 434 -VERELHLLMCQLSQEKPRVKRKKGNKRAVLKLRGSSHSILSPSGFEHKITVQASPTL 492
QY 383 SEGKMSADMSEIARIAATTGNGOFRRRSIQDLTVTGTGEPGQVSSRSSSPSVRMITTS 442
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; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 136
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-136

Query Match          16.0%; Score 482.5; DB 16; Length 330;
Best Local Similarity 38.4%; Pred. No. 3.9e-24;
Matches 107; Conservative 51; Mismatches 98; Indels 23; Gaps 7;

QY 21 APSQVLFEEIDYKEIEVEVVGORGAPGVCKAKWAKOVAIKQISESRKAFIV---- 76
   || : || : || : || : || : || : || : || : || : || : || : || :
Db 4  APAGLQLPQIPPEHLQLEIIIGVGFGKYRVALWRGEEVAVKAAALDPEKDPVTAEQV 63
   || : || : || : || : || : || : || : || : || : || : || : || :
QY 77 --ELRQLSRVNHENIVKLYGACINP--VCLVMEVYAEGGSVNVVLHGAELPYVYTAHAMS 132
   || : || : || : || : || : || : || : || : || : || : || : || :
Db 64  CQEARLFGALQHNNIITALRGACINPPLHCLVMEYAGGALSRLVAGRRVPHV----LVN 119
   || : || : || : || : || : || : || : || : || : || : || : || :
QY 133 WCLQCSQGVAYLHSMOPKALIHRLDKPPNLLLV-----AGTVLKICDFGTACD-IQT 184
   || : || : || : || : || : || : || : || : || : || : || : || :
Db 120 WAVQVARGNNYLHNDAPVPIIHEDLKSINLILILEATENHNLAOTVLKITDFGLAREWHKT 179
   || : || : || : || : || : || : || : || : || : || : || : || :
QY 185 HMTNNKGSAAWPAPEVFGSGNYSKCDVFSWGIIIMVEITRRKPFDEIGGAFRIMWAV- 243
   || : || : || : || : || : || : || : || : || : || : || : || :
Db 180 TKMSAGTGYAWMAPEVIRLSLFKSKSDVMSFGVLLWELLTGEVPYREI--DALAVAYGVA 237
   || : || : || : || : || : || : || : || : || : || : || : || :
QY 244 HNGTRPLIKNLKPKIESLMTRCWSKDPSORPSMEELIVK 282
   || : || : || : || : || : || : || : || : || : || : || : || :
Db 238 MNKLTLPSTCEPFPARLLEECWDDPHGRPDFGSILK 276
   || : || : || : || : || : || : || : || : || : || : || : || :

RESULT 13
US-10-296-115-837
; Sequence 837, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 837
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-837

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Query Match      16.0%; Score 482; DB 15; Length 473;
Best Local Similarity 30.4%; Pred. No. 6.6e-24;
Matches 134; Conservative 81; Mismatches 156; Indels 70; Gaps 18;

QY 20 EAPSQVLNFEEIDYKEIVBEVVGRAFGVCKAKW--RAKDVAIR---QIESERKAF 74
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 18 EMSSLGASVQIKFDLOPFENGCGGSGFVGRVAKVISODKEVAVKLLKIKERAE---73
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2004, 13:58:53 ; Search time 25.1302 Seconds
(without alignments)
1330.044 Million cell updates/sec

Title: US-09-830-144-4

Perfect score: 2580

Sequence: 1 MAAGRRSLQEQPSWTDD.....AEFYRLMSVDKGEQSVVTAP 504

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
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- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2580	100.0	504	2	US-08-752-891-2
2	2580	100.0	504	2	US-09-144-178-2
3	2580	100.0	504	3	US-09-466-854-2
4	2580	100.0	504	4	US-09-519-279-2
5	2580	100.0	504	4	US-10-118-895-2
6	2580	100.0	517	4	US-09-519-279-11
7	2580	100.0	517	4	US-10-118-895-11
8	2577	99.9	513	4	US-09-529-279-43
9	2577	99.9	513	4	US-10-158-895-43
10	2575	99.8	504	2	US-08-752-891-6
11	2575	99.8	504	2	US-09-144-178-6
12	2575	99.8	504	3	US-09-406-854-6
13	391	15.2	217	4	US-09-270-767-32865
14	178	6.9	392	3	US-09-013-881-2
15	178	6.9	392	4	US-09-612-473-2
16	178	6.9	392	4	US-09-724-730-2
17	170.5	6.6	372	4	US-09-973-963-4
18	151	5.9	335	4	US-09-270-767-43565
19	150	5.8	669	4	US-09-270-767-46055
20	147	5.7	1512	4	US-09-328-352-5163
21	146	5.7	241	4	US-09-270-767-32790
22	146	5.7	241	4	US-09-270-767-48007
23	131	5.1	454	4	US-09-538-092-1156
24	128	5.0	286	4	US-09-270-767-61602
25	128	5.0	382	4	US-09-538-092-1086
26	125.5	4.9	546	3	US-08-935-855-20
27	125.5	4.9	546	4	US-09-538-092-827

28 124 4.8 306 2 US-08-822-701-8 Sequence 8, Appli
29 124 4.8 306 3 US-08-935-855-8 Sequence 8, Appli
30 121 4.7 531 4 US-09-248-796A-15560 Sequence 15560, A
31 118 4.6 390 4 US-09-206-646-4 Sequence 4, Appli
32 118 4.6 392 2 US-08-822-701-2 Sequence 2, Appli
33 118 4.6 392 3 US-08-935-855-22 Sequence 22, Appli
34 118 4.6 542 3 US-08-935-855-22 Sequence 22, Appli
35 117.5 4.6 309 3 US-08-822-701-7 Sequence 7, Appli
36 117.5 4.6 309 3 US-08-935-855-7 Sequence 7, Appli
37 117.5 4.6 393 4 US-09-538-092-34 Sequence 34, Appli
38 117 4.5 390 2 US-08-873-093-3 Sequence 3, Appli
39 117 4.5 390 4 US-09-206-646-3 Sequence 3, Appli
40 117 4.5 677 1 US-08-188-582-13 Sequence 13, Appli
41 117 4.5 677 1 US-08-646-715-13 Sequence 13, Appli
42 117 4.5 695 4 US-09-538-092-1164 Sequence 1164, Ap
43 117 4.5 695 4 US-09-248-796A-18020 Sequence 18020, A
44 116 4.5 314 2 US-08-822-701-10 Sequence 10, Appli
45 116 4.5 314 3 US-08-935-855-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-08-752-891-2
; Sequence 2, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiko
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-891-2

Query Match 100.0%; Score 2580; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.5e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRRLSQEQPSWTTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRRLSQEQPSWTTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
QY 61 NCFLYGVFNGYDGNRVTFNFAQRSLAELLGQLNAEHAADVRRVLLQAFDVVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNFAQRSLAELLGQLNAEHAADVRRVLLQAFDVVERSFLES 120
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Db 241 RRIQDYKVKYGYTDDIDLLSAKSPKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
QY 301 GPGQANQEIAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSPTFASGGRARPCPRHEDMTL 360
Db 301 GPGQANQEIAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSPTFASGGRARPCPRHEDMTL 360
QY 361 LVRNFGYPLGEMSOPTSPAPAGRVYPVSPYSSAQSTSKTSVTLNLMSEGLYKALEAAH 420
Db 361 LVRNFGYPLGEMSOPTSPAPAGRVYPVSPYSSAQSTSKTSVTLNLMSEGLYKALEAAH 420
QY 421 AHSASTLDEATPTLTNQSPTLTLOSTNTHQTQSSSSSDGGLFRSRPAHSPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPTLTLOSTNTHQTQSSSSSDGGLFRSRPAHSPPGEDGRVEP 480
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Db 481 YVDFAEFYRLMSVDHGEQSVVVTAP 504

RESULT 2

US-09-144-178-2
; Sequence 2, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-144-178-2

Query Match 100.0%; Score 2580; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 3,5e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRRLSQEQPSWTTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRRLSQEQPSWTTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
QY 61 NCFLYGVFNGYDGNRVTFNFAQRSLAELLGQLNAEHAADVRRVLLQAFDVVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNFAQRSLAELLGQLNAEHAADVRRVLLQAFDVVERSFLES 120
QY 121 IDALAELKASLSQQLPEGVPHQPLPOYQKILERLKTLEIRISGAMAVVAVLLNNKLYV 180
Db 121 IDALAELKASLSQQLPEGVPHQPLPOYQKILERLKTLEIRISGAMAVVAVLLNNKLYV 180
QY 181 ANVTGNRALLCKSTVDGLQVLTQNLNVDHTTENEDELFRLSQLGLDAGIKQVGIICGQEST 240
Db 181 ANVTGNRALLCKSTVDGLQVLTQNLNVDHTTENEDELFRLSQLGLDAGIKQVGIICGQEST 240
QY 241 RRIQDYKVKYGYTDDIDLLSAKSPKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
Db 241 RRIQDYKVKYGYTDDIDLLSAKSPKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
QY 301 GPGQANQEIAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSPTFASGGRARPCPRHEDMTL 360
Db 301 GPGQANQEIAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSPTFASGGRARPCPRHEDMTL 360
QY 361 LVRNFGYPLGEMSOPTSPAPAGRVYPVSPYSSAQSTSKTSVTLNLMSEGLYKALEAAH 420
Db 361 LVRNFGYPLGEMSOPTSPAPAGRVYPVSPYSSAQSTSKTSVTLNLMSEGLYKALEAAH 420
QY 421 AHSASTLDEATPTLTNQSPTLTLOSTNTHQTQSSSSSDGGLFRSRPAHSPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPTLTLOSTNTHQTQSSSSSDGGLFRSRPAHSPPGEDGRVEP 480
QY 481 YVDFAEFYRLMSVDHGEQSVVVTAP 504
Db 481 YVDFAEFYRLMSVDHGEQSVVVTAP 504

RESULT 3

US-09-406-854-2
; Sequence 2, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406.854
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-406-854-2

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Query Match      100.0%; Score 2580; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.5e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGTEHPEDSWLKFRSEN 60

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Db 61 NCFLYGVFNGYDGNRVNMFVAQRLSAELLQLNAEHAADVRRVLLQAFDIVERSFLES 120

Qy 121 IDDALEAKASLSQQLPEGVPOHLPPOYQKILERLKTLEISGAMAVAVLLNNKLYV 180
Db 121 IDDALEAKASLSQQLPEGVPOHLPPOYQKILERLKTLEISGAMAVAVLLNNKLYV 180

Qy 181 ANVGTNRALLCKSTVDGLQVTLNVNDHTTENEDELFRLSQLGLDAGTKQVGIICGQEST 240
Db 181 ANVGTNRALLCKSTVDGLQVTLNVNDHTTENEDELFRLSQLGLDAGTKQVGIICGQEST 240

Qy 241 RRIQDYKVKYGYTIDILLSAKSPPIIAEPIHGAQPLDGVGTGFLVLMSEGLYKALEAAH 300
Db 241 RRIQDYKVKYGYTIDILLSAKSPPIIAEPIHGAQPLDGVGTGFLVLMSEGLYKALEAAH 300

Qy 301 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360

Qy 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVSPVYSSAQSTKSTVTLVLMSEGLYKALEAAH 420
Db 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVSPVYSSAQSTKSTVTLVLMSEGLYKALEAAH 420

Qy 421 AHSASTLDEATPTLTNQSPFTLTQSTNTHTOSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPFTLTQSTNTHTOSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

Qy 481 YVDFAEFRLMSVDHGEQSVVTAP 504
Db 481 YVDFAEFRLMSVDHGEQSVVTAP 504

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RESULT 4

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US-09-529-279-2
; Sequence 2, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-279-2

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Query Match      100.0%; Score 2580; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.5e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGTEHPEDSWLKFRSEN 60
Db 1 MAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGTEHPEDSWLKFRSEN 60

Qy 61 NCFLYGVFNGYDGNRVNMFVAQRLSAELLQLNAEHAADVRRVLLQAFDIVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVNMFVAQRLSAELLQLNAEHAADVRRVLLQAFDIVERSFLES 120

Qy 121 IDDALEAKASLSQQLPEGVPOHLPPOYQKILERLKTLEISGAMAVAVLLNNKLYV 180
Db 121 IDDALEAKASLSQQLPEGVPOHLPPOYQKILERLKTLEISGAMAVAVLLNNKLYV 180

Qy 181 ANVGTNRALLCKSTVDGLQVTLNVNDHTTENEDELFRLSQLGLDAGTKQVGIICGQEST 240
Db 181 ANVGTNRALLCKSTVDGLQVTLNVNDHTTENEDELFRLSQLGLDAGTKQVGIICGQEST 240

Qy 241 RRIQDYKVKYGYTIDILLSAKSPPIIAEPIHGAQPLDGVGTGFLVLMSEGLYKALEAAH 300
Db 241 RRIQDYKVKYGYTIDILLSAKSPPIIAEPIHGAQPLDGVGTGFLVLMSEGLYKALEAAH 300

Qy 301 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQEIAMIDTEFAKQTSLDVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360

Qy 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVSPVYSSAQSTKSTVTLVLMSEGLYKALEAAH 420
Db 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVSPVYSSAQSTKSTVTLVLMSEGLYKALEAAH 420

Qy 421 AHSASTLDEATPTLTNQSPFTLTQSTNTHTOSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
Db 421 AHSASTLDEATPTLTNQSPFTLTQSTNTHTOSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

Qy 481 YVDFAEFRLMSVDHGEQSVVTAP 504
Db 481 YVDFAEFRLMSVDHGEQSVVTAP 504

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RESULT 5

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US-10-158-895-2
; Sequence 2, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

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; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-2

Query Match      100.0%; Score 2580; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.5e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRRLSQEQPQSWTDDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Qy 61 NCFLYGVFNGYDGNRVTFNFAQRLSAELLGQLNAEHAEDVRRVLLQAFDVVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNFAQRLSAELLGQLNAEHAEDVRRVLLQAFDVVERSFLES 120
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Db 181 ANVTNRALLCKSTVDGLQVLTQNLNVNHTTENEDELFRLSQLGLDAGIKQVGIICGQEST 240
Qy 241 RRGDYKVKGYTDDIDLLSAKSPITAEPEIHAQPLDGVGTGFLVLMSEGLYKALEAAH 300
Db 241 RRGDYKVKGYTDDIDLLSAKSPITAEPEIHAQPLDGVGTGFLVLMSEGLYKALEAAH 300
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Db 301 GPGQANQEIAMIDTEFAKQTSLDVAQAQVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
Qy 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVYSSAQSTKTSVTLSLWMPSSQGMVNG 420
Db 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVYSSAQSTKTSVTLSLWMPSSQGMVNG 420
Qy 421 AHSASTLDEATPTLTNQSPITLTQSTNTHQTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
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Db 481 YVDFAEFYRLMSVDHGEQSVVTP 504

RESULT 6
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; PRIOR APPLICATION NUMBER: JP 9/290188

; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; PRIOR APPLICATION NUMBER: JP 9/290188

US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; PRIOR APPLICATION NUMBER: JP 9/290188

RESULT 7
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; PRIOR APPLICATION NUMBER: JP 9/290188
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; ORGANISM: Homo sapiens
US-10-158-895-11

Query Match      100.0%; Score 2580; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60
DB 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60

QY 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120
DB 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120

QY 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180
DB 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180

QY 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240
DB 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240

QY 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
DB 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300

QY 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
DB 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360

QY 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420
DB 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420

QY 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
DB 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

QY 481 YVDFAEFYRLMSVDHGEQSVVTAP 504
DB 481 YVDFAEFYRLMSVDHGEQSVVTAP 504

RESULT 8
US-09-529-279-43
; Sequence 43, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-43

Query Match      99.9%; Score 2577; DB 4; Length 513;
Best Local Similarity 99.8%; Pred. No. 7e-235;
Matches 503; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60
DB 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60

QY 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120
DB 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120

QY 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180
DB 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180

QY 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240
DB 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240

QY 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
DB 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300

QY 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
DB 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360

QY 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420
DB 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420

QY 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
DB 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

QY 481 YVDFAEFYRLMSVDHGEQSVVTAP 504
DB 481 YVDFAEFYRLMSVDHGEQSVVTAP 504

RESULT 9
US-10-158-895-43
; Sequence 43, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Query Match      99.9%; Score 2577; DB 4; Length 513;
Best Local Similarity 99.8%; Pred. No. 7e-235;
Matches 503; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60
DB 1 MAAQRSLQSEQQPSWTDLPLCHLSGVGSASNRYSADGKGTSHPEDSWLKFRSEN 60

QY 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120
DB 61 NCFLYGVFNGYDGNRVTFVQRLSAEALLGQLNAEHAADVRRVLLQAFDVVERSFLS 120

QY 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180
DB 121 IDDAEAKASLQSQLPPEGVPQHLPPOYQKILERLKTLEISGGAMAVAVLNNKLYV 180

QY 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240
DB 181 ANVTGNRALLCKSTVDGLQVTLNVDHTTENEDLFRLSQLGLDAGTKQVGIICQSEST 240

QY 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
DB 241 RRIGDYKVYGYTDDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300

QY 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360
DB 301 GPGQANQBIAMIDTEFAKQTSLSDAVAQAVVDVRVKRIHSDTFASGGERARFCPRHEDMTL 360

QY 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420
DB 361 LVRNFGYPLGEMSQTPSPAPAGGRVVPVSPYSSAOSTSKTSVTLNVPSCQMVNG 420

QY 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
DB 421 AHSASTLDEAPTLTNQSPPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480

QY 481 YVDFAEFYRLMSVDHGEQSVVTAP 504
DB 481 YVDFAEFYRLMSVDHGEQSVVTAP 504
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QY 121 IDALAELKASLSQSLPGVFGHQHLPPOYQKILRLKTLERHISGMAVAVLNNKLYV 180
DB 130 IDALAELKASLSQSLPGVFGHQHLPPOYQKILRLKTLERHISGMAVAVLNNKLYV 189
QY 181 ANVTNRALLCKSVTDGLQVTLNVDHTTENEDELRLSQLGLDAGIKQVGIICGQEST 240
DB 190 ANVTNRALLCKSVTDGLQVTLNVDHTTENEDELRLSQLGLDAGIKQVGIICGQEST 249
QY 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
DB 250 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 309
QY 301 GPGQANOEIAAMIDTEFAKQTSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
DB 310 GPGQANOEIAAMIDTEFAKQTSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 369
QY 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVSSAQSTSKTSVTLSLWPSQGMVNG 420
DB 370 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVSSAQSTSKTSVTLSLWPSQGMVNG 429
QY 421 AHSASTLDEATPTLTNOSPILTLQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
DB 430 AHSASTLDEATPTLTNOSPILTLQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEP 489
QY 481 YVDFAEFYRLWSVDHGQSVVVTAP 504
DB 490 YVDFAEFYRLWSVDHGQSVVVTAP 513

RESULT 10
US-08-752-891-6
; Sequence 6, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-891-6
Query Match 99.8%; Score 2575; DB 2; Length 504;
Best Local Similarity 99.8%; Pred. No. 1.1e-234;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQRRLSLLSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
DB 1 MAQRRLSLLSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
QY 61 NCFLYGVFNQYDGNRVTFVAQRLSAELLIGQLNAEAEADVRVLLQAFDVERSFLES 120
DB 61 NCFLYGVFNQYDGNRVTFVAQRLSAELLIGQLNAEAEADVRVLLQAFDVERSFLES 120
QY 121 IDALAELKASLSQSLPGVFGHQHLPPOYQKILRLKTLERHISGMAVAVLNNKLYV 180
DB 121 IDALAELKASLSQSLPGVFGHQHLPPOYQKILRLKTLERHISGMAVAVLNNKLYV 180
QY 181 ANVTNRALLCKSVTDGLQVTLNVDHTTENEDELRLSQLGLDAGIKQVGIICGQEST 240
DB 181 ANVTNRALLCKSVTDGLQVTLNVDHTTENEDELRLSQLGLDAGIKQVGIICGQEST 240
QY 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
DB 241 RRGIDYKVKYGYTDIDLLSAKSKPIIAEPIHGAQPLDGVTFGLVLMSEGLYKALEAAH 300
QY 301 GPGQANOEIAAMIDTEFAKQTSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
DB 301 GPGQANOEIAAMIDTEFAKQTSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL 360
QY 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVSSAQSTSKTSVTLSLWPSQGMVNG 420
DB 361 LVRNFGYPLGEMSOPTSPAPAGGRVYVPVSSAQSTSKTSVTLSLWPSQGMVNG 420
QY 421 AHSASTLDEATPTLTNOSPILTLQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
DB 421 AHSASTLDEATPTLTNOSPILTLQSTNTHQTSSSSSDGGLFRSRPAHSLPPGEDGRVEP 480
QY 481 YVDFAEFYRLWSVDHGQSVVVTAP 504
DB 481 YVDFAEFYRLWSVDHGQSVVVTAP 504

RESULT 11
US-09-144-178-6
; Sequence 6, Application US/09144178
; Patent No. 5989862
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,178
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid

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; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-144-178-6

Query Match          99.8%; Score 2575; DB 2; Length 504;
Best Local Similarity 99.8%; Pred. No. 1.1e-234;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAQRSLLOSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRSLLOSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
QY 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLGQNAEHAADVRRVLLQAFDVVVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLGQNAEHAADVRRVLLQAFDVVVERSFLES 120
QY 121 IDDAEAKASQSLQEPGVQHPQYQKILERLKTLEIREISGGAMAVVAVLLNNKLYV 180
Db 121 IDDAEAKASQSLQEPGVQHPQYQKILERLKTLEIREISGGAMAVVAVLLNNKLYV 180
QY 181 ANVGNTRALLCKSTVDGLQVTLQNVDDHTTENEDELFRLSQLGLDAGKIKQVGHICQEST 240
Db 181 ANVGNTRALLCKSTVDGLQVTLQNVDDHTTENEDELFRLSQLGLDAGKIKQVGHICQEST 240
QY 241 RRGIDYKVKYGYTDIDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVMSEGLYKALEAAH 300
Db 241 RRGIDYKVKYGYTDIDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVMSEGLYKALEAAH 300
QY 301 GPGQANQETAAIMDTTEFAKQTSLDAVAQAVDVRVKRIHSDTTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQETAAIMDTTEFAKQTSLDAVAQAVDVRVKRIHSDTTFASGGERARFCPRHEDMTL 360
QY 361 LVNFGYPLGEMSQPTSPAPAGGRVYPVSPYSSAQSTKSTVTLVMPSSQGMVNG 420
Db 361 LVNFGYPLGEMSQPTSPAPAGGRVYPVSPYSSAQSTKSTVTLVMPSSQGMVNG 420
QY 421 AHSASTLDEATPTLTNQSTPTLTQSTNTHQTQSSSSSDGGLFRSPAHSLPCEGRVPEP 480
Db 421 AHSASTLDEATPTLTNQSTPTLTQSTNTHQTQSSSSSDGGLFRSPAHSLPCEGRVPEP 480

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RESULT 12

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US-09-406-854-6
; Sequence 6, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiro
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner

```

```

; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,854
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-406-854-6

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Query Match          99.8%; Score 2575; DB 3; Length 504;
Best Local Similarity 99.8%; Pred. No. 1.1e-234;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAQRSLLOSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
Db 1 MAAQRSLLOSQEQPSWTDLPLCHLSGVGSASNRYSADGKGTESHPPEDSWLKFRSEN 60
QY 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLGQNAEHAADVRRVLLQAFDVVVERSFLES 120
Db 61 NCFLYGVFNGYDGNRVTFNVAQRLSAELLGQNAEHAADVRRVLLQAFDVVVERSFLES 120
QY 121 IDDAEAKASQSLQEPGVQHPQYQKILERLKTLEIREISGGAMAVVAVLLNNKLYV 180
Db 121 IDDAEAKASQSLQEPGVQHPQYQKILERLKTLEIREISGGAMAVVAVLLNNKLYV 180
QY 181 ANVGNTRALLCKSTVDGLQVTLQNVDDHTTENEDELFRLSQLGLDAGKIKQVGHICQEST 240
Db 181 ANVGNTRALLCKSTVDGLQVTLQNVDDHTTENEDELFRLSQLGLDAGKIKQVGHICQEST 240
QY 241 RRGIDYKVKYGYTDIDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVMSEGLYKALEAAH 300
Db 241 RRGIDYKVKYGYTDIDLLSAAKSKPIIAEPEIHGAQPLDGVTFGLVMSEGLYKALEAAH 300
QY 301 GPGQANQETAAIMDTTEFAKQTSLDAVAQAVDVRVKRIHSDTTFASGGERARFCPRHEDMTL 360
Db 301 GPGQANQETAAIMDTTEFAKQTSLDAVAQAVDVRVKRIHSDTTFASGGERARFCPRHEDMTL 360
QY 361 LVNFGYPLGEMSQPTSPAPAGGRVYPVSPYSSAQSTKSTVTLVMPSSQGMVNG 420
Db 361 LVNFGYPLGEMSQPTSPAPAGGRVYPVSPYSSAQSTKSTVTLVMPSSQGMVNG 420
QY 421 AHSASTLDEATPTLTNQSTPTLTQSTNTHQTQSSSSSDGGLFRSPAHSLPCEGRVPEP 480
Db 421 AHSASTLDEATPTLTNQSTPTLTQSTNTHQTQSSSSSDGGLFRSPAHSLPCEGRVPEP 480

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QY 481 YVDFAEFRLWSVDHGEQSVVTAP 504
Db 481 YVDFAEFRLWSVDHGEQSVVTAP 504

RESULT 13
US-09-270-767-32865
; Sequence 32865, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-034
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32865
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32865

Query Match 15.2%; Score 391; DB 4; Length 217;
Best Local Similarity 45.7%; Pred. No. 1.1e-28;
Matches 86; Conservative 36; Mismatches 64; Indels 2; Gaps 2;

QY 151 ILERLKTLEETSGGAMAVAVLNNKLYVANVGNTRALLCKSTVDG-LQVTLNVNDHTT 209
Db 14 ILARKEIDVHLSGGAAVIALVHANKLPVAHVGTTRALLCFDNDNAVLRVVLTVDSHL 73

QY 210 ENEBELFRLSQGLDAGTKVIGITCGQESTRIGDYKVYGYTIDILLSAKSKPIIAE 269
Db 74 NNEDELLRLQQLGLDVKNLRNAQYLGNQGTGRLGNLYLVKGLYKAPPTISAAVSBFVIAA 133

QY 270 PEIHAQPLDGVTFGLVLMSEGLYKALEAAHGP-GQANOEIAAMIDTEFAKOTSLDVAQ 328
Db 134 PEIHGEFILLDES CRFLVLVVSAGYKRIQBSKGSYEQTNKQLACLIVENFRKQTDPRMVSQ 193

QY 329 AVVDVRVK 336
Db 194 AVLEBIEQ 201

RESULT 14
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HERewith

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNNOT02
; CLONE: 195647
US-09-013-881-2

Query Match 6.9%; Score 178; DB 3; Length 392;
Best Local Similarity 22.9%; Pred. No. 4.4e-08;
Matches 83; Conservative 65; Mismatches 116; Indels 98; Gaps 18;

QY 3 AQRRELLSQEQPSWTDL---PLCHLSGVGSASNRYSADCKG-----T 44
Db 77 AKRKT---SEBEKNGSEBELVKVKCKASSV-IFGLKGYVAERKGEREQMDAHVILNDIT 132

QY 45 ESHPPEDSWLKRSENNCFLYGVFNGYDGNRVTVNAQRLSAELL--LQLNAEHAADV 102
Db 133 EECRPSSLI-----TRVSYFAVFDGCHGIRASKPAQAQNLHQLNRKPKGVISVEKTV 187

QY 103 RVLVLAQFVWVERSELESIDDAEAKSLQSLPEGVFQHPQVQPKILERLKLTEREI 162
Db 188 KECILDTPKHTDEEL-----KQASSQK-----PAWK----- 214

QY 163 SGAMAVAVLNNKLYVANVGNTRALLCKSTVDGLQ--VTOLNVDTHTTENEDELRLSQ 220
Db 215 -DGSTATCVLAVDNILYIANLGDSTRILCRVNEESQKHAALSKEHNPTQVEERNRIQK 273

QY 221 LGLDAGKIKQVGIIICQESTRIGD--YKVYGYTDIDLLSAKSKPIIAEPIHGAQ-- 276
Db 274 AG---GNVRDGRVLGVLEVSRSIGQYK-RCGVTSV-----PDIRECQLT 315

QY 277 PLDGVTFGLVLMSEGLYKALEAAHGPQGANQBIAMIDTEFAK-----QTSLDVAQAVVD 332
Db 316 PND---RFILLACDGLFKVFT----PEEAVNFILSCLEDEKIQTRGKSAADARVAAACN 368

QY 333 RV 334
Db 369 RL 370

RESULT 15
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06

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